

BLAST score 361 E value 5.0e-34 Match length 222 % identity 38

NCBI Description (AP000003) 450aa long hypothetical fmu protein [Pyrococcus

horikoshii]

Seq. No. 285566

Contig ID 169061_1.R1011 5'-most EST uC-zmflb73244b10b2

Method BLASTX
NCBI GI g2244965
BLAST score 526
E value 1.0e-53
Match length 175
% identity 61

NCBI Description (Z97340) unnamed protein product [Arabidopsis thaliana]

Seq. No. 285567

Contig ID 169092_1.R1011 5'-most EST pwr700450058.h2

Method BLASTX
NCBI GI g3775993
BLAST score 193
E value 1.0e-15
Match length 76
% identity 66

NCBI Description (AJ010460) RNA helicase [Arabidopsis thaliana]

Seq. No. 285568

Contig ID 169095_1.R1011 5'-most EST uC-zmflb73244d08b2

Method BLASTX
NCBI GI g2829887
BLAST score 266
E value 4.0e-23
Match length 141
% identity 38

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 285569

Contig ID 169114_1.R1011 5'-most EST uC-zmflmo17181d10b1

Seq. No. 285570

Contig ID 169178_1.R1011 5'-most EST uC-zmflb73245b07a1

Seq. No. 285571

Contig ID 169212_1.R1011 5'-most EST uC-zmflmo17279g10a1

Seq. No. 285572

Contig ID 169212 2.R1011 5'-most EST uC-zmflb73260e11a1

Seq. No. 285573



Contig ID 169249 1.R1011 5'-most EST uC-zmflb73245f07a1

Seq. No. 285574

Contig ID 169252_1.R1011 5'-most EST wyr700238585.h1

Method BLASTX
NCBI GI g3287695
BLAST score 678
E value 2.0e-71
Match length 157
% identity 79

NCBI Description (AC003979) Similar to hypothetical protein C34B7.2

gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis

thaliana]

Seq. No. 285575

Contig ID 169258_1.R1011 5'-most EST uC-zmflb73245g02a1

Seq. No. 285576

Contig ID 169270 1.R1011 5'-most EST dyk700105576.h1

Method BLASTX
NCBI GI g731675
BLAST score 447
E value 2.0e-44
Match length 165
% identity 52

NCBI Description HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION

>gi_626631_pir__S46811 hypothetical protein YHR074w - yeast

(Saccharomyces cerevisiae) >gi_500832 (U10556) Yhr074wp

[Saccharomyces cerevisiae]

Seq. No. 285577

Contig ID 169273_1.R1011 5'-most EST uC-zmflb73245q12a1

Seq. No. 285578

Contig ID 169287_1.R1011 5'-most EST uC-zmflb73245h10a1

Seq. No. 285579

Contig ID 169304_1.R1011 5'-most EST uC-zmrob73006a02a1

Method BLASTX
NCBI GI g4490738
BLAST score 234
E value 2.0e-19
Match length 74
% identity 54

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 285580

Contig ID 169310_1.R1011 5'-most EST uC-zmflmo17399a03a1



Contig ID 169320_1.R1011 5'-most EST fwa700101412.h1

Method BLASTX
NCBI GI g3608127
BLAST score 400
E value 7.0e-39
Match length 144
% identity 54

NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 285582

Contig ID 169348_1.R1011 5'-most EST uC-zmflmo17033f07a1

Seq. No. 285583

Contig ID 169363_1.R1011 5'-most EST cat700020148.r1

Seq. No. 285584

Contig ID 169372_1.R1011 5'-most EST uC-zmflb73246g07b3

Seq. No. 285585

Contig ID 169418_1.R1011 5'-most EST uC-zmflb73247f02a2

Seq. No. 285586

Contig ID 169419_1.R1011 5'-most EST uC-zmflmo17302g08a1

Method BLASTX
NCBI GI g3805853
BLAST score 545
E value 1.0e-55
Match length 148
% identity 68

NCBI Description (AL031986) putative protein [Arabidopsis thaliana]

Seq. No. 285587

Contig ID 169424_1.R1011 5'-most EST uC-zmflb73247f11a2

Seq. No. 285588

Contig ID 169473_1.R1011 5'-most EST uC-zmflmo17141e09a1

Seq. No. 285589

Contig ID 169540_1.R1011 5'-most EST uC-zmflb73249h11b3

Seq. No. 285590

Contig ID 169555_1.R1011 5'-most EST uC-zmflmo17328f06a1

Seq. No. 285591

Contig ID 169556_1.R1011 5'-most EST uC-zmflmo17247f08a1



Contia ID 169559 1.R1011 $uC-zmf\overline{l}b73250b11a2$ 5'-most EST

Seq. No. 285593

Contig ID 169565 1.R1011 5'-most EST uC-zmflb73268g04a1

285594 Seq. No.

169586 1.R1011 Contig ID 5'-most EST uC-zmromo17031e07a1

285595 Seq. No.

169588 1.R1011 Contig ID 5'-most EST uC-zmflb73250f03a2

285596 Seq. No.

Contig ID 169596 1.R1011 5'-most EST uC-zmflb73250f12a2

285597 Seq. No.

Contig ID 169643 1.R1011 5'-most EST pmx700089217.h1

Method BLASTX g2262107 NCBI GI BLAST score 792 E value 8.0e-85 Match length 161 90 % identity

NCBI Description (AC002343) Ser/Thr protein kinase isolog [Arabidopsis

thaliana]

Seq. No. 285598

Contig ID 169694 1.R1011 5'-most EST cjh700196204.h1

Method BLASTX NCBI GI g4582436 BLAST score 174 E value 3.0e-12 Match length 82

% identity 51

NCBI Description (AC007196) unknown protein [Arabidopsis thaliana]

Seq. No. 285599

Contig ID 169715 1.R1011 5'-most EST uC-zmflb73252c03b3 BLASTX

Method NCBI GI g2494736 BLAST score 819 E value 9.0e-88 Match length 249 65 % identity

NCBI Description GLUCOSE INHIBITED DIVISION PROTEIN A

>gi_1001595_dbj_BAA10223_ (D64000) glucose inhibited

division protein A [Synechocystis sp.]



Contig ID 169735_1.R1011 5'-most EST gct701175682.h1

Seq. No. 285601

Contig ID 169750_1.R1011 5'-most EST uC-zmflb73252g04b3

Seq. No. 285602

Contig ID 169775_1.R1011 5'-most EST uC-zmrob73055f02a1

Seq. No. 285603

Contig ID 169780_1.R1011 5'-most EST uC-zmflb73253c03a1

Method BLASTX
NCBI GI g1353193
BLAST score 502
E value 7.0e-51
Match length 99
% identity 97

NCBI Description O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268

O-methyltransferase (EC 2.1.1.-) - maize $\overline{>}$ gi_ $\overline{40}4070$

(L14063) O-methyltransferase [Zea mays]

Seq. No. 285604

Contig ID 169783_1.R1011 5'-most EST uC-zmflmo17125b12a1

Seq. No. 285605

Contig ID 169788_1.R1011 5'-most EST uC-zmflb73253d02a1

Method BLASTX
NCBI GI g2642448
BLAST score 174
E value 2.0e-12
Match length 39
% identity 90

NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana]

>gi 3169187 (AC004401) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 285606

Contig ID 169792_1.R1011 5'-most EST uC-zmflb73271a03a1

Seq. No. 285607

Contig ID 169802_1.R1011 5'-most EST vux700159743.h1

Seq. No. 285608

Contig ID 169839_1.R1011 5'-most EST uC-zmflb73254c05a1

Method BLASTX
NCBI GI g2832717
BLAST score 298
E value 3.0e-27



Match length 64 % identity 91 NCBI Description (AJ003114) alkaline/neutral invertase [Lolium temulentum] Seq. No. 285609

Contig ID 169840_1.R1011 5'-most EST uC-zmflmo17118d10a1

Seq. No. 285610

Contig ID 169861_1.R1011 5'-most EST uC-zmflb73254h01a1

Method BLASTX
NCBI GI g4455302
BLAST score 403
E value 2.0e-39
Match length 89
% identity 82

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 285611

Contig ID 169910_1.R1011 5'-most EST uC-zmflb73255c06a1

Seq. No. 285612

Contig ID 169915_1.R1011 5'-most EST uC-zmflmo17217e08a1

Seq. No. 285613

Contig ID 169935_1.R1011 5'-most EST uC-zmflmo17057c05a1

Seq. No. 285614

Contig ID 169944_1.R1011 5'-most EST uC-zmflmo17399d03a1

Seq. No. 285615

Contig ID 169977_1.R1011 5'-most EST uC-zmflmo17328a03a1

Seq. No. 285616

Contig ID 170028_1.R1011 5'-most EST vux700161243.h1

Method BLASTX
NCBI GI g2062167
BLAST score 174
E value 6.0e-13
Match length 94
% identity 43

NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis

thaliana]

Seq. No. 285617

Contig ID 170038_1.R1011 5'-most EST afb700380858.h1

Seq. No. 285618

Contig ID 170061 1.R1011



5'-most EST uC-zmflb73257c11a2 Seq. No. 285619 170063 1.R1011 Contig ID 5'-most EST uC-zmromo17007c10a1 Seq. No. 285620 Contig ID 170065 1.R1011 uC-zmflb73257d01a2 5'-most EST 285621 Seq. No. 170067 1.R1011 Contig ID $uC-zmf\overline{l}b73257d02b3$ 5'-most EST Method BLASTX NCBI GI q4455363 BLAST score 180 E value 3.0e-13Match length 54 % identity 61 (AL035524) Medicago nodulin N21-like protein [Arabidopsis NCBI Description thaliana] 285622 Seq. No. 170099 1.R1011 Contig ID 5'-most EST ntr700073484.h1 285623 Seq. No. 170129 1.R1011 Contig ID 5'-most EST $uC-zmf\overline{1}b73296e09a1$ Seq. No. 285624 170135 1.R1011 Contig ID 5'-most EST uC-zmflmo17315b04a1 Seq. No. 285625 170153 1.R1011 Contig ID 5'-most EST ymt700220320.h1 Method BLASTX NCBI GI g283051 BLAST score 627 E value 1.0e-65 Match length 149 84 % identity NCBI Description RNA-directed DNA polymerase (EC 2.7.7.49) - maize transposon (fragment) Seq. No. 285626 Contig ID 170184 1.R1011

Contig ID 170184_1.R1011 5'-most EST pmx700082137.h1

Seq. No. 285627

Contig ID 170214_1.R1011 5'-most EST uC-zmflmo17353g07a1

Seq. No. 285628

Contig ID 170240_1.R1011 5'-most EST xsy700212579.h1



Contig ID 170255_1.R1011 5'-most EST uC-zmflmo17356h11a1

Seq. No. 285630

Contig ID 170295_1.R1011 5'-most EST uC-zmflmo17010f02a1

Seq. No. 285631

Contig ID 170306_1.R1011 5'-most EST uC-zmflb73259e12a1

Method BLASTX
NCBI GI g1177022
BLAST score 304
E value 1.0e-27
Match length 103
% identity 55

NCBI Description HYPOTHETICAL PROTEIN KIAA0052

Seq. No. 285632

Contig ID 170321_1.R1011 5'-most EST uC-zmflmo17311d09a1

Seq. No. 285633

Contig ID 170335_1.R1011 5'-most EST uC-zmflb73273g02a1

Seq. No. 285634

Contig ID 170351_1.R1011 5'-most EST uC-zmflb73260b08b2

Seq. No. 285635

Contig ID 170358_1.R1011 5'-most EST uC-zmflb73260c01a1

Seq. No. 285636

Contig ID 170361_1.R1011 5'-most EST uC-zmflmo17219e08a1

Method BLASTX
NCBI GI g1091678
BLAST score 160
E value 1.0e-10
Match length 63
% identity 44

NCBI Description activator-like transposable element [Pennisetum glaucum]

Seq. No. 285637

Contig ID 170364_1.R1011 5'-most EST uC-zmflb73260c06a1

Seq. No. 285638

Contig ID 170378_1.R1011 5'-most EST pmx700089624.h1

Seq. No. 285639

Contig ID 170389 1.R1011

NCBI GI

E value

BLAST score

g3293547

9.0e-13

177



```
5'-most EST
                   wyr700243737.h1
Seq. No.
                   285640
Contig ID
                   170395 1.R1011
                   uC-zmflb73260e03a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2979553
BLAST score
                   213
E value
                   5.0e-17
Match length
                   98
% identity
                   47
NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]
                   285641
Seq. No.
Contig ID
                   170426 1.R1011
5'-most EST
                   uC-zmromo17111a11a1
Method
                   BLASTX
NCBI GI
                   q3894178
BLAST score
                   301
E value
                   5.0e-27
Match length
                   121
% identity
NCBI Description
                  (AC005312) putative nucleic acid binding protein
                   [Arabidopsis thaliana]
Seq. No.
                   285642
                   170489 1.R1011
Contig ID
5'-most EST
                   kem700\overline{6}11538.h1
Method
                   BLASTX
NCBI GI
                   q3738153
BLAST score
                   319
E value
                   3.0e-29
Match length
                   134
% identity
NCBI Description
                   (AL031852) putative cleavage and polyadenylation
                   specificity factor [Schizosaccharomyces pombe]
                   285643
Seq. No.
                   170500 1.R1011
Contig ID
5'-most EST
                   uC-zmf\overline{l}b73261e03b3
Method
                   BLASTX
                   g3860272
NCBI GI
BLAST score
                   356
E value
                   1.0e-33
Match length
                   84
% identity
                   76
NCBI Description
                   (AC005824) putative suppressor protein [Arabidopsis
                   thaliana] >gi 4314399 gb AAD15609 (AC006232) putative skdl
                   protein [Arabidopsis thaliana]
Seq. No.
                   285644
                   170505 1.R1011
Contig ID
5'-most EST
                   fwa700\overline{0}98312.h1
Method
                   BLASTX
```



Match length 108 % identity 45

NCBI Description (AF072709) putative oxidoreductase [Streptomyces lividans]

Seq. No. 285645

170516 1.R1011 Contig ID tzu700201367.h1 5'-most EST

Method BLASTX NCBI GI q4263722 BLAST score 393 E value 3.0e - 38Match length 142 % identity 65

(AC006223) putative glucan synthase [Arabidopsis thaliana] NCBI Description

Seq. No. 285646

Contig ID 170519 1.R1011 5'-most EST uC-zmflb73261q03b3

Seq. No. 285647

170523 1.R1011 Contig ID $nbm700\overline{4}77592.h1$ 5'-most EST

285648 Seq. No.

Contig ID 170523 2.R1011 5'-most EST uC-zmflb73261g09b3

Method BLASTX NCBI GI q3702327 BLAST score 207 2.0e-16 E value Match length 90

47 % identity

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 285649

Contig ID 170530 1.R1011 5'-most EST uC-zmflb73261h06b3

Seq. No. 285650

170551 1.R1011 Contig ID 5'-most EST xsy700211725.hl

Seq. No. 285651

170656 1.R1011 Contig ID 5'-most EST uC-zmflmo17240e04a1

Method BLASTX NCBI GI g3080374 BLAST score 154 E value 4.0e-10 Match length 112 27 % identity

NCBI Description (AL022580) putative protein [Arabidopsis thaliana]

Seq. No. 285652

170677 1.R1011 Contig ID 5'-most EST uC-zmflb73263f09a1



Contig ID 170689_1.R1011 5'-most EST wyr700240902.h1

Seq. No. 285654

Contig ID 170707_1.R1011 5'-most EST uC-zmflb73265b12b4

Method BLASTX
NCBI GI g4038037
BLAST score 234
E value 2.0e-19
Match length 139
% identity 5

NCBI Description (AC005936) hypothetical protein [Arabidopsis thaliana]

Seq. No. 285655

Contig ID 170719_1.R1011 5'-most EST uC-zmflb73265d04b4

Seq. No. 285656

Contig ID 170766_1.R1011 5'-most EST uwc700150613.h1

Method BLASTX
NCBI GI g3033398
BLAST score 562
E value 1.0e-57
Match length 134
% identity 81

NCBI Description (AC004238) putative phosphoribosylaminoimidazolecarboxamide

formyltransferase [Arabidopsis thaliana]

Seq. No. 285657

Contig ID 170767_1.R1011 5'-most EST uC-zmflb73266a01a2

Seq. No. 285658

Contig ID 170780_1.R1011 5'-most EST gct701176485.h1

Seq. No. 285659

Contig ID 170786_1.R1011 5'-most EST ymt700223165.h1

Seq. No. 285660

Contig ID 170788_1.R1011 5'-most EST wyr700242927.h1

Seq. No. 285661

Contig ID 170829 1.R1011 5'-most EST uC-zmflb73372a12a1

Method BLASTX
NCBI GI 94138581
BLAST score 583
E value 5.0e-60
Match length 149
% identity 37

NCBI Description (X98474) mitochondrial energy transfer protein [Solanum



tuberosum]

Seq. No. 285663

Contig ID 170857 1.R1011 5'-most EST xmt700263104.h1

Seq. No. 285664

Contig ID 170858_1.R1011 5'-most EST rvt700548662.h1

Seq. No. 285665

Contig ID 170865_1.R1011 5'-most EST wty700172323.h1

Seq. No. 285666

Contig ID 170873_1.R1011 5'-most EST uC-zmflb73266f10a2

Method BLASTX
NCBI GI g2864625
BLAST score 285
E value 2.0e-25
Match length 141
% identity 52

NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 285667

Contig ID 170908_1.R1011 5'-most EST uC-zmflb73266h10b2

Method BLASTX
NCBI GI g4585991
BLAST score 462
E value 8.0e-53
Match length 137
% identity 69

NCBI Description (AC005287) very similar to mouse Dhm1 and Dhm2 [Arabidopsis

thaliana]

Seq. No. 285668

Contig ID 170992 1.R1011 5'-most EST xmt700258589.h1

Seq. No. 285669

Contig ID 170995_1.R1011 5'-most EST uC-zmflb73267f12a1

Seq. No. 285670

Contig ID 170999_1.R1011 5'-most EST xsy700211573.h1

Method BLASTX
NCBI GI g4587579
BLAST score 214
E value 4.0e-17
Match length 89



% identity

NCBI Description (AC006550) F1003.1 [Arabidopsis thaliana]

Seq. No.

285671

Contig ID 5'-most EST 171015 1.R1011 uC-zmflb73267h07b2

Seq. No.

285672

Contig ID 5'-most EST 171023 1.R1011 uC-zmflb73267h09a1

Seq. No.

285673

Contig ID 5'-most EST 171033 1.R1011 uC-zmflb73268b01a1

Seq. No.

285674

Contig ID 5'-most EST 171045 1.R1011 uC-zmflb73268c05a1

Seq. No.

285675

Contig ID 5'-most EST 171047 1.R1011 uC-zmflmo17249b12a1

Seq. No.

285676

Contig ID 5'-most EST 171087 1.R1011 uer700582714.h1

Seq. No.

285677

Contig ID 5'-most EST 171107 1.R1011 uC-zmflb73269b12a1

Method BLASTX NCBI GI g4584547

BLAST score E value

199

Match length

3.0e-1560

% identity

60 NCBI Description (AL049608) potassium transporter-like protein [Arabidopsis thaliana]

Seq. No.

285678

Contig ID 5'-most EST

171148 1.R1011 uC-zmflmo17346a09a1

Method NCBI GI BLAST score BLASTX g2723471 266

E value Match length

4.0e-23 79

% identity

70 NCBI Description (D87819) sucrose transporter [Oryza sativa]

Seq. No.

285679

Contig ID 5'-most EST 171187 1.R1011 uC-zmflb73365d10a1

Seq. No.

285680

Contig ID 5'-most EST 171197 1.R1011 rvt700549094.h1



171236 1.R1011 Contig ID uC-zmflb73271d01a1 5'-most EST

285682 Seq. No.

171270 1.R1011 Contig ID uC-zmflb73271g05a1 5'-most EST

285683 Seq. No.

171272 1.R1011 Contig ID uC-zmflmo17341h06a1 5'-most EST

285684 Seq. No.

171277 1.R1011 Contig ID $xmt700\overline{2}58758.h1$ 5'-most EST

285685 Seq. No.

171309 1.R1011 Contig ID 5'-most EST $uC-zmf\overline{1}b73272c06a1$

285686 Seq. No.

171311 1.R1011 Contig ID $uC-zmf\overline{l}b73272c09a1$ 5'-most EST

BLASTX Method g4490317 NCBI GI BLAST score 301 4.0e-27 E value 131 Match length 48 % identity

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

285687 Seq. No.

171334 1.R1011 Contig ID uC-zmflb73272f01a1 5'-most EST

Method BLASTX NCBI GI q2654870 BLAST score 730 2.0e-77 E value Match length 144 93 % identity

NCBI Description (AF015302) RbohAOsp [Oryza sativa]

285688 Seq. No.

171365 1.R1011 Contig ID 5'-most EST uC-zmflb73273a02a1

Seq. No. 285689

171370 1.R1011 Contig ID uC-zmflb73355e07a15'-most EST

Seq. No. 285690

171378 1.R1011 Contiq ID $uC-zmf\overline{1}b73273b05a1$ 5'-most EST

BLASTX Method NCBI GI g3250675 BLAST score 343



E value 3.0e-32 Match length 152 % identity 45

NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 285691

Contig ID 171383_1.R1011 5'-most EST uC-zmflmo17209d01a1

Seq. No. 285692

Contig ID 171383_2.R1011 5'-most EST uC-zmflb73273b12a1

Seq. No. 285693

Contig ID 171418_1.R1011 5'-most EST uC-zmflb73273f12a1

Seq. No. 285694

Contig ID 171436_1.R1011 5'-most EST uC-zmflb73274a01a1

Seq. No. 285695

Contig ID 171454_1.R1011 5'-most EST uC-zmflb73274b09a1

Seq. No. 285696

Contig ID 171471_1.R1011 5'-most EST uer700581956.h1

Method BLASTX
NCBI GI g4140691
BLAST score 147
E value 4.0e-09
Match length 95
% identity 29

NCBI Description (AF101972) zeatin O-glucosyltransferase [Phaseolus lunatus]

Seq. No. 285697

Contig ID 171484_1.R1011 5'-most EST uC-zmflb73274e08a1

Seq. No. 285698

Contig ID 171530_1.R1011 5'-most EST uC-zmflmo17012d01a1

Seq. No. 285699

Contig ID 171538_1.R1011 5'-most EST uC-zmflb73303d08a2

Seq. No. 285700

Contig ID 171547_1.R1011 5'-most EST uC-zmflmo17300c04a1

Seq. No. 285701

Contig ID 171573_1.R1011 5'-most EST cat700020973.r1

Seq. No. 285702



Contig ID 171582_1.R1011 5'-most EST uC-zmflb73276b12a1

Seq. No. 285703

Contig ID 171616_1.R1011 5'-most EST uC-zmflb73345e07a2

Seq. No. 285704

Contig ID 171623_1.R1011 5'-most EST uC-zmflb73276g07a1

Seq. No. 285705

Contig ID 171625_1.R1011 5'-most EST uC-zmflb73333e09a1

Seq. No. 285706

Contig ID 171630_1.R1011 5'-most EST uC-zmflmo17018a03a1

Seq. No. 285707

Contig ID 171639_1.R1011 5'-most EST uC-zmflb73277b08a1

Seq. No. 285708

Contig ID 171654_1.R1011 5'-most EST nbm700468443.h1

Method BLASTN
NCBI GI g3821794
BLAST score 40
E value 6.0e-13

Match length 72 % identity 89

NCBI Description Zea mays gene encoding protein kinase CK2 alpha subunit

Seq. No. 285709

Contig ID 171664_1.R1011 5'-most EST uC-zmflb73277g09b1

Method BLASTX
NCBI GI g585451
BLAST score 152
E value 2.0e-10
Match length 36
% identity 78

NCBI Description MALATE OXIDOREDUCTASE (NAD), MITOCHONDRIAL 62 KD ISOFORM PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME)

(NAD-ME) >gi_1076667_pir__B53318 malate dehydrogenase (decarboxylating) (EC 1.1.1.39) 62K chain precursor, mitochondrial - potato >gi_438249_emb_CAA80559_ (Z23023)

malate dehydrogenase [Solanum tuberosum]

Seq. No. 285710

Contig ID 171690_1.R1011 5'-most EST uC-zmflb73278b02a2

Seq. No. 285711

Contig ID 171695_1.R1011 5'-most EST uC-zmflmo17334e02a1



Contig ID 171698_1.R1011 5'-most EST uC-zmflb73278b11a2

Seq. No. 285713

Contig ID 171714_1.R1011 5'-most EST uC-zmflb73278d06a2

Method BLASTX
NCBI GI g2696227
BLAST score 248
E value 4.0e-21
Match length 58
% identity 76

NCBI Description (D55711) chitinase [Oryza sativa]

Seq. No. 285714

Contig ID 171717_1.R1011 5'-most EST uC-zmflb73278d12a2

Method BLASTX
NCBI GI g2979555
BLAST score 182
E value 2.0e-13
Match length 100
% identity 43

NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]

Seq. No. 285715

Contig ID 171718_1.R1011 5'-most EST uC-zmrob73062e05a1

Seq. No. 285716

Contig ID 171734_1.R1011 5'-most EST uC-zmflb73278f07a2

Seq. No. 285717

Contig ID 171742_1.R1011 5'-most EST uC-zmflb73278g05a2

Seq. No. 285718

Contig ID 171770_1.R1011 5'-most EST cyk700047560.f1

Seq. No. 285719

Contig ID 171775_1.R1011 5'-most EST uC-zmflb73279b08a2

Seq. No. 285720

Contig ID 171775_2.R1011 5'-most EST hbs701185383.h1

Seq. No. 285721

Contig ID 171842_1.R1011 5'-most EST uC-zmflb73280a08a1

Seq. No. 285722

Contig ID 171863 1.R1011



```
uC-zmflb73280b10b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3415115
BLAST score
                  481
                  2.0e-48
E value
Match length
                  139
% identity
NCBI Description
                 (AF081202) villin 2 [Arabidopsis thaliana]
                  285723
Seq. No.
Contig ID
                  171913 1.R1011
5'-most EST
                  uC-zmflb73280e05a1
                  285724
Seq. No.
Contig ID
                  171924 1.R1011
                  pmx700086545.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3980254
BLAST score
                  230
E value
                  6.0e-19
                  100
Match length
% identity
                  44
NCBI Description
                  (AJ006053) peroxisomal membrane protein [Arabidopsis
                  thaliana]
Seq. No.
                  285725
                  171931 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73280f03a1
                  285726
Seq. No.
                  171938 1.R1011
Contig ID
5'-most EST
                  hvj700620161.hl
Seq. No.
Contig ID
                   171940 1.R1011
5'-most EST
                  uC-zmflb73280f08b2
                  285728
Seq. No.
                   171943 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73280f11a1
                   285729
Seq. No.
                   171964 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73280h01b2
                  BLASTX
Method
NCBI GI
                  g4039155
BLAST score
                   655
```

8.0e-83 E value 198 Match length 80 % identity

NCBI Description (AF104258) putative copper-inducible 35.6 kDa protein

[Festuca rubra]

Seq. No. 285730

171973 1.R1011 Contig ID 5'-most EST uC-zmflb73280h11a1



Contig ID 171976_1.R1011 5'-most EST uC-zmflb73280h12b2

Seq. No. 285732

Contig ID 172016_1.R1011 5'-most EST uC-zmflmo17001g01a1

Seq. No. 285733

Contig ID 172019_1.R1011 5'-most EST xyt700346308.h1

Seq. No. 285734

Contig ID 172036_1.R1011 5'-most EST uC-zmflb73282f11a1

Seq. No. 285735

Contig ID 172052_1.R1011 5'-most EST uC-zmflb73282h05a1

Seq. No. 285736

Contig ID 172053_1.R1011 5'-most EST uC-zmflmo17079b07a1

Method BLASTX
NCBI GI g4220533
BLAST score 198
E value 2.0e-15
Match length 78
% identity 54

NCBI Description (AL035356) putative mitochondrial uncoupling protein

[Arabidopsis thaliana]

Seq. No. 285737

Contig ID 172072_1.R1011 5'-most EST uC-zmflb73283a10b2

Seq. No. 285738

Contig ID 172088_1.R1011 5'-most EST uC-zmflb73283b11a1

Seq. No. 285739

Contig ID 172106_1.R1011 5'-most EST uC-zmflb73283d01a1

Seq. No. 285740

Contig ID 172156_1.R1011 5'-most EST uC-zmflb73283f11b2

Method BLASTX
NCBI GI g4538929
BLAST score 287
E value 1.0e-25
Match length 139
% identity 47

NCBI Description (AL049483) putative nucleic acid binding protein

[Arabidopsis thaliana]

Seq. No. 285741



172189 1.R1011 Contig ID uC-zmflb73283h08b2 5'-most EST

285742 Seq. No.

172210 1.R1011 Contig ID uC-zmflb73284b10a1 5'-most EST

285743 Seq. No.

172229 1.R1011 Contig ID $sem700\overline{9}30274.h1$ 5'-most EST

BLASTX Method NCBI GI g3142300 BLAST score 163 2.0e-11 E value 65 Match length 52 % identity

(AC002411) Contains similarity to pre-mRNA processing NCBI Description

protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this

gene. [Arabidopsis thaliana]

285744 Seq. No.

172278 1.R1011 Contig ID 5'-most EST hbs701185506.h1

285745 Seq. No.

172281 1.R1011 Contig ID uC-zmflmo17258e01a1 5'-most EST

285746 Seq. No.

Contig ID 172294 1.R1011 uC-zmflb73285d08a1 5'-most EST

285747 Seq. No.

172315 1.R1011 Contig ID 5'-most EST

uC-zmflmo17057g10a1 Method BLASTX

NCBI GI q3885336 BLAST score 162 5.0e-11E value Match length 86 % identity

(AC005623) receptor-like protein kinase [Arabidopsis NCBI Description

thaliana]

Seq. No. 285748

172320 1.R1011 Contig ID uC-zmflmo17330e08a1 5'-most EST

285749 Seq. No.

172331 1.R1011 Contig ID uC-zmflb73285g10b1 5'-most EST

Method BLASTN NCBI GI g288611 BLAST score 63 E value 9.0e-27 151 Match length



% identity 85

NCBI Description Z.mays PG gene for polygalacturonase

Seq. No.

285750

Contig ID 5'-most EST 172423 1.R1011

Method

uC-zmfImo17065c09a1

NCBI GI

BLASTN g483489

BLAST score E value

240

Match length

1.0e-132 324

% identity

95

NCBI Description Z.mays IBP1 mRNA for initiator-binding protein

Seq. No.

285751

Contig ID 5'-most EST 172432 1.R1011 uC-zmflb73292b11a1

Seq. No.

285752

Contig ID 5'-most EST 172436 1.R1011

 $uC-zmf\overline{1}b73292c03a1$

Seq. No.

285753

Contig ID 5'-most EST 172447 1.R1011 uC-zmflb73292d04a1

Seq. No.

285754

Contig ID 5'-most EST 172452 1.R1011 cat700017558.r1

285755

Seq. No. Contig ID 5'-most EST

172479 1.R1011 pmx700089573.h1

Seq. No.

285756

Contig ID

172483 1.R1011

5'-most EST

uC-zmflb73303a03a2

Seq. No.

285757

Contig ID 5'-most EST 172498 1.R1011 uC-zmflb73294b03a1

285758

Seq. No. Contig ID

172503 1.R1011

5'-most EST

uC-zmflb73294b10a1

Seq. No.

Seq. No.

285759

Contig ID

172505 1.R1011 uC-zmflb73294c02a1

5'-most EST

285760

Contig ID

172513 1.R1011

5'-most EST

wyr700238883.h1

Seq. No.

285761

Contig ID

172561 1.R1011

5'-most EST

uC-zmflb73295a06b2



BLASTX Method NCBI GI q66009 Ž11 BLAST score 1.0e-17 E value Match length 51 98 % identity glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C, NCBI Description cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH (AA 1-337) [Zea mays] 285762 Seq. No. 172598 1.R1011 Contig ID wuj700282040.hl 5'-most EST 285763 Seq. No. 172618 1.R1011 Contig ID uC-zmflb73295f02b2 5'-most EST

Seq. No. 285764

Contig ID 172620_1.R1011 5'-most EST xdb700339304.h1

Seq. No. 285765

Contig ID 172636 1.R1011 5'-most EST uC-zmflb73295g12b2

Seq. No. 285766

Contig ID 172677_1.R1011 5'-most EST uC-zmflmo17069b11a1

Seq. No. 285767

Contig ID 172701_1.R1011 5'-most EST uC-zmflb73296c06b2

Method BLASTX
NCBI GI g4544404
BLAST score 147
E value 2.0e-09
Match length 94
% identity 40

NCBI Description (AC007047) unknown protein [Arabidopsis thaliana]

Seq. No. 285768

Contig ID 172739_1.R1011 5'-most EST uC-zmflb73296e05b2

Method BLASTX
NCBI GI 94063743
BLAST score 328
E value 2.0e-30
Match length 136
% identity 54

NCBI Description (AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No. 285769

Contig ID 172746_1.R1011 5'-most EST uC-zmflb73296e10a1

Seq. No. 285770



Contig ID	
5'-most	EST

172833_1.R1011 tfd700571527.h1

Seq. No.

285771

Contig ID 5'-most EST

172856_1.R1011 uC-zmflb73297e10a1

Seq. No.
Contig ID
5'-most EST

285772

172864_1.R1011 cat700016074.r1

Seq. No. Contig ID

285773

172870_1.R1011 uC-zmflb73297g01a1

Seq. No.

285774

Contig ID 5'-most EST

5'-most EST

172887_1.R1011 uC-zmflmo17331b05a1

Seq. No.

285775

Contig ID 5'-most EST

172912_1.R1011 uC-zmflb73298c02a1

Seq. No.

285776

Contig ID 5'-most EST

172915_1.R1011 uC-zmflb73298c06a1

Method BLASTX NCBI GI q3201627

BLAST score
E value

288

Match length

9.0e-26 92

57

% identity NCBI Description

(AC004669) putative SWH1 protein [Arabidopsis thaliana]

Seq. No.

285777

Contig ID 5'-most EST

172925_1.R1011 uC-zmflb73298d06a1

Seq. No.

285778

Contig ID 5'-most EST

172954_1.R1011 uC-zmflb73298h01a1

Seq. No.

285779

Contig ID 5'-most EST

172992_1.R1011 uC-zmflb73299d04a1

Seq. No.

285780

Contig ID 5'-most EST

173009_1.R1011 uC-zmflb73299f08a1

Seq. No. Contig ID 285781

5'-most EST

173021_1.R1011 uC-zmflb73299g10a1

Seq. No.

285782

173065_1.R1011 uC-zmflb73300d10a1

Contig ID 5'-most EST



```
285783
Seq. No.
                  173188 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73301e04b2
                  BLASTX
Method
                  q4557273
NCBI GI
BLAST score
                  237
                  2.0e-30
E value
Match length
                  118
% identity
NCBI Description
                  aspartylglucosaminidase precursor
                  >gi_114276_sp_P20933_ASPG_HUMAN
                  N4-(BETA-N-ACETYLGLUCOSAMINYL)-L-ASPARAGINASE PRECURSOR
                   (GLYCOSYLASPARAGINASE) (ASPARTYLGLUCOSAMINIDASE)
                   (N4-(N-ACETYL-BETA-GLUCOSAMINYL)-L-ASPARAGINE AMIDASE)
                   (AGA) >gi_67759_pir__MUHUGD
                  N4-(beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26)
                  precursor - human >gi_28534_emb_CAA39029_ (X55330)
                  N4-(beta-N-acetylglucosaminyl)-L- asparaginase [Homo
                  sapiens] >gi_34760_emb_CAA39288_ (X55762)
                  glycosylasparaginase precursor (AA -23 to 323) [Homo
                  sapiens]
                  285784
Seq. No.
                  173191 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17122c07a1
                  285785
Seq. No.
Contig ID
                  173192 1.R1011
5'-most EST
                  tzu700204674.h1
Method
                  BLASTX
NCBI GI
                  g2160782
BLAST score
                  501
E value
                   2.0e-96
Match length
                   207
% identity
                  (AF001505) putative ammonium transporter OsAMT1p [Oryza
NCBI Description
                  sativa]
                   285786
Seq. No.
                   173224 1.R1011
Contig ID
                  ntr700073979.h1
5'-most EST
                   285787
Seq. No.
                  173236 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17247g09a1
                   285788
Seq. No.
```

173314 1.R1011 Contig ID $uC-zmf\overline{l}mo17424d12a1$ 5'-most EST

285789 Seq. No.

173339 1.R1011 Contig ID fwa700099535.h1 5'-most EST

Seq. No. 285790

173347 1.R1011 Contig ID



uC-zmflb73351b08a1 5'-most EST

285791 Seq. No.

173354 1.R1011 Contig ID 5'-most EST uC-zmfImo17180f07a1

285792 Seq. No.

Contig ID 173362 1.R1011 5'-most EST uC-zmfImo17158b04a1

Seq. No. 285793

Contig ID 173385 1.R1011 5'-most EST uC-zmflb73303f12a2

Method BLASTX NCBI GI q1169544 BLAST score 144 E value 4.0e-09 Match length 56 % identity 52

ERD1 PROTEIN PRECURSOR >gi_541859_pir__JN0901 ERD1 protein - Arabidopsis thaliana >gi_497629_dbj_BAA04506_ (D17582) NCBI Description

ERD1 protein [Arabidopsis thaliana]

Seq. No. 285794

Contig ID 173426 1.R1011 5'-most EST uC-zmflb73304e02a1

Seq. No. 285795

173506 1.R1011 Contig ID uC-zmflb73305e06a1 5'-most EST

285796 Seq. No.

173509 1.R1011 Contig ID uC-zmflmo17007b10a1 5'-most EST

Seq. No. 285797

173518 1.R1011 Contig ID $wen700\overline{3}32160.h1$ 5'-most EST

Method BLASTX NCBI GI g1707642 BLAST score 523 E value 2.0e-53 153 Match length

% identity 65

NCBI Description (Y07748) TMK [Oryza sativa]

Seq. No. 285798

173531 1.R1011 Contig ID 5'-most EST uC-zmflb73305g02a1

285799 Seq. No.

Contig ID 173535 1.R1011 5'-most EST $uC-zmf\overline{l}b73305g04b2$

Seq. No. 285800

Contig ID 173640 1.R1011 uC-zmflmo17160h04a1 5'-most EST



```
285801
Seq. No.
                   173644 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73306f04b1
                  BLASTX
Method
NCBI GI
                  g118103
BLAST score
                   630
                   7.0e-66
E value
Match length
                  130
% identity
                   91
NCBI Description
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi 170440
                   (M55019) cyclophilin [Lycopersicon esculentum]
Seq. No.
                   285802
                   173661 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73306g09a1
                   285803
Seq. No.
Contig ID
                   173670 1.R1011
5'-most EST
                   uC-zmflmo17114f11a1
Seq. No.
                   285804
Contig ID
                   173683 1.R1011
5'-most EST
                   vux700161863.h1
Method
                  BLASTX
NCBI GI
                  a541855
BLAST score
                   427
E value
                   4.0e-42
Match length
                  138
% identity
                   55
NCBI Description cycloartenol synthase (EC 5.4.99.8) - Arabidopsis thaliana
                   285805
Seq. No.
Contig ID
                   173692 1.R1011
5'-most EST
                   ymt700221886.h1
Method
                  BLASTX
NCBI GI
                   g3482933
BLAST score
                   513
                   1.0e-76
E value
Match length
                  186
                   73
% identity
                  (AC003970) Similar to cdc2 protein kinases [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   285806
                   173703 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73307d05b1
                   285807
Seq. No.
                   173715 1.R1011
Contig ID
```

5'-most EST xsy700213563.h1

BLASTX Method NCBI GI g1351877 BLAST score 177 E value 9.0e-13 Match length 85



% identity 46 ALCOHOL DEHYDROGENASE II >gi_82845_pir__S20911 alcohol NCBI Description dehydrogenase (EC 1.1.1.1) II - yeast (Kluyveromyces marxianus var. lactis) >gi_2833_emb_CAA45739_ (X64397) Alcohol Dehydrogenase II [Kluyveromyces lactis] 285808 Seq. No. 173723 1.R1011 Contig ID 5'-most EST pmx700083166.h1 Method BLASTX NCBI GI g3776003 BLAST score 568 1.0e-58 E value Match length 162 64 % identity (AJ010465) RNA helicase [Arabidopsis thaliana] NCBI Description 285809 Seq. No. Contig ID 173727 1.R1011 5'-most EST $xjt700\overline{0}95907.h1$ Method BLASTX g3335359 NCBI GI BLAST score 246 E value 5.0e-2186 Match length 59 % identity NCBI Description (AC003028) unknown protein [Arabidopsis thaliana] 285810 Seq. No. 173751 1.R1011 Contig ID 5'-most EST uC-zmfImo17103h11a1BLASTX Method NCBI GI g2055230 BLAST score 150 E value 1.0e-09 Match length 83 % identity 47 NCBI Description (AB000130) SRC2 [Glycine max] Seq. No. 285811 173761 1.R1011 Contig ID uC-zmfImo17418e10a15'-most EST 285812 Seq. No. 173792 1.R1011 Contig ID uC-zmflmo17121a10a1 5'-most EST Seq. No. 285813

Contig ID 173807_1.R1011 5'-most EST uC-zmflb73324b01a1

Seq. No. 285814

Contig ID 173832_1.R1011 5'-most EST gwl700613634.h1

Seq. No. 285815

Contig ID 173886 1.R1011



67

% identity

```
5'-most EST
                  uC-zmflmo17220d06a1
                  285816
Seq. No.
Contig ID
                  173890 1.R1011
                  uC-zmflb73325f12a1
5'-most EST
                  BLASTX
Method
                  q2760333
NCBI GI
                  153
BLAST score
E value
                  1.0e-20
                  125
Match length
                  47
% identity
                  (AC002130) F1N21.18 [Arabidopsis thaliana]
NCBI Description
                  285817
Seq. No.
Contig ID
                  173900 1.R1011
                  uC-zmflb73325q12a1
5'-most EST
                  285818
Seq. No.
                  173915 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17234g07a1
                  285819
Seq. No.
Contig ID
                  173915 2.R1011
5'-most EST
                  uC-zmflmo17133d12a1
                  285820
Seq. No.
                  173935 1.R1011
Contig ID
                  uC-zmflb73326c03a1
5'-most EST
                  285821
Seq. No.
Contig ID
                  173948 1.R1011
5'-most EST
                  uC-zmflmo17129b03a1
                  285822
Seq. No.
Contig ID
                  173979 1.R1011
5'-most EST
                  uC-zmromo17119c08a1
Method
                  BLASTX
NCBI GI
                   q2739168
                  218
BLAST score
E value
                   1.0e-17
Match length
                  78
% identity
                   50
NCBI Description (AF032386) aldose-1-epimerase-like protein [Nicotiana
                   tabacum]
Seq. No.
                   285823
                   174035 1.R1011
Contig ID
                  uC-zmflmo17382d09a1
5'-most EST
                  BLASTX
Method
                   g3367523
NCBI GI
BLAST score
                  154
E value
                   5.0e-10
                   43
Match length
```

NCBI Description (AC004392) ESTs gb_AA728658 and gb_N95943 come from this

gene. [Arabidopsis thaliana]



Contig ID 174057_1.R1011 5'-most EST uC-zmflb73333b01a1

Method BLASTX
NCBI GI g1055162
BLAST score 296
E value 1.0e-26
Match length 96
% identity 51

NCBI Description (U40029) coded for by C. elegans cDNA ykl6b1.3; coded for

by C. elegans cDNA yk8g6.5; coded for by C. elegans cDNA yk8g6.3; coded for by C. elegans cDNA yk6d3.5; coded for by

C. elegans cDNA yk6d3.3; coded for by C. elegans cDNA

yk7e12.5; co

Seq. No. 285825

Contig ID 174074_1.R1011 5'-most EST uC-zmflb73333c06a1

Seq. No. 285826

Contig ID 174079_1.R1011 5'-most EST uC-zmflmo17354g10a1

Seq. No. 285827

Contig ID 174157_1.R1011 5'-most EST uC-zmflb73337d01a1

Seq. No. 285828

Contig ID 174201_1.R1011 5'-most EST uC-zmflmo17238h09a1

Method BLASTX
NCBI GI 94581164
BLAST score 210
E value 9.0e-17
Match length 91
% identity 45

NCBI Description (AC006220) putative polyprotein [Arabidopsis thaliana]

Seq. No. 285829

Contig ID 174253_1.R1011 5'-most EST uC-zmflb73338f03a1

Seq. No. 285830

Contig ID 174310_1.R1011 5'-most EST uC-zmflb73339d11a1

Seq. No. 285831

Contig ID 174313_1.R1011 5'-most EST uC-zmflb73365e11a1

Seq. No. 285832

Contig ID 174320_1.R1011 5'-most EST uC-zmflb73378h11a2

Seq. No. 285833

Contig ID 174321_1.R1011 5'-most EST uC-zmflb73339f06a1



```
285834
Seq. No.
Contig ID
                  174356 1.R1011
5'-most EST
                  uC-zmromo17100d10a1
                  285835
Seq. No.
Contig ID
                  174366 1.R1011
5'-most EST
                  uC-zmflb73341d02a2
                  285836
Seq. No.
Contig ID
                  174375_1.R1011
                  uC-zmflmo17194d03a1
5'-most EST
                  BLASTX
Method
                  q1223579
NCBI GI
BLAST score
                  189
                  6.0e-14
E value
Match length
                  81
% identity
                  41
NCBI Description
                  (X96481) cDNA101 [Arabidopsis thaliana]
                  285837
Seq. No.
                  174380 1.R1011
Contig ID
5'-most EST
                  ceu700422822.h1
                  285838
Seq. No.
Contig ID
                  174426 1.R1011
5'-most EST
                  uC-zmflb73342c07a2
                  285839
Seq. No.
Contig ID
                  174429 1.R1011
                  uC-zmfImo17132f09a1
5'-most EST
Seq. No.
                  285840
Contig ID
                  174463 1.R1011
5'-most EST
                  uC-zmflb73344a09a2
                  285841
Seq. No.
                  174492 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73344d12a2
                  285842
Seq. No.
                  174497 1.R1011
Contig ID
                  arm700460780.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4468804
BLAST score
                  293
                   2.0e-26
E value
                  117
Match length
                   50
% identity
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]
```

174513-1.R1011 Contig ID 5'-most EST xsy700212868.h1

Method BLASTX NCBI GI g4572671 BLAST score 526



E value 1.0e-53 Match length 176 % identity 59

NCBI Description (AC006954) putative cyclic nucleotide regulated ion channel

[Arabidopsis thaliana]

Seq. No. 285844

Contig ID 174529_1.R1011 5'-most EST uC-zmflb73344h09a2

Seq. No. 285845

Contig ID 174546_1.R1011 5'-most EST uC-zmflb73345b11a2

Method BLASTX
NCBI GI g4455338
BLAST score 595
E value 1.0e-61
Match length 153
% identity 65

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 285846

Contig ID 174562_1.R1011 5'-most EST uC-zmflb73345d12a2

Method BLASTX
NCBI GI g2459408
BLAST score 231
E value 5.0e-19
Match length 65
% identity 66

NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]

>gi 2924769 (AC002334) unknown protein [Arabidopsis

thaliana]

Seq. No. 285847

Contig ID 174563_1.R1011 5'-most EST uC-zmflb73345e01a2

Method BLASTX
NCBI GI g4337040
BLAST score 263
E value 7.0e-23
Match length 87
% identity 61

NCBI Description (AF124159) molybdopterin synthase sulphurylase [Arabidopsis

thaliana] >gi_4337042_gb_AAD18051_ (AF124160) molybdopterin synthase sulphurylase [Arabidopsis thaliana]

Seq. No. 285848

Contig ID 174589_1.R1011 5'-most EST uC-zmflb73346a06a2

Method BLASTX
NCBI GI g3953458
BLAST score 795
E value 5.0e-85
Match length 214
% identity 74

NCBI Description (AC002328) F20N2.3 [Arabidopsis thaliana]

```
285849
Seq. No.
                   174694 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17290c12a1
                   285850
Seq. No.
                   174719 1.R1011
Contig ID
                   uC-zmflmo17300a10a1
5'-most EST
                   BLASTX
Method
                   g3492803
NCBI GI
                   371
BLAST score
                   3.0e - 35
E value
Match length
                   88
% identity
                   75
                  (AJ002479) ENBP1 [Medicago truncatula]
NCBI Description
                   285851
Seq. No.
                   174738 1.R1011
Contig ID
                   uC-zmf\overline{1}b73348d01a3
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2642448
BLAST score
                   192
                   1.0e-14
E value
                   98
Match length
                   47
% identity
                   (AC002391) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3169187 (AC004401) hypothetical protein [Arabidopsis
                   thaliana]
                   285852
Seq. No.
                   174778 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73349a01a2
                   285853
Seq. No.
                   174791 1.R1011
Contig ID
                   yyf700\overline{3}48186.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3877252
BLAST score
                   224
E value
                   4.0e-23
Match length
                   113
% identity
                   51
NCBI Description (Z93382) F45G2.10 [Caenorhabditis elegans]
```

Contig ID 174864_1.R1011 5'-most EST xdb700338918.h1

Seq. No. 285855

Contig ID 174897_1.R1011 5'-most EST uC-zmflb73350f01a1

Seq. No. 285856

Contig ID 174905_1.R1011 5'-most EST uC-zmflmo17306h01a1

Seq. No. 285857



```
174914 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73350g07a1
                  285858
Seq. No.
                  174947_1.R1011
Contig ID
                  uC-zmrob73034e02a1
5'-most EST
                  BLASTX
Method
                  g294845
NCBI GI
BLAST score
                  1129
                  1.0e-124
E value
                  298
Match length
% identity
                  70
                  (L13655) membrane protein [Saccharum hybrid cultivar
NCBI Description
                  H65-7052]
                  285859
Seq. No.
                  174947 2.R1011
Contig ID
                  wty700164733.hl
5'-most EST
                  BLASTX
Method
                   g3292830
NCBI GI
                   171
BLAST score
                   5.0e-12
E value
Match length
                   116
                   41
% identity
                  (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
                   285860
Seq. No.
                   175053 1.R1011
Contig ID
                   uC-zmflmo17209e02a1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q517492
                   44
BLAST score
                   3.0e-15
E value
Match length
                   88
                   88
% identity
NCBI Description Z.Mays Zm38 gene, intron
                   285861
Seq. No.
                   175066 1.R1011
Contig ID
                   uC-zmflb73412b11a1
5'-most EST
Seq. No.
                   285862
                   175087 1.R1011
Contig ID
                   sem700930222.h1
5'-most EST
Seq. No.
                   285863
```

Contig ID 175106_1.R1011 5'-most EST uC-zmflb73355d01a1

Seq. No. 285864

Contig ID 175136_1.R1011 5'-most EST uC-zmflmo17010c09a1

Seq. No. 285865

Contig ID 175144_1.R1011 5'-most EST uC-zmflmo17316g04a1



285866 Seq. No. 175160 1.R1011 Contig ID 5'-most EST uC-zmflb73356b03a2 285867 Seq. No. 175182 1.R1011 Contig ID $xsy700\overline{2}11321.h1$ 5'-most EST 285868 Seq. No. 175193 1.R1011 Contig ID uC-zmflb73356e08a2 5'-most EST BLASTX Method q4056490 NCBI GI BLAST score 310 E value 2.0e-28 154 Match length 46 % identity (AC005896) hypothetical protein [Arabidopsis thaliana] NCBI Description 285869 Seq. No. 175196 1.R1011 Contig ID tfd700571637.hl 5'-most EST Method BLASTX NCBI GI q2832632 317 BLAST score E value 3.0e-29 Match length 142 54 % identity NCBI Description (AL021711) hypothetical protein [Arabidopsis thaliana] 285870 Seq. No. 175273 2.R1011 Contig ID uC-zmflb73361f12a2 5'-most EST Seq. No. 285871 175275 1.R1011 Contig ID 5'-most EST xyt700342623.h1 285872 Seq. No. 175288 1.R1011 Contig ID $uC-zmf\overline{1}b73359h04a2$ 5'-most EST BLASTX Method g2826900 NCBI GI BLAST score 648 5.0e-68 E value Match length 145 % identity 88 (AB004461) DNA polymerase alpha catalytic subunit [Oryza NCBI Description

sativa]
Seg. No. 285873

Seq. No. 285873 Contig ID 175294_1.R1011 5'-most EST nbm700466826.h1

Seq. No. 285874

Contig ID 175304_1.R1011 5'-most EST uC-zmflb73360b03a1



Contig ID 175311_1.R1011 5'-most EST uC-zmflb73360b11a1

Seq. No. 285876

Contig ID 175322_1.R1011 5'-most EST uC-zmromo17017a08a1

Method BLASTX
NCBI GI g1351762
BLAST score 235
E value 2.0e-19
Match length 64
% identity 66

NCBI Description HYPOTHETICAL 18.6 KD PROTEIN YCF36 >gi_1016155 (U30821)

ycf36 gene product [Cyanophora paradoxa]

Seq. No. 285877

Contig ID 175334_1.R1011 5'-most EST uC-zmflb73360g05a1

Seq. No. 285878

Contig ID 175388_1.R1011 5'-most EST pmx700086489.h1

Method BLASTX
NCBI GI g3402697
BLAST score 384
E value 2.0e-37
Match length 86
% identity 84

NCBI Description (AC004261) putative phosphatidylinositol-4-phosphate

5-kinase [Arabidopsis thaliana]

Seq. No. 285879

Contig ID 175394_1.R1011 5'-most EST uC-zmflb73361d01a2

Seq. No. 285880

Contig ID 175409_1.R1011 5'-most EST uC-zmflb73361e11a2

Method BLASTX
NCBI GI g3033393
BLAST score 251
E value 2.0e-21
Match length 73
% identity 62

NCBI Description (AC004238) putative phosphatidylinositol-glycan-class C

(PIGC) [Arabidopsis thaliana]

Seq. No. 285881

Contig ID 175422 2.R1011 5'-most EST ntr700073605.h1

Seq. No. 285882

Contig ID 175468_1.R1011 5'-most EST xyt700345564.h1

Method BLASTX



q2827715 NCBI GI 548 BLAST score 9.0e-77E value Match length 180 84 % identity

(AL021684) receptor protein kinase - like protein NCBI Description

[Arabidopsis thaliana]

Seq. No. 285883

175489 1.R1011 Contig ID 5'-most EST uC-zmflb73362e11a2

Method BLASTX g4455232 NCBI GI 294 BLAST score 2.0e-26 E value 150 Match length 39 % identity

(AL035523) putative protein [Arabidopsis thaliana] NCBI Description

285884 Seq. No.

175524 1.R1011 Contig ID uC-zmflb73363a07a1 5'-most EST

285885 Seq. No.

175558 1.R1011 Contig ID 5'-most EST uC-zmflb73363e09a1

285886 Seq. No.

175569 1.R1011 Contig ID 5'-most EST uC-zmflb73363f12a1

285887 Seq. No.

175590 1.R1011 Contig ID 5'-most EST uC-zmflb73365a07a1

BLASTX Method NCBI GI q3128167 BLAST score 179 E value 4.0e-13 Match length 74

% identity

(AC004521) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi 3212874 (AC004005) hypothetical protein [Arabidopsis

thaliana]

285888 Seq. No.

Contig ID 175635 1.R1011 uC-zmflb73410h02a1 5'-most EST

BLASTX Method NCBI GI q1616659 261 BLAST score E value 9.0e-23 Match length 61 79 % identity

NCBI Description (U49387) adenylosuccinate synthetase [Triticum aestivum]

Seq. No. 285889

175646_1.R1011 Contig ID



5'-most	EST	uC-zmflb73365g11a1

 Seq. No.
 285890

 Contig ID
 175653_1.R1011

 5'-most EST
 uC-zmflb73366b02a1

 Seq. No.
 285891

 Contig ID
 175667_1.R1011

 5'-most EST
 uC-zmflmo17150e03a1

 Seq. No.
 285892

 Contig ID
 175694_1.R1011

 5'-most EST
 uC-zmflb73366g03a1

 Seq. No.
 285893

 Contig ID
 175722_1.R1011

 5'-most EST
 uC-zmrob73062a12a1

 Seq. No.
 285894

 Contig ID
 175748_1.R1011

 5'-most EST
 uC-zmflb73389h12a1

 Seq. No.
 285896

 Contig ID
 175767_1.R1011

 5'-most EST
 uC-zmflb73367h06a1

 Seq. No.
 285900

 Contig ID
 175810_1.R1011

 5'-most EST
 uC-zmflb73397c09a1

 Seq. No.
 285901

 Contig ID
 175844_1.R1011

 5'-most EST
 uC-zmflb73371a12a1

 Seq. No.
 285902

 Contig ID
 175860_1.R1011

 5'-most EST
 uC-zmromo17028g10a1

 Seq. No.
 285903

 Contig ID
 175860_2.R1011

 5'-most EST
 uC-zmrob73033b10a1



```
285904
Seq. No.
                   175870 1.R1011
Contig ID
                   xsy700\overline{2}17163.h1
5'-most EST
                   285905
Seq. No.
                   175878 1.R1011
Contig ID
                   uC-zmf1b73372a01a1
5'-most EST
                   BLASTX
Method
                   g4262148
NCBI GI
                   214
BLAST score
                   4.0e-17
E value
                   81
Match length
                   49
% identity
                   (AC005275) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                   285906
Seq. No.
                   175913 1.R1011
Contig ID
                   uC-zmf\overline{1}b73372g02a1
5'-most EST
                   BLASTX
Method
                   g2444180
NCBI GI
                   152
BLAST score
                   4.0e-10
E value
                   49
Match length
                   59
% identity
NCBI Description (U94785) unconventional myosin [Helianthus annuus]
                   285907
Seq. No.
                    175928 1.R1011
Contig ID
5'-most EST
                    uC-zmromo17010b09a1
                    285908
Seq. No.
                    175940 1.R1011
Contig ID
                    uC-zmf\overline{1}b73376b05a2
5'-most EST
Seq. No.
                    285909
                    175948 1.R1011
Contig ID
5'-most EST
                    uC-zmflb73376f09a2
                    285910
Seq. No.
                    175960 1.R1011
Contig ID
                    uC-zmflmo17025g01a1
5'-most EST
                    285911
Seq. No.
                    175975 1.R1011
Contig ID
                    uC-zmflb73376f01a2
5'-most EST
                    285912
Seq. No.
                    175987 1.R1011
Contig ID
                    uC-zmf\overline{l}mo17340e05a1
5'-most EST
                    BLASTX
Method
                    g2104529
NCBI GI
                    203
BLAST score
```

6.0e-16

69

49

E value

Match length

% identity



NCBI Description (AF001308) putative hexose transporter [Arabidopsis thaliana]

Seq. No. 285913

Contig ID 176002_1.R1011 5'-most EST xsy700210648.h1

Seq. No. 285914

Contig ID 176022_1.R1011 5'-most EST uC-zmflb73378c05a2

Seq. No. 285915

Contig ID 176099_1.R1011 5'-most EST xdb700338067.h1

Seq. No. 285916

Contig ID 176166_1.R1011 5'-most EST uC-zmromo17102a06a1

Seq. No. 285917

Contig ID 176171_1.R1011 5'-most EST uC-zmflb73380e01a1

Method BLASTX
NCBI GI g2281090
BLAST score 172
E value 4.0e-12

Match length 81 % identity 46

NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No. 285918

Contig ID 176242_1.R1011 5'-most EST uC-zmflb73387e11a1

Seq. No. 285919

Contig ID 176256_1.R1011 5'-most EST rvt700551569.h1

Seq. No. 285920

Contig ID 176297_1.R1011 5'-most EST uC-zmflb73389d11a1

Seq. No. 285921

Contig ID 176307_1.R1011 5'-most EST uC-zmflb73389f10a1

Seq. No. 285922

Contig ID 176308_1.R1011 5'-most EST uC-zmrob73024h03a1

Seq. No. 285923

Contig ID 176344_1.R1011 5'-most EST uC-zmflmo17239f11a1

Seq. No. 285924

Contig ID 176348_1.R1011 5'-most EST uC-zmflb73391h03a1



Contig ID 176422_1.R1011 5'-most EST uC-zmflb73397d12a1

Seq. No. 285926

Contig ID 176429_1.R1011 5'-most EST uC-zmflmo17304b04a1

Seq. No. 285927

Contig ID 176456 1.R1011 5'-most EST uC-zmflb73397h06a1

Seq. No. 285928

Contig ID 176459_1.R1011 5'-most EST uC-zmflmo17334g01a1

Method BLASTX
NCBI GI g2262105
BLAST score 200
E value 2.0e-15
Match length 54
% identity 65

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 285929

Contig ID 176472_1.R1011 5'-most EST uC-zmflb73401b09a1

Seq. No. 285930

Contig ID 176474_1.R1011 5'-most EST uC-zmflmo17122b11a1

Seq. No. 285931

Contig ID 176492_1.R1011 5'-most EST uC-zmflb73401e02a1

Seq. No. 285932

Contig ID 176498_1.R1011 5'-most EST uC-zmflb73401e11a1

Seq. No. 285933

Contig ID 176513_1.R1011 5'-most EST yne700379012.h1

Seq. No. 285934

Contig ID 176516_1.R1011 5'-most EST uC-zmflb73418b03a1

Seq. No. 285935

Contig ID 176574_1.R1011 5'-most EST uC-zmflb73403g01a1

Seq. No. 285936

Contig ID 176574_2.R1011 5'-most EST gct701179421.h1

Seq. No. 285937



Contig ID 176582 1.R1011 5'-most EST uC-zmflb73404a04a1

Method BLASTN
NCBI GI g2623247
BLAST score 39
E value 1.0e-12
Match length 86
% identity 87

NCBI Description Zea mays SU1 isoamylase (sugary1) gene, complete cds

Seq. No. 285938

Contig ID 176626_1.R1011 5'-most EST uC-zmflmo17017d05a1

Method BLASTX
NCBI GI g2065531
BLAST score 173
E value 3.0e-12
Match length 62
% identity 56

NCBI Description (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No. 285939

Contig ID 176626_2.R1011 5'-most EST hbs701181052.h1

Seq. No. 285940

Contig ID 176658_1.R1011 5'-most EST gwl700618019.h1

Seq. No. 285941

Contig ID 176673_1.R1011 5'-most EST uC-zmflb73405d03a2

Seq. No. 285942

Contig ID 176698_1.R1011 5'-most EST uC-zmflmo17159e07a1

Seq. No. 285943

Contig ID 176707_1.R1011 5'-most EST uC-zmflmo17270g05a1

Method BLASTX
NCBI GI g3377517
BLAST score 298
E value 5.0e-27
Match length 119
% identity 50

NCBI Description (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]

Seq. No. 285944

Contig ID 176753_1.R1011 5'-most EST uC-zmromo17111a10a1

Seq. No. 285945

Contig ID 176755_1.R1011 5'-most EST uC-zmflmo17270g10a1

Method BLASTN NCBI GI g4185305



BLAST score 37 E value 2.0e-11 Match length 53 % identity 92

NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No. 285946

Contig ID 176811_1.R1011 5'-most EST uC-zmflmo17248h10a1

Seq. No. 285947

Contig ID 176819_1.R1011 5'-most EST uC-zmflb73410g09a1

Method BLASTX
NCBI GI g1890315
BLAST score 150
E value 1.0e-09
Match length 44
% identity 64

NCBI Description (Y11790) peroxidase ATP25a [Arabidopsis thaliana]

Seq. No. 285948

Contig ID 176840_1.R1011 5'-most EST uC-zmflb73411b09a1

Seq. No. 285949

Contig ID 176853_1.R1011 5'-most EST uC-zmflmo17203c09a1

Seq. No. 285950

Contig ID 176857_1.R1011 5'-most EST uC-zmflmo17367h01a1

Method BLASTX
NCBI GI 94544409
BLAST score 399
E value 2.0e-38
Match length 104
% identity 67

NCBI Description (AC006955) putative transcription factor [Arabidopsis thaliana] >gi_4585920_gb_AAD25580.1_AC007211 2 (AC007211)

putative scarecrow homolog [Arabidopsis thaliana]

Seq. No. 285951

Contig ID 176858_1.R1011 5'-most EST uC-zmflb73411e10a1

Method BLASTX
NCBI GI g3650037
BLAST score 293
E value 3.0e-36
Match length 93
% identity 85

NCBI Description (AC005396) auxin-responsive GH3-like protein [Arabidopsis

thaliana]



```
Seq. No.
                   285952
Contig ID
                   176877 1.R1011
5'-most EST
                  uC-zmflmo17337g01a1
                  285953
Seq. No.
                  176967 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73413c10a1
                  285954
Seq. No.
                  176976 1.R1011
Contig ID
5'-most EST
                  uC-zmrob73051h02a1
Method
                  BLASTN
                  g2224845
NCBI GI
BLAST score
                  230
E value
                  1.0e-126
Match length
                  288
% identity
                   95
NCBI Description Zea mays mRNA for anionic peroxidase
Seq. No.
                   285955
                  177012 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73413h12a1
Seq. No.
                   285956
Contig ID
                  177012 2.R1011
5'-most EST
                  qmh700025961.f1
                  285957
Seq. No.
                  177015 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17179a11a1
Seq. No.
                  285958
                  177039 1.R1011
Contig ID
                  uC-zmf\overline{l}b73414e03a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q421843
BLAST score
                  284
E value
                   2.0e-25
Match length
                  86
% identity
                   60
NCBI Description protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana
                   >gi 217861 dbj BAA01715 (D10909) serine/threonine protein
                  kinase [Arabidopsis thaliana]
                  285959
Seq. No.
                  177074_1.R1011
                  uC-zmflmo17211a05a1
Method
                  BLASTX
```

Contig ID 5'-most EST

g3894385 NCBI GI BLAST score 195 E value 6.0e-15 Match length 91 % identity

NCBI Description (AF053994) Hcr2-OA [Lycopersicon esculentum]

Seq. No. 285960

177094 1.R1011 Contig ID



```
wyr700240124.hl
5'-most EST
                  285961
Seq. No.
                  177104 1.R1011
Contig ID
                  uC-zmflb73415f06a1
5'-most EST
                  285962
Seq. No.
                  177149 1.R1011
Contig ID
                  uC-zmrob73054e09a1
5'-most EST
                  BLASTX
Method
                  g3702332
NCBI GI
                  169
BLAST score
                  6.0e-12
E value
Match length
                  64
                  50
% identity
                 (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
                  285963
Seq. No.
                  177156 1.R1011
Contig ID
                  uC-zmflb73416d03a1
5'-most EST
                  285964
Seq. No.
                  177204 1.R1011
Contig ID
                  uC-zmflb73417a06a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g172320
BLAST score
                  530
                  9.0e-54
E value
                  233
Match length
                  46
% identity
NCBI Description (M83553) excision repair protein [Saccharomyces cerevisiae]
                  285965
Seq. No.
                  177240 1.R1011
Contig ID
                  uC-zmflb73417f02a1
5'-most EST
Seq. No.
                  285966
                  177243 1.R1011
Contig ID
                  uC-zmflmo17129e09a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2160712
BLAST score
                  174
                   2.0e-12
E value
                  39
Match length
                   87
% identity
NCBI Description (U82966) Ca2+-ATPase [Oryza sativa]
Seq. No.
                   285967
                   177270 1.R1011
Contig ID
                  uC-zmflb73418a10a1
5'-most EST
Seq. No.
                   285968
                   177314 1.R1011
Contig ID
                  uC-zmflb73418g04a1
5'-most EST
```

39836

285969

177368 1.R1011

Seq. No.

Contig ID



5'-most EST	uC-zmflmo17001f06a1	
Seq. No. Contig ID 5'-most EST	285970 177392 1.R1011 xsy700213339.h1	
Seq. No. Contig ID 5'-most EST	285971 177412_1.R1011 uC-zmflmo17007g03a1	
Seq. No. Contig ID 5'-most EST	285972 177419_1.R1011 uC-zmflmo17007g11a1	
Seq. No. Contig ID 5'-most EST	285973 177471_1.R1011 uC-zmflmo17009a07a1	

Seq. No.	285974
Contig ID	177474_1.R1011
5'-most EST	uC-zmflmo17009a10a1

Seq. No.	285975
Contig ID	177484 1.R1011
5'-most EST	$uC-zmf\overline{l}mo17009c02a1$

Seq. No.	285976
Contig ID	177499 1.R1011
5'-most EST	uC-zmfImo17324f04a1

Seq. No.	285977	
Contig ID	177524 1.R1011	
5'-most EST	$ceu700\overline{4}22855.h1$	

Seq. No.	285978
Contig ID	177534 1.R1011
5'-most EST	uC-zmflmo17010a09a1

Seq. No.	285979
Contig ID	177563 1.R1011
5'-most EST	uC-zmfImo17129b04a1

Seq. No.	285980
Contig ID	177572 1.R1011
5'-most EST	xjt700096065.h1

Seq. No.	285981
Contig ID	177590 1.R1011
5'-most EST	uC-zmfImo17131e02a1

Seq. No.	285982
Contig ID	177611 1.R1011
5'-most EST	$wyr700\overline{2}42803.h1$

 Seq. No.
 285983

 Contig ID
 177615_1.R1011

 5'-most EST
 uC-zmflmo17065c04a1



Contig ID 177664_2.R1011 5'-most EST uC-zmflmo17012b07a1

Seq. No. 285985

Contig ID 177670_1.R1011 5'-most EST uC-zmflmo17012c03a1

Seq. No. 285986

Contig ID 177681_1.R1011 5'-most EST uC-zmflmo17012d04a1

Method BLASTX
NCBI GI g3236240
BLAST score 226
E value 2.0e-18
Match length 62
% identity 71

NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

Seq. No. 285987

Contig ID 177687_1.R1011 5'-most EST uC-zmflmo17245b09a1

Method BLASTX
NCBI GI g3402684
BLAST score 357
E value 7.0e-34
Match length 91
% identity 74

NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No. 285988

Contig ID 177688_1.R1011 5'-most EST uC-zmflmo17012e02a1

Seq. No. 285989

Contig ID 177693_1.R1011 5'-most EST uC-zmflmo17012e08a1

Seq. No. 285990

Contig ID 177727 1.R1011 5'-most EST uC-zmflmo17012h07a1

Method BLASTX
NCBI GI g3482914
BLAST score 364
E value 9.0e-42
Match length 191
% identity 53

NCBI Description (AC003970) Similar to nodulins and lipase [Arabidopsis

thaliana]

Seq. No. 285991

Contig ID 177746_1.R1011 5'-most EST zuv700355530.h1

Seq. No. 285992

Contig ID 177771 1.R1011



5'-most EST uC-zmflmo17016c07a1

Seq. No. 285993

Contig ID 177786_1.R1011 5'-most EST uC-zmrob73060f06a1

Method BLASTX
NCBI GI g3928150
BLAST score 153
E value 5.0e-10
Match length 35

% identity 89

NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]

Seq. No. 285994

Contig ID 177796_1.R1011 5'-most EST tfd700571750.h1

Method BLASTN
NCBI GI g22330
BLAST score 385
E value 0.0e+00
Match length 439
% identity 97

NCBI Description Z.mays Zmhoxla mRNA for homeobox protein

Seq. No. 285995

Contig ID 177825_1.R1011 5'-most EST uC-zmflmo17250c02a1

Seq. No. 285996

Contig ID 177829_1.R1011 5'-most EST uC-zmflmo17017b09a1

Seq. No. 285997

Contig ID 177836_1.R1011 5'-most EST uC-zmflmo17017c11a1

Seq. No. 285998

Contig ID 177883_1.R1011 5'-most EST uC-zmflmo17017h08a1

Seq. No. 285999

Contig ID 177927_1.R1011 5'-most EST xmt700262080.h1

Seq. No. 286000

Contig ID 177960_1.R1011 5'-most EST uC-zmflmo17019a06a1

Seq. No. 286001

Contig ID 177985_1.R1011 5'-most EST uC-zmflmo17342b12a1

Seq. No. 286002

Contig ID 177988_1.R1011 5'-most EST uC-zmflmo17019e02a1

Seq. No. 286003



```
178001 1.R1011
Contig ID
                  uC-zmflmo17019e07a1
5'-most EST
                  286004
Seq. No.
                  178056 1.R1011
Contig ID
                  ntr700074829.h1
5'-most EST
                  BLASTX
Method
                  g4249662
NCBI GI
                   220
BLAST score
                   1.0e-17
E value
                   90
Match length
```

% identity 54 NCBI Description (AF089810) Altered Response to Gravity [Arabidopsis

thaliana]

Seq. No. 286005

Contig ID 178062_1.R1011 5'-most EST gct701180492.h1

Seq. No. 286006

Contig ID 178102_1.R1011 5'-most EST xjt700092221.h1

Method BLASTX
NCBI GI g1076625
BLAST score 330
E value 1.0e-30
Match length 113
% identity 57

NCBI Description glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) precursor

- common tobacco >gi_473102_emb CAA82271_ (Z28697)

beta-1,3-glucanase [Nicotiana tabacum]

Seq. No. 286007

Contig ID 178134_1.R1011 5'-most EST uC-zmflmo17022f12a1

Seq. No. 286008

Contig ID 178140_1.R1011 5'-most EST uC-zmflmo17022g07a1

Seq. No. 286009

Contig ID 178182_1.R1011 5'-most EST uC-zmflmo17023d03a1

Method BLASTX
NCBI GI g1172704
BLAST score 386
E value 3.0e-37
Match length 108
% identity 69

NCBI Description PEPTIDE TRANSPORTER PTR2-B (HISTIDINE TRANSPORTING PROTEIN)

>gi_633940 (L39082) transport protein [Arabidopsis

thaliana] >gi 4406786 gb AAD20096_ (AC006532) histidine

transport protein PTR2-B [Arabidopsis thaliana]

Seq. No. 286010

Contig ID 178186_1.R1011 5'-most EST uC-zmflmo17023d08a1



Contig ID

286011

178195 1.R1011

```
uC-zmflmo17023e06a1
5'-most EST
                  BLASTX
Method
                  q3582328
NCBI GI
                  295
BLAST score
                  2.0e-26
E value
                  100
Match length
                  51
% identity
                  (AC005496) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  286012
Seq. No.
                  178202 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17023f01a1
                   286013
Seq. No.
                  178208 1.R1011
Contig ID
5'-most EST
                   gct701170705.h1
                   286014
Seq. No.
                   178213 1.R1011
Contig ID
                   uC-zmflmo17023g02a1
5'-most EST
                   286015
Seq. No.
                   178213 2.R1011
Contig ID
5'-most EST
                   wyr700242665.hl
                   286016
Seq. No.
                   178218 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17023g08a1
                   286017
Seq. No.
                   178270 1.R1011
Contig ID
                   uC-zmfImo17175c03a1
5'-most EST
                   BLASTN
Method
                   g2198852
NCBI GI
                   37
BLAST score
                   2.0e-11
E value
                   57
Match length
% identity
                   91
                   Zea mays cystathionine gamma-synthase (CGS1) gene, complete
NCBI Description
                   286018
Seq. No.
                   178271 1.R1011
Contig ID
5'-most EST
                   dyk700102228.h1
Method
                   BLASTX
NCBI GI
                   q4512624
BLAST score
                   296
                   1.0e-26
E value
Match length
                   67
% identity
                   (AC004793) Strong similarity to gi_3033401 F19I3.29
NCBI Description
                   putative potassium transporter from Arabidopsis thaliana
                   BAC gb AC004238
```



Contig ID 178277_1.R1011 5'-most EST cat700016242.r1

Seq. No. 286020

Contig ID 178288_1.R1011 5'-most EST uC-zmflmo17355f10a1

Seq. No. 286021

Contig ID 178289_1.R1011 5'-most EST uC-zmflmo17024f10a1

Method BLASTX
NCBI GI g4567285
BLAST score 209
E value 2.0e-16
Match length 57
% identity 70

NCBI Description (AC006841) hypothetical protein [Arabidopsis thaliana]

Seq. No. 286022

Contig ID 178291_1.R1011 5'-most EST uC-zmflmo17024f12a1

Seq. No. 286023

Contig ID 178295_1.R1011 5'-most EST xjt700093942.h1

Method BLASTX
NCBI GI g2674203
BLAST score 283
E value 5.0e-25
Match length 105
% identity 56

NCBI Description (AF036328) CLP protease regulatory subunit CLPX

[Arabidopsis thaliana]

Seq. No. 286024

Contig ID 178298_1.R1011 5'-most EST uC-zmflmo17024g09a1

Method BLASTX
NCBI GI g4115925
BLAST score 861
E value 2.0e-92
Match length 192
% identity 86

NCBI Description (AF118222) contains similarity to RNA recognition motifs

(Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi 4539439 emb CAB40027.1 (AL049523) RNA-binding protein

[Arabidopsis thaliana]

Seq. No. 286025

Contig ID 178298_2.R1011 5'-most EST tzu700201589.h1

Seq. No. 286026

Contig ID 178308_1.R1011 5'-most EST uC-zmflmo17024h12a1



Contig ID 178323_1.R1011 5'-most EST uC-zmflmo17396h06a1

Method BLASTX
NCBI GI g129232
BLAST score 342
E value 4.0e-32
Match length 64
% identity 91

NCBI Description ORYZAIN BETA CHAIN PRECURSOR >gi 67645 pir KHRZOB oryzain

(EC 3.4.22.-) beta precursor - rice

>gi 218183 dbj BAA14403_ (D90407) oryzain beta precursor

[Oryza sativa]

Seq. No. 286028

Contig ID 178346_1.R1011 5'-most EST uC-zmflmo17301c10a1

Seq. No. 286029

Contig ID 178393_1.R1011 5'-most EST uC-zmflmo17027b09a1

Seq. No. 286030

Contig ID 178404_1.R1011 5'-most EST uC-zmflmo17027d12a1

Seq. No. 286031

Contig ID 178417_1.R1011 5'-most EST uC-zmflmo17260e05a1

Method BLASTX
NCBI GI g4371280
BLAST score 279
E value 1.0e-33
Match length 117
% identity 68

NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 286032

Contig ID 178446_1.R1011 5'-most EST uC-zmflmo17028c08a1

Seq. No. 286033

Contig ID 178475_1.R1011 5'-most EST uC-zmflmo17352e07a1

Seq. No. 286034

Contig ID 178496 1.R1011 5'-most EST vux700160229.h1

Seq. No. 286035

Contig ID 178526_1.R1011 5'-most EST uC-zmflmo17033c12a1

Method BLASTX
NCBI GI g1946355
BLAST score 200
E value 1.0e-15
Match length 63



% identity NCBI Description

56
(U93215) maize transposon MuDR mudrA protein isolog
[Arabidopsis thaliana] >gi_2880040 (AC002340) maize
transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No. 286036

Contig ID 178538_1.R1011 5'-most EST uC-zmflmo17033e04a1

Seq. No. 286037

Contig ID 178545_2.R1011 5'-most EST cat700016024.r1

Seq. No. 286038

Contig ID 178578_1.R1011 5'-most EST uC-zmromo17026e12a1

Seq. No. 286039

Contig ID 178591_1.R1011 5'-most EST uC-zmflmo17034d05a1

Seq. No. 286040

Contig ID 178620_1.R1011 5'-most EST xdb700341263.h1

Seq. No. 286041

Contig ID 178621_1.R1011 5'-most EST uC-zmflmo17069b05a1

Seq. No. 286042

Contig ID 178625_1.R1011 5'-most EST uC-zmflmo17034h09a1

Seq. No. 286043

Contig ID 178626_1.R1011 5'-most EST uC-zmflmo17156b07a1

Method BLASTN
NCBI GI g1617473
BLAST score 155
E value 1.0e-81
Match length 319
% identity 88

NCBI Description Z.mays mRNA for Rb1 protein

Seq. No. 286044

Contig ID 178663_1.R1011 5'-most EST uC-zmflmo17035f01a1

Seq. No. 286045

Contig ID 178710_1.R1011 5'-most EST uC-zmflmo17047g03a1

Seq. No. 286046

Contig ID 178717_1.R1011 5'-most EST uC-zmflmo17036c12a1

Seq. No. 286047



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178739 1.R1011
Contig ID
                   uC-zmflmo17036f11a1
5'-most EST
                   286048
Seq. No.
                   178750 1.R1011
Contig ID
                   xdb700\overline{3}39859.h1
5'-most EST
                   286049
Seq. No.
                   178766 1.R1011
Contig ID
                   tzu700201609.hl
5'-most EST
                   286050
Seq. No.
                   178780 1.R1011
Contig ID
                   uC-zmflmo17037c06a1
5'-most EST
                   286051
Seq. No.
                   178791 1.R1011
Contig ID
                   uC-zmf\overline{l}mo17037d08a1
5'-most EST
                   BLASTX
Method
                   q2792248
NCBI GI
                   284
BLAST score
                   2.0e-25
E value
Match length
                   142
% identity
                    42
NCBI Description (AF032702) NBS-LRR type resistance protein [Oryza sativa]
                    286052
Seq. No.
                    178814 1.R1011
Contig ID
                    uC-zmf\overline{l}mo17057e09a1
5'-most EST
                    286053
Seq. No.
                    178861 1.R1011
Contig ID
                    uC-zmflmo17188b10a1
 5'-most EST
                    286054
Seq. No.
                    178941 1.R1011
 Contig ID
                    cat700\overline{0}20213.r1
 5'-most EST
                    286055
 Seq. No.
                    178943 1.R1011
 Contig ID
                    uC-zmflmo17039e09a1
 5'-most EST
                    BLASTX
 Method
                    g2335097
 NCBI GI
                    166
 BLAST score
                    9.0e-12
 E value
                    41
 Match length
                    76
 % identity
                   (AC002339) putative receptor-like protein kinase
 NCBI Description
                     [Arabidopsis thaliana]
```

Contig ID 178945_1.R1011 5'-most EST qmh700029889.f1

Seq. No. 286057

Contig ID 178945_2.R1011 5'-most EST uC-zmflmo17039e11a1



Contig ID 178986_1.R1011 5'-most EST uC-zmflmo17040d04a1

Seq. No. 286059

Contig ID 179008_1.R1011 5'-most EST uC-zmflmo17040g02a1

Seq. No. 286060

Contig ID 179025_1.R1011 5'-most EST uC-zmflmo17040h08a1 Method BLASTN

Method BLASTN
NCBI GI g4185305
BLAST score 43
E value 6.0e-15
Match length 51
% identity 96

NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21

(sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No. 286061

Contig ID 179027_1.R1011 5'-most EST uC-zmflmo17289d02a1

Seq. No. 286062

Contig ID 179046 1.R1011 5'-most EST uC-zmflmo17041d01a1

Seq. No. 286063

Contig ID 179066_1.R1011 5'-most EST uC-zmflmo17041g01a1

Seq. No. 286064

Contig ID 179099_1.R1011 5'-most EST uC-zmflmo17042c10a1

Seq. No. 286065

Contig ID 179118_1.R1011 5'-most EST uC-zmflmo17180h05a1

Seq. No. 286066

Contig ID 179131_1.R1011 5'-most EST uC-zmflmo17043g07a1

Seq. No. 286067

Contig ID 179144_1.R1011 5'-most EST uC-zmflmo17123e05a1

Method BLASTX
NCBI GI g3426064
BLAST score 174
E value 6.0e-23
Match length 124
% identity 52

NCBI Description (AJ007588) monooxygenase [Arabidopsis thaliana]



>gi_4467141_emb_CAB37510_ (AL035540) monooxygenase 2 (MO2)
[Arabidopsis thaliana]

Seq. No. 286068

Contig ID 179159_1.R1011 5'-most EST uC-zmflmo17043d01a1

Seq. No. 286069

Contig ID 179184_1.R1011 5'-most EST uC-zmflmo17043g04a1

Seq. No. 286070

Contig ID 179214_1.R1011 5'-most EST uC-zmflmo17044b04a1

Seq. No. 286071

Contig ID 179247_1.R1011 5'-most EST uC-zmflmo17224h08a1

Seq. No. 286072

Contig ID 179260_1.R1011 5'-most EST uC-zmflmo17044f06a1

Seq. No. 286073

Contig ID 179273_1.R1011 5'-most EST uC-zmromo17068h01a1

Seq. No. 286074

Contig ID 179278_1.R1011 5'-most EST uC-zmrob73058f10a1

Method BLASTX
NCBI GI g3641838
BLAST score 173
E value 5.0e-27
Match length 96
% identity 67

NCBI Description (AL023094) putative protein (fragment) [Arabidopsis

thaliana]

Seq. No. 286075

Contig ID 179295_1.R1011 5'-most EST uC-zmromo17102a08a1

Seq. No. 286076

Contig ID 179297_1.R1011 5'-most EST uC-zmflmo17045c03a1

Seq. No. 286077

Contig ID 179342_1.R1011 5'-most EST hbs701183372.h1

Seq. No. 286078

Contig ID 179346_1.R1011 5'-most EST uC-zmflmo17046b08a1

Method BLASTX
NCBI GI g2244867
BLAST score 212

4.0e-17 E value 75 Match length 51 % identity (Z97337) hydroxynitrile lyase [Arabidopsis thaliana] NCBI Description 286079 Seq. No. 179371 1.R1011 Contig ID $uC-zmf\overline{1}mo17046e12a1$ 5'-most EST 286080 Seq. No. 179405_1.R1011 Contig ID uC-zmflmo17047b05a1 5'-most EST BLASTX Method g2979550 NCBI GI 192 BLAST score 3.0e-19 E value 106 Match length 57 % identity (AC003680) putative 7-ethoxycoumarin O-deethylase NCBI Description [Arabidopsis thaliana] 286081 Seq. No. 179499_1.R1011 Contig ID uC-zmromo17066c02a1 5'-most EST BLASTX Method g2979562 NCBI GI BLAST score 242 2.0e-20 E value 75 Match length % identity (AC003680) unknown protein [Arabidopsis thaliana] NCBI Description >gi_3386623 (AC004665) unknown protein [Arabidopsis thaliana] 286082 Seq. No. 179502 1.R1011 Contig ID uC-zmflmo17049f06a1 5'-most EST

286083 Seq. No.

179529 1.R1011 Contiq ID uC-zmflmo17052c04a1 5'-most EST

BLASTX Method g3860245 NCBI GI 185 BLAST score 1.0e-13 E value 71 Match length

% identity

(AC005824) putative argonaute protein [Arabidopsis NCBI Description

thaliana]

286084 Seq. No.

179562 1.R1011 Contig ID uC-zmflmo17052g10a1 5'-most EST

286085 Seq. No.

179598 1.R1011 Contig ID uC-zmflmo17053c10a1 5'-most EST



BLASTX Method q1785621 NCBI GI 190 BLAST score 3.0e-14E value 65 Match length 55 % identity

(Z84202) AtPK2324 [Arabidopsis thaliana] >gi_2465927 NCBI Description (AF024650) receptor-like serine/threonine kinase [Arabidopsis thaliana] >gi_4249408 (AC006072) putative

serine/threonine protein kinase [Arabidopsis thaliana]

286086 Seq. No.

179613 1.R1011 Contig ID uC-zmflmo17053e04a1 5'-most EST

286087 Seq. No.

179616 1.R1011 Contig ID uC-zmfImo17053e07a15'-most EST

286088 Seq. No.

179620 1.R1011 Contig ID uC-zmflmo17053e12a1 5'-most EST

286089 Seq. No.

179638 1.R1011 Contig ID uC-zmflmo17053g08a15'-most EST

286090 Seq. No.

179655 1.R1011 Contig ID uC-zmflmo17310c12a1 5'-most EST

Method BLASTX NCBI GI q3128168 241 BLAST score 3.0e-20E value Match length 105 % identity 52

(AC004521) putative carboxyl-terminal peptidase NCBI Description

[Arabidopsis thaliana]

286091 Seq. No.

179660 1.R1011 Contig ID yne700378632.h1 5'-most EST

286092 Seq. No.

Contig ID 179664 1.R1011 $uC-zmf\overline{l}mo17175b05a1$ 5'-most EST

BLASTX Method q3549626 NCBI GI 366 BLAST score 9.0e-35 E value 179 Match length

% identity 44

NCBI Description (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]

286093 Seq. No.

179691 1.R1011 Contig ID 5'-most EST uC-zmflmo17357g03a1



Seq. No. 286094
Contig ID 179695_1.R1011
5'-most EST gct701173760.h1

Seq. No. 286095
Contig ID 179724_1.R1011
5'-most EST uC-zmflmo17055b01a1
Method BLASTX

Method BLASTX
NCBI GI g3036802
BLAST score 187
E value 9.0e-14
Match length 47
% identity 74

NCBI Description (AL022373) putative protein [Arabidopsis thaliana] >gi 3805864 emb CAA21484 (AL031986) putative protein

[Arabidopsis thaliana]

Seq. No. 286096

Contig ID 179733_1.R1011 5'-most EST uC-zmflmo17056c03a1

Seq. No. 286097

Contig ID 179734_1.R1011 5'-most EST uC-zmflmo17055b11a1

Seq. No. 286098

Contig ID 179746_1.R1011 5'-most EST uC-zmflmo17055d01a1

Seq. No. 286099

Contig ID 179749_1.R1011 5'-most EST gct701178759.h2

Method BLASTX
NCBI GI g4581111
BLAST score 146
E value 3.0e-09
Match length 128
% identity 26

NCBI Description (AC005825) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No. 286100

Contig ID 179756_1.R1011 5'-most EST uC-zmflmo17055e03a1

Seq. No. 286101

Contig ID 179792_1.R1011 5'-most EST uC-zmflmo17104a02a1

Method BLASTN
NCBI GI g22227
BLAST score 38
E value 1.0e-11
Match length 102
% identity 84

NCBI Description Z.mays CAB48 gene for chlorophyll a/b binding protein



```
286102
Seq. No.
                  179801 1.R1011
Contig ID
                  uC-zmflmo17056a10a1
5'-most EST
                  286103
Seq. No.
                  179820 1.R1011
Contig ID
                  uC-zmflmo17056c09a1
5'-most EST
                  286104
Seq. No.
                  179860 1.R1011
Contig ID
                  uC-zmflmo17056g12a1
5'-most EST
                  286105
Seq. No.
                  179884 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17057b09a1
                  BLASTX
Method
                  q1653033
NCBI GI
                   201
BLAST score
                   2.0e-15
E value
                   53
Match length
                   68
% identity
                  (D90910) hypothetical protein [Synechocystis sp.]
NCBI Description
                   286106
Seq. No.
                   179886 1.R1011
Contig ID
                   uC-zmfImo17336f07a1
5'-most EST
                   286107
Seq. No.
                   179927 1.R1011
Contig ID
                   uC-zmflmo17057g06a1
5'-most EST
Method
                   BLASTX
                   q3892057
NCBI GI
                   345
BLAST score
                   2.0e-32
E value
                   79
Match length
% identity
NCBI Description (AC002330) hypothetical protein [Arabidopsis thaliana]
                   286108
Seq. No.
                   179979 1.R1011
Contig ID
5'-most EST
                   uC-zmfImo17315e08a1
                   286109
Seq. No.
                   180005 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17058g06a1
                   BLASTX
Method
NCBI GI
                   q4239692
BLAST score
                   218
E value
                   2.0e-17
Match length
                   55
 % identity
NCBI Description (AJ132745) hypothetical protein [Arabidopsis thaliana]
```

39851

286110

180006 1.R1011

hbs701186075.hl

Seq. No.

Contig ID 5'-most EST



286111 Seq. No. 180022 1.R1011 Contig ID $uC-zmf\overline{l}mo17327f11a1$ 5'-most EST 286112 Seq. No. 180032 1.R1011 Contig ID uC-zmflmo17273h06a1 5'-most EST 286113 Seq. No. 180034 1.R1011 Contig ID uC-zmflmo17059b04a1 5'-most EST 286114 Seq. No. 180060 1.R1011 Contig ID $uC-zmf\overline{1}mo17109g10a1$ 5'-most EST 286115 Seq. No. 180073 1.R1011 Contig ID uC-zmf1mo17287b12a15'-most EST 286116 Seq. No. 180080 1.R1011 Contig ID uC-zmf1mo17218b03a15'-most EST 286117 Seq. No. 180082 1.R1011 Contig ID uC-zmfImo17059g02a15'-most EST 286118 Seq. No. 180118 1.R1011 Contig ID uC-zmflmo17060c03a1 5'-most EST 286119 Seq. No. 180134_1.R1011 Contig ID $uC-zmf\overline{l}mo17060d11a1$ 5'-most EST BLASTX Method g2252830 NCBI GI 244 BLAST score E value 2.0e-20 73 Match length 59 % identity NCBI Description (AF013293) weak similarity to receptor protein kinase [Arabidopsis thaliana] 286120 Seq. No. 180186_1.R1011 Contig ID 5'-most EST gct701176980.hl Seq. No. 286121 180208 1.R1011 Contig ID $uC-zmf\overline{l}mo17062d10a1$ 5'-most EST BLASTX Method

Method BLASTX
NCBI GI g2262105
BLAST score 159
E value 1.0e-10
Match length 50
% identity 56



```
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
                   286122
Seq. No.
                   180214 1.R1011
Contig ID
                   uC-zmf1mo17062e04a1
5'-most EST
                   286123
Seq. No.
                   180263_1.R1011
Contig ID
                   uC-zmf\overline{l}mo17426a09a1
5'-most EST
                   BLASTX
Method
                   g3953471
NCBI GI
                   160
BLAST score
                   9.0e-11
E value
                   48
Match length
                   67
% identity
                  (AC002328) F2202.16 [Arabidopsis thaliana]
NCBI Description
                   286124
Seg. No.
                   180303 1.R1011
Contig ID
                   uC-zmf1mo17194e12a1
5'-most EST
                   286125
Seq. No.
                   180337 1.R1011
Contig ID
                   uC-zmflmo17363g04a1
5'-most EST
                   286126
Seq. No.
                   180357 1.R1011
Contig ID
                   uC-zmromo17111c02a1
5'-most EST
                   286127
Seq. No.
                   180367 1.R1011
Contig ID
                   hvj700623549.hl
5'-most EST
                   286128
Seq. No.
                   180377 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17065g09a1
                   286129
Seq. No.
                   180402 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17155f06a1
                    286130
Seq. No.
                    180421 1.R1011
Contig ID
                   uC-zmf1mo17066f09a1
5'-most EST
                    286131
Seq. No.
                    180462 1.R1011
Contig ID
                    rvt700\overline{5}50714.h1
 5'-most EST
Method
                    BLASTX
                    g3445441
 NCBI GI
                    188
 BLAST score
                    7.0e-14
 E value
                   109
 Match length
```

% identity

35

39853

NCBI Description (AJ010169) Ariadne-2 protein [Drosophila melanogaster]

Seq. No. Contig ID



Contig ID	180509_1.R1011
5'-most EST	uC-zmflmo17068b05a1
Seq. No.	286133
Contig ID	180512_1.R1011
5'-most EST	uC-zmflmo17068b11a1
Seq. No.	286134
Contig ID	180534_1.R1011
5'-most EST	uC-zmflmo17068e07a1
Seq. No.	286135
Contig ID	180539_1.R1011
5'-most EST	uC-zmflmo17382h08a1
Seq. No.	286136
Contig ID	180567_1.R1011
5'-most EST	uC-zmflmo17069b07a1
Seq. No.	286137
Contig ID	180569_1.R1011
5'-most EST	uC-zmflmo17150g04a1
Seq. No.	286138
Contig ID	180601_1.R1011
5'-most EST	uC-zmflmo17069f03a1
Seq. No.	286139
Contig ID	180602_1.R1011
5'-most EST	uC-zmflmo17069f04a1
Seq. No.	286140
Contig ID	180607_1.R1011
5'-most EST	uC-zmromo17007h12a1
Seq. No.	286141
Contig ID	180646_1.R1011
5'-most EST	uC-zmflmo17070c02a1
Seq. No.	286142
Contig ID	180671_1.R1011
5'-most EST	uC-zmflmo17070e06a1
Seq. No.	286143
Contig ID	180706_1.R1011
5'-most EST	nbm700470471.h1
Seq. No.	286144
Contig ID	180736_1.R1011
5'-most EST	pwr700451043.h1
Seq. No.	286145
Contig ID	180736_2.R1011
5'-most EST	uC-zmflmo17339h02a1

39854

286146 180737_1.R1011



5'-most	EST	uC-zmrob73053a03a1
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Seq.	No	٠.	286147
- ــ ــ ــ ــ ــ	<u> </u>	TD	100774

Contig ID 180774_1.R1011 5'-most EST xsy700210941.h1

Seq. No. 286148

Contig ID 180777_1.R1011 5'-most EST uC-zmflmo17334d05a1

Seq. No. 286149

Contig ID 180828_1.R1011 5'-most EST uC-zmflmo17075d08a1

Seq. No. 286150

Contig ID 180886_1.R1011 5'-most EST uC-zmflmo17079h04a1

Seq. No. 286151

Contig ID 180908_1.R1011 5'-most EST uC-zmflmo17420g04a1

Seq. No. 286152

Contig ID 180930_1.R1011 5'-most EST uC-zmrob73050f12a1

Seq. No. 286153

Contig ID 180976_1.R1011 5'-most EST uC-zmflmo17339f02a1

Seq. No. 286154

Contig ID 180989_1.R1011 5'-most EST uC-zmflmo17079a08a1

Method BLASTN
NCBI GI g1061307
BLAST score 312
E value 1.0e-175
Match length 416
% identity 94

NCBI Description Z.mays Dof3 mRNA

Seq. No. 286155

Contig ID 181000_1.R1011 5'-most EST cjh700193809.h1

Seq. No. 286156

Contig ID 181005_1.R1011 5'-most EST uC-zmflmo17079c01a1

Seq. No. 286157

Contig ID 181017_1.R1011 5'-most EST uC-zmflmo17079d01a1

Seq. No. 286158

Contig ID 181042_1.R1011 5'-most EST uC-zmflmo17079g07a1

286159 Seq. No. 181086 1.R1011 Contig ID uC-zmflmo17083c08a1 5'-most EST BLASTN Method NCBI GI g3821780 BLAST score 36 1.0e-10 E value Match length 36 % identity 100 NCBI Description Xenopus laevis cDNA clone 27A6-1 Seq. No. 181094 1.R1011 Contig ID 5'-most EST uC-zmflmo17334f09a1 Method BLASTX NCBI GI g282994 BLAST score 698 8.0e-74E value Match length 155 % identity 85 protein [Hordeum vulgare]

NCBI Description Sip1 protein - barley >gi_167100 (M77475) seed imbibition

Seq. No. 286161 181113 1.R1011 Contig ID uC-zmflmo17083h09a1 5'-most EST Method BLASTX q4584541 NCBI GI 152

BLAST score E value 6.0e-10 47 Match length 55 % identity

NCBI Description (AL049608) 3-hydroxyisobutyryl-coenzyme A hydrolase-like

protein [Arabidopsis thaliana]

286162 Seq. No.

181124 1.R1011 Contig ID 5'-most EST uC-zmflmo17269a09a1

Seq. No. 286163

181124 2.R1011 Contig ID uC-zmflmo17234c10a1 5'-most EST

286164 Seq. No.

181161 1.R1011 Contig ID uC-zmflmo17084f04a1 5'-most EST

286165 Seq. No.

181215 1.R1011 Contig ID 5'-most EST uC-zmflmo17085f07a1

286166 Seq. No.

181236 1.R1011 Contig ID 5'-most EST uC-zmflmo17085h06a1

Method BLASTX NCBI GI q4544431 225 BLAST score



E value 2.0e-18 Match length 62 % identity 68

NCBI Description (AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No. 286167

Contig ID 181275_1.R1011 5'-most EST uC-zmflmo17086d10a1

Seq. No. 286168

Contig ID 181285_1.R1011 5'-most EST uC-zmflmo17086e10a1

Seq. No. 286169

Contig ID 181318_1.R1011 5'-most EST uC-zmflmo17087b07a1

Seq. No. 286170

Contig ID 181327_1.R1011 5'-most EST uC-zmflmo17419c03a1

Seq. No. 286171

Contig ID 181348_1.R1011 5'-most EST uC-zmromo17111g02a1

Method BLASTX
NCBI GI g1708424
BLAST score 211
E value 5.0e-17
Match length 58
% identity 64

NCBI Description ISOFLAVONE REDUCTASE HOMOLOG >gi_1230614 (U48590) isoflavone reductase-like protein [Lupinus albus]

Seq. No. 286172

Contig ID 181394_1.R1011 5'-most EST uC-zmflmo17210f12a1

Seq. No. 286173

Contig ID 181418 1.R1011 5'-most EST uC-zmflmo17090b02a1

Seq. No. 286174

Contig ID 181521_1.R1011 5'-most EST uC-zmflmo17139g11a1

Seq. No. 286175

Contig ID 181583_1.R1011 5'-most EST uC-zmflmo17323b11a1

Seq. No. 286176

Contig ID 181609_1.R1011 5'-most EST uC-zmflmo17290g06a1

Seq. No. 286177

Contig ID 181619_1.R1011 5'-most EST xsy700214467.h1



Contig ID 181642_1.R1011 5'-most EST uC-zmflmo17327h09a1

Seq. No. 286179

Contig ID 181644_1.R1011 5'-most EST cat700019046.r1

Seq. No. 286180

Contig ID 181657_1.R1011 5'-most EST cat700019418.r1

Seq. No. 286181

Contig ID 181667_1.R1011 5'-most EST uC-zmflmo17103h05a1

Seq. No. 286182

Contig ID 181673_1.R1011 5'-most EST uC-zmflmo17217a12a1

Seq. No. 286183

Contig ID 181699_1.R1011 5'-most EST uC-zmflmo17104e05a1

Method BLASTX
NCBI GI g3445397
BLAST score 306
E value 7.0e-28
Match length 83
% identity 72

NCBI Description (AJ010166) S-domain receptor-like protein kinase [Zea mays]

Seq. No. 286184

Contig ID 181708_1.R1011 5'-most EST uC-zmflmo17104g04a1

Seq. No. 286185

Contig ID 181725_1.R1011

5'-most EST uC-zmflmo17107b03a1

Method BLASTX
NCBI GI g3522946
BLAST score 195
E value 6.0e-15
Match length 62
% identity 56

NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 286186

Contig ID 181731_1.R1011 5'-most EST uC-zmflmo17290d03a1

Seq. No. 286187

Contig ID 181740_1.R1011 5'-most EST uC-zmflmo17107f08a1

Method BLASTX
NCBI GI g4335756
BLAST score 305
E value 1.0e-27



Match length 80 % identity 79

NCBI Description (AC006284) putative ankyrin [Arabidopsis thaliana]

Seq. No. 286188

Contig ID 181746_1.R1011 5'-most EST uC-zmflmo17107h03a1

Method BLASTX
NCBI GI g4572671
BLAST score 150
E value 5.0e-14
Match length 71
% identity 58

NCBI Description (AC006954) putative cyclic nucleotide regulated ion channel

[Arabidopsis thaliana]

Seq. No. 286189

Contig ID 181772_1.R1011 5'-most EST gct701176291.h1

Seq. No. 286190

Contig ID 181809_1.R1011 5'-most EST uC-zmflmo17239f03a1

Seq. No. 286191

Contig ID 181818_1.R1011 5'-most EST uC-zmflmo17328g08a1

Seq. No. 286192

Contig ID 181828_1.R1011 5'-most EST uC-zmrob73022f08a1

Seq. No. 286193

Contig ID 181832_1.R1011 5'-most EST wty700170714.h1

Seq. No. 286194

Contig ID 181849_1.R1011 5'-most EST uC-zmflmo17223b08a1

Seq. No. 286195

Contig ID 181852_1.R1011 5'-most EST pmx700081932.h1

Method BLASTX
NCBI GI g3874214
BLAST score 353
E value 2.0e-33
Match length 129
% identity 56

NCBI Description (Z83217) Similarity to Yeast E1-E2 ATPase YEL031W

(SW:YED1_YEAST); cDNA EST EMBL:D27574 comes from this gene;

cDNA EST EMBL:D33757 comes from this gene; cDNA EST EMBL:D34256 comes from this gene; cDNA EST EMBL:D37288

comes from

Seq. No. 286196

Contig ID 181864_1.R1011



```
uC-zmflmo17111d08a1
 5'-most EST
                    286197
 Seq. No.
                    181865 1.R1011
 Contiq ID
                    uC-zmromo17027c09a1
 5'-most EST
                    286198
 Seq. No.
                    181882 1.R1011
 Contig ID
                    uC-zmflmo17111g09a1
 5'-most EST
                    286199
 Seq. No.
                    181893 1.R1011
 Contig ID
                    uC-zmf\overline{l}mo17337d02a1
 5'-most EST
                    286200
 Seq. No.
                    181920 1.R1011
 Contig ID
                    uC-zmflmo17204c11a1
 5'-most EST
                    286201
 Seq. No.
                    181937 1.R1011
 Contig ID
                    uC-zmflmo17112g09a1
 5'-most EST
                    BLASTX
 Method
                    g496164
 NCBI GI
                    296
 BLAST score
                    9.0e-27
 E value
                    61
 Match length
                    95
  % identity
                    (L26305) ribosome-inactivating protein [Zea mays]
 NCBI Description
                    >gi_1096509_prf__2111429A ribosome-inactivating protein
                     [Zea mays]
                    286202
  Seq. No.
                     181951_1.R1011
  Contig ID
                     uC-zmflmo17113b07a1
  5'-most EST
                    BLASTX
 Method
                    g3763933
  NCBI GI
  BLAST score
                     162
                     9.0e-11
  E value
                     45
  Match length
  % identity
  NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]
                     286203
  Seq. No.
                     181960 1.R1011
  Contig ID
                     uC-zmromo17111d02a1
  5'-most EST
                     286204
  Seq. No.
                     182015 1.R1011
  Contig ID
                     uC-zmflmo17427e10a1
  5'-most EST
                     286205
  Seq. No.
                     182046 1.R1011
  Contig ID
                     vux700156934.hl
  5'-most EST
                     286206
Seq. No.
```

39860

182087 1.R1011

uC-zmf1mo17403a01a1

Contig ID

5'-most EST



```
Seq. No.
                  286207
Contig ID
                  182130 1.R1011
5'-most EST
                  uC-zmflmo17152c06a1
Method
                  BLASTX
NCBI GI
                  g3461814
BLAST score
                  206
                  6.0e-16
E value
                  57
Match length
% identity
                  67
NCBI Description (AC004138) hypothetical protein [Arabidopsis thaliana]
                  286208
Seq. No.
Contig ID
                  182158 1.R1011
5'-most EST
                  uC-zmromo17049c10a1
                  286209
Seq. No.
                  182167 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17122e05a1
```

Contig ID 182187_1.R1011 5'-most EST uC-zmflmo17139e11a1

Seq. No. 286211

Contig ID 182189 1.R1011 5'-most EST uC-zmflmo17117h12a1

Seq. No. 286212

Contig ID 182225_1.R1011 5'-most EST uC-zmflmo17336a10a1

Seq. No. 286213

Contig ID 182236_1.R1011 5'-most EST uC-zmflmo17118f09a1

Seq. No. 286214

Contig ID 182242 1.R1011 5'-most EST uC-zmflmo17342d09a1

Method BLASTX
NCBI GI g2244787
BLAST score 303
E value 2.0e-27
Match length 106
% identity 57

NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 286215

Contig ID 182245_1.R1011 5'-most EST dyk700105601.h1

Method BLASTX
NCBI GI g4115534
BLAST score 187
E value 6.0e-14
Match length 103
% identity 41

NCBI Description (AB012114) UDP-glycose:flavonoid glycosyltransferase [Vigna



mungo]

Seq. No. 286217

Contig ID 182255 1.R1011 5'-most EST uC-zmflmo17121a02a1

Seq. No. 286218

Contig ID 182263_1.R1011 5'-most EST uC-zmflmo17121b12a1

Seq. No. 286219

Contig ID 182316_1.R1011 5'-most EST uC-zmflmo17122b03a1

Seq. No. 286220

Contig ID 182442_1.R1011 5'-most EST uC-zmflmo17234a12a1

Seq. No. 286221

Contig ID 182444_1.R1011 5'-most EST uC-zmflmo17247d08a1

Seq. No. 286222

Contig ID 182457_1.R1011 5'-most EST uC-zmromo17011b06a1

Seq. No. 286223

Contig ID 182531_1.R1011 5'-most EST uC-zmflmo17127f11a1

Seq. No. 286224

Contig ID 182534_1.R1011 5'-most EST uC-zmflmo17127g03a1

Seq. No. 286225

Contig ID 182558 1.R1011 5'-most EST xdb700340742.h1

Method BLASTX
NCBI GI g4539335
BLAST score 165
E value 2.0e-11
Match length 53
% identity 43

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 286226

Contig ID 182586_1.R1011 5'-most EST uC~zmflmo17129f09a1

Seq. No. 286227

Contig ID 182588 1.R1011 5'-most EST uC-zmflmo17359b09a1



Contig ID 182643_1.R1011 5'-most EST uC-zmflmo17234e01a1

Seq. No. 286229

Contig ID 182649_1.R1011 5'-most EST uC-zmflmo17130f07a1

Seq. No. 286230

Contig ID 182659_1.R1011 5'-most EST uC-zmflmo17130g06a1

Seq. No. 286231

Contig ID 182719_1.R1011 5'-most EST uC-zmflmo17131f12a1

Method BLASTX
NCBI GI g2809241
BLAST score 290
E value 4.0e-26
Match length 74
% identity 72

NCBI Description (AC002560) F21B7.10 [Arabidopsis thaliana]

Seq. No. 286232

Contig ID 182764_1.R1011 5'-most EST uC-zmflmo17317g04a1

Method BLASTX
NCBI GI g3738285
BLAST score 275
E value 3.0e-24
Match length 108
% identity 50

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 286233

Contig ID 182780_1.R1011 5'-most EST uC-zmflmo17292f11a1

Seq. No. 286234

Contig ID 182781_1.R1011 5'-most EST uC-zmflmo17132f06a1

Method BLASTX
NCBI GI g4467124
BLAST score 175
E value 1.0e-12
Match length 119
% identity 31

NCBI Description (AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No. 286235

Contig ID 182798_1.R1011 5'-most EST uC-zmflmo17318f09a1

Method BLASTX
NCBI GI g2924509
BLAST score 477
E value 5.0e-48
Match length 141



% identity 66

NCBI Description (AL022023) subtilisin proteinase - like [Arabidopsis

thaliana]

Seq. No. 286236

Contig ID 182803_1.R1011 5'-most EST uC-zmflmo17281b02a1

Seq. No. 286237

Contig ID 182818_1.R1011 5'-most EST uC-zmflmo17399d11a1

Method BLASTN
NCBI GI g4140643
BLAST score 142
E value 7.0e-74
Match length 178
% identity 95

NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

complete sequence

Seq. No. 286238

Contig ID 182866_1.R1011 5'-most EST uC-zmflmo17319h06a1

Seq. No. 286239

Contig ID 182879_1.R1011 5'-most EST uC-zmflmo17134d01a1

Seq. No. 286240

Contig ID 182882_1.R1011 5'-most EST uC-zmflmo17134d07a1

Method BLASTX
NCBI GI g1743412
BLAST score 450
E value 2.0e-64
Match length 159
% identity 78

NCBI Description (Y09826) amino acid transporter [Solanum tuberosum]

Seq. No. 286241

Contig ID 182892 2.R1011 5'-most EST tfd700572479.h1

Seq. No. 286242

Contig ID 182893_1.R1011 5'-most EST uC-zmflmo17134e11a1

Seq. No. 286243

Contig ID 182903_1.R1011 5'-most EST uC-zmflmo17134g01a1

Seq. No. 286244

Contig ID 182976_1.R1011 5'-most EST xmt700262392.h1

Seq. No. 286245

Contig ID 182983_1.R1011



```
5'-most EST
                   uC-zmflmo17135h03a1
                   286246
 Seq. No.
                   182992 1.R1011
 Contig ID
 5'-most EST
                   uC-zmflmo17139a08a1
                   286247
 Seq. No.
                   183003 1.R1011
 Contig ID
 5'-most EST
                   dyk700105820.h1
                   286248
 Seq. No.
 Contig ID
                   183068 1.R1011
                   uC-zmflmo17140c05a1
 5'-most EST
                   286249
 Seq. No.
                   183086 1.R1011
 Contig ID
 5'-most EST
                   uC-zmflmo17140e10a1
Seq. No.
                   286250
                   183090 1.R1011
 Contig ID
 5'-most EST
                   uC-zmflmo17140f03a1
                   286251
Seq. No.
                   183109 1.R1011
 Contig ID
5'-most EST
                   uC-zmflmo17211g05a1
                   286252
 Seq. No.
                   183116 1.R1011
 Contig ID
 5'-most EST
                  ceu700423053.hl
                   BLASTX
Method
NCBI GI
                   g4587597
BLAST score
                   204
                   1.0e-15
E value
Match length
                   112
 % identity
 NCBI Description (AC006951) putative MAP kinase phosphatase [Arabidopsis
                   thaliana]
                   286253
 Seq. No.
 Contig ID
                   183123 1.R1011
 5'-most EST
                   uC-zmflmo17326f08a1
                   286254
 Seq. No.
                   183131 1.R1011
 Contig ID
 5'-most EST
                   uC-zmromo17006f02a1
 Method
                   BLASTX
 NCBI GI
                   g4584358
 BLAST score
                   282
 E value
                   4.0e-25
                   75
 Match length
 % identity
                   80
 NCBI Description (AC006420) unknown protein [Arabidopsis thaliana]
```

Seq. No. 286255

Contig ID 183155_1.R1011 5'-most EST wyr700239981.h1

Method BLASTX



NCBI GI g4455198 BLAST score 221 E value 9.0e-18 Match length 88 % identity 58

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 286256

Contig ID 183210_1.R1011 5'-most EST uC-zmflmo17150c11a1

Seq. No. 286257

Contig ID 183244_1.R1011 5'-most EST vux700156764.h1

Seq. No. 286258

Contig ID 183262_1.R1011 5'-most EST uC-zmflmo17151a05a1

Seq. No. 286259

Contig ID 183294_1.R1011 5'-most EST uer700577286.h1

Method BLASTX
NCBI GI g3287696
BLAST score 304
E value 1.0e-27
Match length 76
% identity 68

NCBI Description (AC003979) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from Pisum sativum. This ORF may be

part of a larger gene that lies in the overlapping region.

[Arabidopsis thaliana]

Seq. No. 286260

Contig ID 183294_2.R1011 5'-most EST uC-zmflmo17364f07a1

5'-most EST uC-zmflmo1
Method BLASTX
NCBI GI g3287696
BLAST score 204
E value 3.0e-18
Match length 66

Match length 66 % identity 68

NCBI Description (AC003979) Strong similarity to phosphoribosylanthranilate

transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region.

[Arabidopsis thaliana]

Seq. No. 286261

Contig ID 183301_1.R1011 5'-most EST uC-zmflmo17151e05a1

Seq. No. 286262

Contig ID 183309 1.R1011 5'-most EST uC-zmflmo17151f04a1

Seq. No. 286263

Contig ID 183333 1.R1011



```
uC-zmflmo17205b10a1
5'-most EST
                  BLASTX
Method
                  g1732517
NCBI GI
                  368
BLAST score
                   8.0e-35
E value
                   145
Match length
                   55
% identity
                  (U62745) putative cytoskeletal protein [Arabidopsis
NCBI Description
                   thaliana]
                   286264
Seq. No.
                   183352 1.R1011
Contig ID
                   uC-zmflmo17292c03a1
5'-most EST
                   286265
Seq. No.
                   183426 1.R1011
Contig ID
                   uC-zmflmo17374d07a1
5'-most EST
                   286266
Seq. No.
                   183448 1.R1011
Contig ID
                   uC-zmf1mo17153e07a1
5'-most EST
                   286267
Seq. No.
                   183450 1.R1011
Contig ID
                   uC-zmf\overline{l}mo17153e09a1
5'-most EST
                   BLASTX
Method
                   q4510349
NCBI GI
                   144
BLAST score
                   4.0e-09
E value
Match length
                   35
                   83
% identity
                   (AC006921) putative bZIP transcription factor [Arabidopsis
NCBI Description
                   thaliana]
                   286268
Seq. No.
                   183500 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17398b01a1
                   BLASTX
Method
                   q3738306
NCBI GI
BLAST score
                   240
                   7.0e-20
E value
Match length
                   91
 % identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
                    286269
 Seq. No.
                    183500 2.R1011
 Contig ID
                    zuv700353144.h1
 5'-most EST
 Method
                    BLASTX
                    q3738306
 NCBI GI
                    415
 BLAST score
                    6.0e-41
 E value
                   108
 Match length
                    71
 % identity
 NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
```

39867

286270

Seq. No.

```
Contig ID
                  183503 1.R1011
                  uC-zmflmo17291a11a1
5'-most EST
                  286271
Seq. No.
                  183524 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17343b10a1
                  286272
Seq. No.
                  183541 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17155a08a1
Method
                  BLASTN
                  g3264610
NCBI GI
BLAST score
                  359
                  0.0e+00
E value
Match length
                  363
% identity
                  100
NCBI Description Zea mays seven in absentia homolog mRNA, partial cds
                  286273
Seq. No.
Contig ID
                  183568 1.R1011
5'-most EST
                  uC-zmflmo17334b05a1
Seq. No.
                  286274
```

Contig ID 183587_1.R1011 5'-most EST uC-zmflmo17155f04a1

 Seq. No.
 286275

 Contig ID
 183596_1.R1011

 5'-most EST
 uC-zmflmo17156g05a1

 Seq. No.
 286276

 Contig ID
 183610_1.R1011

 5'-most EST
 uC-zmromo17011a11a1

 Method
 BLASTN

Method BLASTN
NCBI GI g3320103
BLAST score 121
E value 1.0e-61
Match length 274
% identity 84

NCBI Description Zea mays mRNA for calcium-dependent protein kinase

 Seq. No.
 286277

 Contig ID
 183628_1.R1011

 5'-most EST
 uC-zmrob73054f09a1

 Method
 BLASTX

 NCBI GI
 g2131733

 BLAST score
 153

BLAST score 153 E value 1.0e-09 Match length 146 % identity 32

NCBI Description hypothetical protein YLL035w - yeast (Saccharomyces

cerevisiae) >gi_1360224_emb_CAA97484_ (Z73140) ORF YLL035w

[Saccharomyces cerevisiae]

Seq. No. 286278

Contig ID 183642_1.R1011 5'-most EST uC-zmflmo17367b03a1



Seq. No. 286279

Contig ID 183698 1.R1011 5'-most EST uC-zmflmo17157c11a1

286280 Seq. No.

Contig ID 183746 1.R1011 uC-zmflmo17157h10a1 5'-most EST

286281 Seq. No.

183805 1.R1011 Contig ID 5'-most EST uC-zmflmo17158g01a1

BLASTX Method NCBI GI q4206787 BLAST score 216 1.0e-18 E value 77 Match length 73 % identity

NCBI Description (AF112863) syntaxin-related protein Nt-syr1 [Nicotiana

tabacum]

286282 Seq. No.

Contig ID 183833 1.R1011 5'-most EST uC-zmflmo17159b03a1

286283 Seq. No.

183859 1.R1011 Contig ID 5'-most EST uC-zmflmo17159e02a1

Method BLASTX NCBI GI g113363 BLAST score 166 1.0e-11 E value 72 Match length % identity 44

NCBI Description ALCOHOL DEHYDROGENASE 1 >gi_279445_pir__DEPJA1 alcohol dehydrogenase (EC 1.1.1.1) 1 - garden petunia

>gi_20506_emb_CAA38039_ (X54106) alcohol dehydrogenase

[Petunia x hybrida]

286284 Seq. No.

183899 1.R1011 Contig ID 5'-most EST fdz701164929.h1

Seq. No. 286285

Contig ID 183915 1.R1011 uC-zmflmo17160d10a1 5'-most EST

BLASTX Method g4416302 NCBI GI BLAST score 207 2.0e-16 E value Match length 116 % identity 44

NCBI Description (AF105716) copia-type pol polyprotein [Zea mays]

286286 Seq. No.

Contig ID 183921_1.R1011 5'-most EST uC-zmflmo17160e05a1



```
286287
Seq. No.
Contig ID
                  183968 1.R1011
5'-most EST
                  uC-zmflmo17163c03a1
                  286288
Seq. No.
                  184021 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17168a03a1
                  286289
Seq. No.
Contig ID
                  184071_1.R1011
5'-most EST
                  uC-zmflmo17168h05a1
Method
                  BLASTX
NCBI GI
                  q2262172
BLAST score
                  154
E value
                  6.0e-10
Match length
                  35
% identity
                  83
NCBI Description (AC002329) predicted protein of unknown function
                  [Arabidopsis thaliana]
Seq. No.
                  286290
                  184108 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17169e11a1
                  BLASTX
Method
                  q1777386
NCBI GI
BLAST score
                  367
E value
                  4.0e-58
Match length
                  219
% identity
                  56
NCBI Description (U39301) caffeic acid O-methyltransferase [Pinus taeda]
Seq. No.
                  286291
Contig ID
                  184112 1.R1011
5'-most EST
                  uC-zmflmo17169e10a1
Seq. No.
                  286292
                  184235 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17172b12a1
                  286293
Seq. No.
                  184267 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17428g07a1
Method
                  BLASTX
NCBI GI
                  g3413706
BLAST score
                  285
E value
                  3.0e-25
Match length
                  92
% identity
NCBI Description (AC004747) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  286294
```

Contig ID 184311_1.R1011 5'-most EST uC-zmflmo17174c10a1

Seq. No. 286295

Contig ID 184331_1.R1011

```
uC-zmflmo17174f02a1
5'-most EST
                  286296
Seq. No.
                  184353 1.R1011
Contig ID
                  uC-zmf1mo17175a02a1
5'-most EST
                  286297
Seq. No.
                  184361 1.R1011
Contig ID
                  uC-zmrob73006e05a1
5'-most EST
                  BLASTN
Method
NCBI GI
                  q1263159
                  82
BLAST score
                  4.0e-38
E value
                  130
Match length
                  91
% identity
NCBI Description O.sativa DNA for LRK2 gene
                  286298
Seq. No.
                  184362 1.R1011
Contig ID
                  uC-zmf\overline{1}mo17175c02a1
5'-most EST
                  286299
Seq. No.
                  184430 1.R1011
Contig ID
                  uC-zmflmo17177b10a1
5'-most EST
                  286300
Seq. No.
                  184475 1.R1011
Contig ID
                  uC-zmflmo17177g12a1
5'-most EST
```

Seq. No.	286301
Contig ID	184478 1.R1011
5'-most EST	uC-zmfImo17177h04a1

Seq. No.	286302
Contig ID	184553 1.R1011
5'-most EST	$uC-zmf\overline{l}mo17318a02a1$

Seq. No.	286303
Contig ID	184558 1.R1011
5'-most EST	uC-zmrob73023h07a1

Seq. No.	286304
Contig ID	184575 1.R1011
5'-most EST	$uC-zmf\overline{1}mo17323b03a1$
Method	BLASTX
NCBI GI	g4204268
BLAST score	321
E value	1.0e-29
Match length	74
% identity	76

NCBI Description (AC005223) 62134 [Arabidopsis thaliana]

 Seq. No.
 286305

 Contig ID
 184580_1.R1011

 5'-most EST
 uC-zmflmo17180d04a1

Seq. No. 286306



```
184619 1.R1011
Contig ID
                   uC-zmf\overline{l}mo17180h07a1
5'-most EST
                    286307
Seq. No.
                    184630 1.R1011
Contig ID
                    uC-zmfImo17181b01b1
5'-most EST
                    BLASTX
Method
                    g1075616
NCBI GI
                    150
BLAST score
                    4.0e-12
E value
Match length
                    90
                    44
% identity
                    carboxyl-terminal processing proteinase precursor - Synechocystis sp. (PCC 6803) >gi_493215 (L25250) protease
NCBI Description
                    [Synechocystis sp.] >gi_1001562_dbj_BAA10189_ (D64000)
                    carboxyl-terminal processing protease [Synechocystis sp.]
                    286308
Seq. No.
                    184639 1.R1011
Contig ID
                    uC-zmfImo17181b12b1
5'-most EST
                    286309
Seq. No.
                    184655 1.R1011
Contig ID
                    uC-zmflmo17181d05b1
5'-most EST
                    286310
Seq. No.
                    184693 1.R1011
Contig ID
                    uC-zmf\overline{l}mo17181h03b1
5'-most EST
                    BLASTX
Method
                    g3298474
NCBI GI
                    792
BLAST score
                    7.0e-85
E value
                    163
Match length
% identity
NCBI Description (AB012765) ovpl [Oryza sativa]
                    286311
Seq. No.
                    184779 1.R1011
Contig ID
5'-most EST
                    uC-zmflmo17188d02a1
                     BLASTX
Method
                     g2673908
NCBI GI
                     196
BLAST score
                     5.0e-15
E value
                     83
Match length
 % identity
NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
```

184783 1.R1011 Contig ID uC-zmflmo17188d08a1 5'-most EST

286313 Seq. No.

184797 1.R1011 Contig ID $uC-zmf\overline{l}mo17188f06a1$ 5'-most EST

286314 Seq. No.

184807 1.R1011 Contig ID



5'-most EST uC-zmflmo17320e02a1

Method BLASTX
NCBI GI g2462107
BLAST score 168
E value 2.0e-11
Match length 179
% identity 27

NCBI Description (Y10909) stage V sporulation protein K [Bacillus cereus]

Seq. No. 286315

Contig ID 184847_1.R1011 5'-most EST nbm700466570.h1

Method BLASTX
NCBI GI g4539660
BLAST score 176
E value 1.0e-12
Match length 71
% identity 45

NCBI Description (AF061282) polyprotein [Sorghum bicolor]

Seq. No. 286316

Contig ID 184950_1.R1011 5'-most EST uC-zmflmo17192b02a1

Seq. No. 286317

Contig ID 184977_1.R1011 5'-most EST cat700018530.r1

Seq. No. 286318

Contig ID 185004_1.R1011 5'-most EST nbm700474161.h1

Seq. No. 286319

Contig ID 185021_1.R1011 5'-most EST uC-zmrob73064c12a1

Seq. No. 286320

Contig ID 185070_1.R1011 5'-most EST uC-zmromo17029h04a1

Method BLASTX
NCBI GI g3980254
BLAST score 259
E value 3.0e-22
Match length 81
% identity 53

NCBI Description (AJ006053) peroxisomal membrane protein [Arabidopsis

thaliana]

Seq. No. 286321

Contig ID 185074_1.R1011 5'-most EST uC-zmflmo17194g03a1

Seq. No. 286322

Contig ID 185076_1.R1011 5'-most EST uC~zmflmo17194g06a1

Seq. No. 286323



Contig ID	185201_1.R1011
5'-most EST	uC-zmflmo17202b09a1
Seq. No.	286324
Contig ID	185224_1.R1011
5'-most EST	uC-zmflmo17217d09a1
Seq. No.	286325
Contig ID	185248_1.R1011
5'-most EST	uC-zmflmo17202g05a1
Seq. No.	286326
Contig ID	185384_1.R1011
5'-most EST	uC~zmflmo17244f05a1
Seq. No.	286327
Contig ID	185405_1.R1011
5'-most EST	uC-zmflmo17391a12a1
Seq. No.	286328
Contig ID	185419_1.R1011
5'-most EST	uC-zmromo17008f02a1
Seq. No.	286329
Contig ID	185481_1.R1011
5'-most EST	uC-zmflmo17272d01a1
Seq. No.	286330
Contig ID	185533_1.R1011
5'-most EST	uC-zmflmo17206f07a1
Seq. No.	286331
Contig ID	185627_1.R1011
5'-most EST	uC-zmflmo17209h08a1
Seq. No.	286332
Contig ID	185640_1.R1011
5'-most EST	uC-zmflmo17210a12a1
Seq. No.	286333
Contig ID	185654_1.R1011
5'-most EST	uC-zmflmo17210c04a1
Seq. No.	286334
Contig ID	185667_1.R1011
5'-most EST	uC-zmflmo17210d07a1
Seq. No.	286335
Contig ID	185668_1.R1011
5'-most EST	uC-zmflmo17210d08a1
Seq. No.	286336
Contig ID	185682 1.R1011
5'-most EST	uC-zmflmo17210e12a1
Seq. No.	286337
Contig ID	185703_1.R1011



5'-most EST uC-zmflmo17210h02a1

Seq. No. 286338

Contig ID 185760_1.R1011 5'-most EST uC-zmflmo17391h04a1

Seq. No. 286339

Contig ID 185779_1.R1011 5'-most EST xdb700341323.h1

Seq. No. 286340

Contig ID 185786_1.R1011 5'-most EST uC-zmflmo17264d08a2

Seq. No. 286341

Contig ID 185799_1.R1011 5'-most EST uC-zmflmo17333d03a1

Seq. No. 286342

Contig ID 185808_1.R1011 5'-most EST uC-zmflmo17326e08a1

Seq. No. 286343

Contig ID 185842_1.R1011 5'-most EST uC-zmflmo17212f09a1

Seq. No. 286344

Contig ID 185866_1.R1011 5'-most EST uC-zmflmo17311d01a1

Method BLASTX
NCBI GI g4249382
BLAST score 202
E value 1.0e-15
Match length 57
% identity 63

NCBI Description (AC005966) Strong similarity to gi 3337350 F13P17.3

putative permease from Arabidopsis thaliana BAC

gb_AC004481. [Arabidopsis thaliana]

Seq. No. 286345

Contig ID 185937_1.R1011 5'-most EST uC-zmflmo17215c03a1

Seq. No. 286346

Contig ID 185939_1.R1011 5'-most EST wyr700240529.h1

Seq. No. 286347

Contig ID 185945_1.R1011 5'-most EST uC~zmflmo17215c12a1

Seq. No. 286348

Contig ID 185992_1.R1011 5'-most EST uC-zmflmo17217a03a1

Seq. No. 286349

Contig ID 186002_1.R1011



```
uC-zmromo17113d12a1
5'-most EST
                   286350
Seq. No.
                   186007 1.R1011
Contig ID
                   nbm700468703.hl
5'-most EST
                   286351
Seq. No.
                   186037 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17218a01a1
                   286352
Seq. No.
                   186104_1.R1011
Contig ID
                   uC-zmf\overline{l}mo17219a01a1
5'-most EST
                   BLASTX
Method
                   g3941289
NCBI GI
                   160
BLAST score
                   6.0e-11
E value
                   36
Match length
                   72
% identity
NCBI Description (AF018093) similarity to SCAMP37 [Pisum sativum]
                   286353
Seq. No.
                   186110 1.R1011
Contig ID
                   uC-zmflmo17219a09a1
5'-most EST
                   286354
Seq. No.
                   186122 1.R1011
Contig ID
                   xsy700\overline{2}08122.h1
5'-most EST
                   286355
Seq. No.
                   186125 1.R1011
Contig ID
                   uC-zmflmo17219c09a1
5'-most EST
                   286356
Seq. No.
                   186176 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17220a05a1
                   286357
Seq. No.
                   186260 1.R1011
Contig ID
                   uC-zmflmo17394e11a1
5'-most EST
                   BLASTX
Method
                   g2262103
NCBI GI
                   370
BLAST score
                   3.0e - 35
E value
                   103
Match length
% identity
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
Seq. No.
                    286358
                    186285 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17221e07a1
                   BLASTX
Method
NCBI GI
                    g3219815
                    183
BLAST score
                    2.0e-13
E value
```

39876

67

55

Match length

% identity



MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT NCBI Description TIM22 HOMOLOG >gi 2104453 emb_CAB08780_ (Z95397) unknown [Schizosaccharomyces pombe]

286359 Seq. No.

186311 1.R1011 Contig ID $uC-zmf\overline{l}mo17221h01a1$ 5'-most EST

286360 Seq. No.

186336 1.R1011 Contig ID uC-zmflmo17222b08a1 5'-most EST

286361 Seq. No.

186338 1.R1011 Contig ID uC-zmflmo17222b11a1 5'-most EST

286362 Seq. No.

186404 1.R1011 Contig ID uC-zmrob73061d05a1 5'-most EST

286363 Seq. No.

186415 1.R1011 Contig ID uC-zmflmo17223b10a1 5'-most EST

286364 Seq. No.

186454 1.R1011 Contig ID $uC-zmf\overline{l}mo17396d01a1$ 5'-most EST

BLASTX Method q2980806 NCBI GI 281 BLAST score 9.0e-25E value 69 Match length

74 % identity

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

286365 Seq. No.

Contig ID 186459 1.R1011 cyk700048263.fl 5'-most EST

286366 Seq. No.

186485 1.R1011 Contig ID uC-zmflmo17228c12a1 5'-most EST

BLASTN Method g1653477 NCBI GI 459 BLAST score 0.0e + 00E value Match length 479 99 % identity

NCBI Description Synechocystis sp. PCC6803 complete genome, 16/27,

1991550-2137258

286367 Seq. No.

186506 1.R1011 Contia ID $uC-zmf\overline{l}mo17341b02a1$ 5'-most EST

286368 Seq. No.

186562 1.R1011 Contig ID



```
uC-zmflmo17225g10a1
5'-most EST
Method
                  BLASTX
                  g1652644
NCBI GI
BLAST score
                  445
E value
                  4.0e-44
Match length
                  84
% identity
NCBI Description (D90907) hypothetical protein [Synechocystis sp.]
                  286369
Seq. No.
Contig ID
                  186571 1.R1011
5'-most EST
                  uC-zmflmo17225g07a1
Method
                  BLASTN
NCBI GI
                  g1652844
BLAST score
                  395
E value
                  0.0e + 00
                   490
Match length
% identity
                  94
NCBI Description Synechocystis sp. PCC6803 complete genome, 11/27,
                  1311235-1430418
                  286370
Seq. No.
                  186576 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17231a11a1
Method
                  BLASTX
                  g1001311
NCBI GI
BLAST score
                  1055
E value
                  1.0e-138
                  249
Match length
% identity
NCBI Description (D64006) hypothetical protein [Synechocystis sp.]
                   286371
Seq. No.
                  186596 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17226f06a1
                  286372
Seq. No.
                  186608 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17226d02a1
                  BLASTN
Method
                  g1001396
NCBI GI
BLAST score
                  461
E value
                   0.0e+00
Match length
                   477
% identity
NCBI Description Synechocystis sp. PCC6803 complete genome, 18/27,
                  2267260-2392728
Seq. No.
                  286373
                  186613 1.R1011
Contig ID
                  uC-zmflmo17226d10a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g132642
BLAST score
                   668
                  3.0e-70
E value
Match length
                  135
% identity
                   99
```

NCBI Description



```
NCBI Description 50S RIBOSOMAL PROTEIN L10 >gi_79728_pir__S13068 ribosomal
                   protein L10 - Synechocystis sp. (PCC 6803)
                   >gi_47475_emb_CAA37317_ (X53178) rpl10 (AA 1-173) [Synechocystis PCC6803] >gi_1652496_dbj_BAA17417_ (D90906)
                    50S ribosomal protein L10 [Synechocystis sp.]
                   >gi_227224_prf__1617100A ribosomal protein L10
                    [Synechocystis sp.]
                    286374
Sea. No.
                    186633 1.R1011
Contig ID
                    uC-zmf\overline{l}mo17226f12a1
5'-most EST
                    BLASTX
Method
                    q1652948
NCBI GI
                    1059
BLAST score
                    1.0e-116
E value
                    199
Match length
                    98
% identity
                   (D90909) hypothetical protein [Synechocystis sp.]
NCBI Description
                    286375
Seq. No.
                    186647 1.R1011
Contig ID
                    uC-zmflmo17231h04a1
5'-most EST
                    BLASTN
Method
                    g1651650
NCBI GI
                    417
BLAST score
                    0.0e + 00
E value
                    417
Match length
                    100
% identity
NCBI Description Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
                    286376
Seq. No.
                    186698 1.R1011
Contig ID
                    uC-zmflmo17227e12a1
 5'-most EST
                    BLASTX
Method
                    q1651783
NCBI GI
                    378
 BLAST score
 E value
                    3.0e-36
 Match length
                    74
                    97
 % identity
 NCBI Description (D90900) arginase [Synechocystis sp.]
                    286377
 Seq. No.
                    186727 1.R1011
 Contig ID
                    uC-zmflmo17230e08a1
 5'-most EST
                     286378
 Seq. No.
                     186738 1.R1011
 Contig ID
                    uC-zmf\overline{1}mo17228c05a1
 5'-most EST
                    BLASTX
 Method
                     q1001660
 NCBI GI
                     709
 BLAST score
                     6.0e-75
 E value
                     159
 Match length
                     90
 % identity
                    (D64002) uroporphyrin-III C-methyltransferase
```

[Synechocystis sp.]



Seq. No. 286379

Contig ID 186740_1.R1011 5'-most EST uC-zmflmo17228c08a1

Method BLASTX
NCBI GI g1001708
BLAST score 675
E value 1.0e-76
Match length 147
% identity 100

NCBI Description (D64004) NifS [Synechocystis sp.]

Seq. No. 286380

Contig ID 186741_1.R1011 5'-most EST uC-zmflmo17228c09a1

Seq. No. 286381

Contig ID 186753_1.R1011 5'-most EST uC-zmflmo17228d12a1

Method BLASTN
NCBI GI g1652127
BLAST score 256
E value 1.0e-142
Match length 264
% identity 99

NCBI Description Synechocystis sp. PCC6803 complete genome, 5/27,

524346-630554

Seq. No. 286382

Contig ID 186768_1.R1011 5'-most EST uC-zmflmo17228f10a1

Method BLASTX
NCBI GI g2492510
BLAST score 923
E value 1.0e-100
Match length 184
% identity 99

NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG 1

>gi_1001602_dbj_BAA10230_ (D64000) cell division protein

FtsH [Synechocystis sp.]

Seq. No. 286383

Contig ID 186769_1.R1011 5'-most EST uC-zmflmo17228f11a1

Seq. No. 286384

Contig ID 186770_1.R1011 5'-most EST uC-zmflmo17228f12a1

Seq. No. 286385

Contig ID 186845_1.R1011 5'-most EST uC-zmflmo17255f07a1

Seq. No. 286386

Contig ID 186932_1.R1011 5'-most EST uC-zmflmo17231c08a1

Method BLASTX NCBI GI g1651951



```
BLAST score
                   635
                   1.0e-66
E value
                   127
Match length
                   97
% identity
                   (D90901) hypothetical protein [Synechocystis sp.]
NCBI Description
                   286387
Seq. No.
                   186945 1.R1011
Contig ID
                   uC-zmf\overline{l}mo17231e03a1
5'-most EST
                   BLASTX
Method
                   g2506463
NCBI GI
BLAST score
                   754
                   2.0e-80
E value
                   151
Match length
                   97
% identity
                   FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE 2 (FD-GOGAT)
NCBI Description
                   >gi_1100774_dbj_BAA11379_ (D78371) ferredoxin-dependent
                   glutamate synthase [Synechocystis sp.]
                   >gi_1653782_dbj_BAA18693_ (D90916) ferredoxin-dependent
                   glutamate synthase [Synechocystis sp.]
                   286388
Seq. No.
                   186952 1.R1011
Contig ID
                   uC-zmf\overline{l}mo17231e12a1
5'-most EST
                   BLASTX
Method
                   q3122377
NCBI GI
                   491
BLAST score
                   9.0e-50
E value
                   87
Match length
                   100
% identity
                   PROBABLE LIPOATE-PROTEIN LIGASE B (LIPOATE BIOSYNTHESIS
NCBI Description
                   PROTEIN B) >gi_1653711_dbj_BAA18623_ (D90915) LipB
                   [Synechocystis sp.]
                   286389
Seq. No.
                   186954_1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17231f02a1
                   BLASTX
Method
                   a2500624
NCBI GI
                   645
BLAST score
                   1.0e-67
E value
                   135
Match length
% identity
                   DNA-DIRECTED RNA POLYMERASE DELTA CHAIN
NCBI Description
                   >gi_1652442_dbj_BAA17364_ (D90905) RNA polymerase beta
                   prime subunit [Synechocystis sp.]
                    286390
 Seq. No.
                    186964 1.R1011
 Contig ID
                    uC-zmflmo17231g06a1
 5'-most EST
                    BLASTX
Method
                    q1653894
NCBI GI
                    850
 BLAST score
                    1.0e-91
 E value
                    169
Match length
                    96
 % identity
 NCBI Description (D90917) antiviral protein [Synechocystis sp.]
```



```
286391
Seq. No.
                  186993 1.R1011
Contig ID
                  uC-zmfImo17233c01a1
5'-most EST
                  BLASTX
Method
                  q4539452
NCBI GI
                  723
BLAST score
                  1.0e-76
E value
Match length
                  182
                   75
% identity
                   (AL049500) putative phosphoribosylanthranilate transferase
NCBI Description
                   [Arabidopsis thaliana]
                   286392
Seq. No.
                   187010 1.R1011
Contig ID
                   ymt700222088.h1
5'-most EST
                   286393
Seq. No.
                   187018 1.R1011
Contig ID
                   uC-zmflmo17233e10a1
5'-most EST
                   286394
Seq. No.
                   187045 1.R1011
Contig ID
                   uC-zmflmo17233h07a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4454465
                   323
BLAST score
                   1.0e-29
E value
                   169
Match length
% identity
                   37
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
                   286395
Seq. No.
                   187115_1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17234g08a1
                   286396
Seq. No.
                   187135 1.R1011
Contig ID
                   qw1700613631.h1
5'-most EST
                   286397
Seq. No.
                   187148 1.R1011
Contig ID
                   hvj700619166.hl
5'-most EST
                   286398
Seq. No.
                   187156 1.R1011
 Contig ID
                   uC-zmflmo17236e01a1
 5'-most EST
                   286399
 Seq. No.
                   187187 1.R1011
```

Contig ID uC-zmflmo17334h09a1 5'-most EST

286400 Seq. No.

187188 1.R1011 Contig ID 5'-most EST uC-zmflmo17238a04a1

286401 Seq. No.



```
187192 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17238a10a1
                  BLASTX
Method
                  q4335739
NCBI GI
                   216
BLAST score
                  2.0e-17
E value
                  69
Match length
                   59
% identity
NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]
                   286402
Seq. No.
                   187205 1.R1011
Contig ID
                   uC-zmflmo17403c10a1
5'-most EST
Seq. No.
                   286403
                   187302 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17239q01a1
Seq. No.
                   286404
                   187344 1.R1011
Contig ID
                   uC-zmflmo17368d07a1
5'-most EST
                   286405
Seq. No.
                   187376 1.R1011
Contig ID
                   zla700\overline{3}80628.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                   g4510387
BLAST score
                   176
                   9.0e-13
E value
                   50
Match length
% identity
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
                   286406
Seq. No.
                   187393 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17241a08b1
                   286407
Seq. No.
                   187400 2.R1011
Contig ID
                   pmx700086424.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4164149
BLAST score
                   490
                   2.0e-49
E value
Match length
                   166
% identity
                   65
NCBI Description (AB014056) iron-superoxide dismutase [Oryza sativa]
Seq. No.
                   286408
                   187403 1.R1011
Contig ID
5'-most EST
                   xsy700211344.h1
Seq. No.
                   286409
```

Contig ID 187492_1.R1011 5'-most EST uC-zmflmo17241h12b1

Method BLASTX NCBI GI g4467137



BLAST score 248 E value 4.0e-21 Match length 99 % identity 53

NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Šeq. No. 286410

Contig ID 187497_1.R1011 5'-most EST uC~zmflmo17243a06a1

Seq. No. 286411

Contig ID 187498 1.R1011 5'-most EST uC-zmflmo17243a08a1

Seq. No. 286412

Contig ID 187502_1.R1011 5'-most EST uer700581002.h1

Seq. No. 286413

Contig ID 187578_1.R1011 5'-most EST ceu700425717.h2

Seq. No. 286414

Contig ID 187590_1.R1011 5'-most EST uC-zmflmo17244f06a1

Seq. No. 286415

Contig ID 187591_1.R1011 5'-most EST uC-zmflmo17244f07a1

Seq. No. 286416

Contig ID 187678_1.R1011 5'-most EST uC-zmflmo17247b06a1

Method BLASTX
NCBI GI g2244876
BLAST score 488
E value 3.0e-49
Match length 154
% identity 66

NCBI Description (Z97338) hypothetical protein [Arabidopsis thaliana]

Seq. No. 286417

Contig ID 187753 1.R1011 5'-most EST uC-zmflmo17248e06a1

Seq. No. 286418

Contig ID 187817_1.R1011 5'-most EST uC-zmflmo17310c08a1

Seq. No. 286419

Contig ID 187887_1.R1011 5'-most EST uC-zmflmo17250e01a1

Seq. No. 286420

Contig ID 188027_1.R1011 5'-most EST uC-zmflmo17253a04a1

Method BLASTN



NCBI GI g1652492 BLAST score 327 0.0e + 00E value 395 Match length 96 % identity NCBI Description Synechocystis sp. PCC6803 complete genome, 8/27, 920916-1056466 Seq. No. 286421 Contig ID 188036 1.R1011 5'-most EST uC-zmflmo17253b07a1 Method BLASTX g1001157 708

NCBI GI g1001157
BLAST score 708
E value 6.0e-75
Match length 132
% identity 98

NCBI Description (D64001) hypothetical protein [Synechocystis sp.]

Seq. No. 286422

Contig ID 188061_1.R1011 5'-most EST uC-zmflmo17253f03a1

Seq. No. 286423

Contig ID 188067_1.R1011 5'-most EST uC-zmflmo17253g04a1

Method BLASTN
NCBI GI g1651650
BLAST score 480
E value 0.0e+00
Match length 492
% identity 100

NCBI Description Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859

Seq. No. 286424

Contig ID 188078_1.R1011 5'-most EST uC-zmflmo17255a04a1

Method BLASTN
NCBI GI g1652360
BLAST score 386
E value 0.0e+00
Match length 410
% identity 99

NCBI Description Synechocystis sp. PCC6803 complete genome, 7/27,

781449-920915

Seq. No. 286425

Contig ID 188137_1.R1011 5'-most EST uC-zmflmo17256c06b1

Seq. No. 286426

Contig ID 188202_1.R1011 5'-most EST uC-zmflmo17258f01a1

Method BLASTX
NCBI GI g3386605
BLAST score 219
E value 1.0e-17



58 Match length % identity

NCBI Description

(AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No. Contig ID 5'-most EST 286427

188224 1.R1011 uC-zmflmo17260c01a1

Seq. No. Contig ID 5'-most EST 286428

188235_1.R1011 uC-zmf1mo17377b02a1

Seq. No. Contig ID 5'-most EST 286429

188256_1.R1011 uC-zmflmo17260f10a1

Seq. No. Contig ID 5'-most EST 286430

188388 1.R1011 $uC-zmf\overline{l}mo17263g04a2$

Seq. No. Contig ID 5'-most EST 286431

188538_1.R1011 uC-zmfImo17264h12a1

Seq. No. Contig ID 5'-most EST 286432

188542 1.R1011 uC-zmfImo17265a03a2

Seq. No. Contig ID 5'-most EST 286433

188544 1.R1011 uC-zmflmo17265a05a1

Seq. No. Contig ID 5'-most EST 286434

188558 1.R1011 uC-zmflmo17279g12a1

Seq. No. Contig ID 5'-most EST 286435

188645 1.R1011 uC-zmflmo17265g09a2

Seq. No. Contig ID 5'-most EST 286436

188669 1.R1011 uC-zmflmo17426c04a1

Seq. No. Contig ID 5'-most EST 286437

188709 1.R1011 uC-zmflmo17266g06a1

Seq. No. Contig ID 5'-most EST 286438

188822 1.R1011 uC-zmflmo17268g12a1

Seq. No. Contig ID 5'-most EST 286439

188841 1.R1011 uC-zmrob73059c05a1

Seq. No.

286440

BLAST score

Match length

E value

487

133

3.0e-49



```
Contig ID
                  188850 1.R1011
5'-most EST
                  uC-zmflmo17269d11a1
Seq. No.
                  286441
                  188886 1.R1011
Contig ID
                  uC-zmflmo17270b12a1
5'-most EST
Method
                  BLASTX
                  g4455302
NCBI GI
                  511
BLAST score
                  1.0e-51
E value
Match length
                  120
% identity
                  79
NCBI Description (AL035528) putative protein [Arabidopsis thaliana]
                  286442
Seq. No.
                  188886 2.R1011
Contig ID
5'-most EST
                  ceu700427608.hl
                  BLASTX
Method
                  g4455302
NCBI GI
BLAST score
                  380
                  6.0e-37
E value
Match length
                  90
% identity
                  74
NCBI Description (AL035528) putative protein [Arabidopsis thaliana]
Seq. No.
                  286443
Contig ID
                  188920 1.R1011
5'-most EST
                  uC-zmflmo17394b10a1
Seq. No.
                  286444
                  189010 1.R1011
Contig ID
                  uer700\overline{5}82574.h1
5'-most EST
                  286445
Seq. No.
                  189034 1.R1011
Contig ID
5'-most EST
                  uC-zmfImo17274a02a1
Seq. No.
                  286446
Contig ID
                  189129 1.R1011
5'-most EST
                  uC-zmflmo17275h02a1
Seq. No.
                  286447
Contig ID
                  189192 1.R1011
5'-most EST
                  uC-zmflmo17278a07a1
                  286448
Seq. No.
Contig ID
                  189198 1.R1011
5'-most EST
                  rvt700550576.h1
                  286449
Seq. No.
Contig ID
                  189232 1.R1011
5'-most EST
                  uC-zmflmo17279d01a1
Method
                  BLASTX
NCBI GI
                  q136632
```



% identity NCBI Description

UBIQUITIN-ACTIVATING ENZYME E1 1 >gi_100841_pir__A38373

ubiquitin--protein ligase (EC 6.3.2.19) E1 - wheat

>gi_285451_pir__A42873 ubiquitin-activating enzyme E1, UBA1
- Wheat >gi_170780 (M55604) ubiquitin-activating enzyme E1

[Triticum aestivum]

Seq. No. 286450

Contig ID 189241_1.R1011 5'-most EST uC-zmflmo17279e05a1

Seq. No. 286451

Contig ID 189253_1.R1011 5'-most EST uC-zmflmo17279g05a1

Seq. No. 286452

Contig ID 189308_1.R1011 5'-most EST cjh700195290.h1

Seq. No. 286453

Contig ID 189368_1.R1011 5'-most EST ymt700221196.h1

Method BLASTX
NCBI GI g3132825
BLAST score 819
E value 5.0e-88
Match length 156
% identity 99

NCBI Description (AF063403) putative cytosine-5 DNA methyltransferase [Zea

mays]

Seq. No. 286454

Contig ID 189387_1.R1011 5'-most EST uC-zmflmo17281f10b1

Seq. No. 286455

Contig ID 189396 1.R1011 5'-most EST uC-zmflmo17281g06b1

Seq. No. 286456

Contig ID 189511_1.R1011 5'-most EST uC-zmflmo17286e01a1

Seq. No. 286457

Contig ID 189549 1.R1011 5'-most EST uC-zmflmo17287a11a1

Seq. No. 286458

Contig ID 189584_1.R1011 5'-most EST uC-zmflmo17287e12a1

Seq. No. 286459

Contig ID 189585_1.R1011 5'-most EST uC-zmflmo17287f01a1

Seq. No. 286460

Contig ID 189618 1.R1011



dyk700106613.hl 5'-most EST 286461 Seq. No. 189647 1.R1011 Contig ID uC-zmflmo17289d07a1 5'-most EST 286462 Seq. No. 189727 1.R1011 Contig ID hvj700620945.hl 5'-most EST 286463 Seq. No. 189801_1.R1011 Contig ID uC-zmflmo17344a01a15'-most EST 286464 Seq. No. 189814 1.R1011 Contig ID uC-zmflmo17291g01a1 5'-most EST 286465 Seq. No. 189858 1.R1011 Contig ID uC-zmf1mo17292c04a15'-most EST 286466 Seq. No. 189896_1.R1011 Contig ID $uC-zmf\overline{l}mo17426c02a1$ 5'-most EST 286467 Seq. No. 189925 1.R1011 Contig ID uC-zmfImo17300c02a15'-most EST 286468 Seq. No. 189937 1.R1011 Contig ID uC-zmflmo17300d10a1 5'-most EST 286469 Seq. No. 189952_1.R1011 Contig ID uC-zmflmo17300f05a1 5'-most EST 286470 Seq. No. 190078 1.R1011 Contig ID uC-zmflmo17302g02a1 5'-most EST 286471 Seq. No. 190100 1.R1011 Contig ID xsy700211019.hl 5'-most EST 286472 Seq. No. 190110 1.R1011 Contig ID cat700021583.rl 5'-most EST BLASTX Method

q2982283 NCBI GI 158 BLAST score 2.0e-10 E value 44 Match length 66

% identity

NCBI Description (AF051226) PREG-like protein [Picea mariana]



Seq. No. 286473

Contig ID 190115_1.R1011 5'-most EST xmt700265460.h1

Seq. No. 286474

Contig ID 190195_1.R1011 5'-most EST uC-zmflmo17305d07a1

Seq. No. 286475

Contig ID 190224_1.R1011 5'-most EST uC-zmflmo17305g04a1

Seq. No. 286476

Contig ID 190239_1.R1011 5'-most EST cat700018620.r1

Seq. No. 286477

Contig ID 190253_1.R1011 5'-most EST uC-zmflmo17306b02a1

Method BLASTX
NCBI GI g1076288
BLAST score 323
E value 7.0e-30
Match length 83
% identity 69

NCBI Description amino acid permease AAP3 - Arabidopsis thaliana

Seq. No. 286478

Contig ID 190339_1.R1011 5'-most EST uC-zmflmo17365b07a1

Seq. No. 286479

Contig ID 190435_1.R1011 5'-most EST uC-zmflmo17311f02a1

Seq. No. 286480

Contig ID 190508_1.R1011 5'-most EST uC-zmflmo17315a10a1

Seq. No. 286481

Contig ID 190526 1.R1011 5'-most EST gct701174396.h1

Seq. No. 286482

Contig ID 190618_1.R1011 5'-most EST gct701175363.h1

Seq. No. 286483

Contig ID 190643_1.R1011 5'-most EST rvt700551909.h1

Seq. No. 286484

Contig ID 190644_1.R1011 5'-most EST uC-zmflmo17317c03a1

Seq. No. 286485

Contig ID 190654_1.R1011



5'-most EST uC-zmflmo17317d01a1

Seq. No. 286486

Contig ID 190739_1.R1011 5'-most EST uC-zmflmo17318e08a1

Seq. No. 286487

Contig ID 190749_1.R1011 5'-most EST uC-zmflmo17318f07a1

Seq. No. 286488

Contig ID 190793_1.R1011 5'-most EST uC-zmflmo17319b11a1

Seq. No. 286489

Contig ID 190831_1.R1011 5'-most EST uC-zmrob73062f02a1

Method BLASTX
NCBI GI g2580499
BLAST score 328
E value 3.0e-30
Match length 76
% identity 80

NCBI Description (U67186) NADPH: ferrihemoprotein oxidoreductase

[Eschscholzia californica]

Seq. No. 286490

Contig ID 190834_1.R1011 5'-most EST uC-zmflmo17319g01a1

Seq. No. 286491

Contig ID 190878_1.R1011 5'-most EST uC-zmflmo17320c05a1

Seq. No. 286492

Contig ID 190907_1.R1011 5'-most EST uC-zmflmo17320f02a1

Seq. No. 286493

Contig ID 190921_1.R1011 5'-most EST uC-zmflmo17320g07a1

Seq. No. 286494

Contig ID 190983_1.R1011 5'-most EST uC-zmflmo17321e09a1

Seq. No. 286495

Contig ID 190986_1.R1011 5'-most EST uC-zmflmo17321e12a1

Seq. No. 286496

Contig ID 191014_1.R1011 5'-most EST uC-zmromo17107a11a1

Seq. No. 286497

Contig ID 191049_1.R1011 5'-most EST uC-zmflmo17322e01a1



Seq. No. 286498

Contig ID 191051_1.R1011 5'-most EST gct701173428.h2

Seq. No. 286499

Contig ID 191085_1.R1011 5'-most EST uC-zmrob73057h03a1

Seq. No. 286500

Contig ID 191130_1.R1011 5'-most EST uC-zmflmo17323e08a1

Method BLASTN
NCBI GI 9498772
BLAST score 43
E value 5.0e-15
Match length 79
% identity 89

NCBI Description Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein

Seq. No. 286501

Contig ID 191138_1.R1011 5'-most EST ceu700431789.h1

Seq. No. 286502

Contig ID 191208_1.R1011 5'-most EST ypc700803983.h1

Seq. No. 286503

Contig ID 191255_1.R1011 5'-most EST cat700020331.r1

Seq. No. 286504

Contig ID 191258_1.R1011 5'-most EST ceu700433844.h1

Seq. No. 286505

Contig ID 191259_1.R1011 5'-most EST uC-zmflmo17326b05a1

Method BLASTX
NCBI GI g2832643
BLAST score 292
E value 2.0e-26
Match length 117
% identity 50

NCBI Description (AL021710) hypothetical protein [Arabidopsis thaliana]

Seq. No. 286506

Contig ID 191339_1.R1011 5'-most EST uC-zmflmo17327d04a1

Seq. No. 286507

Contig ID 191359_1.R1011 5'-most EST uC-zmflmo17327f04b1

Seq. No. 286508

Contig ID 191472_1.R1011



```
5'-most EST
                  uC-zmflmo17329a08a1
                  BLASTX
Method
                  g1491615
NCBI GI
                  184
BLAST score
                   2.0e-13
E value
                   117
Match length
                   38
% identity
                  (X99923) male sterility 2-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   286509
Seq. No.
                   191487_1.R1011
Contig ID
                   nbm700465055.h1
5'-most EST
                   286510
Seq. No.
                   191541 1.R1011
Contig ID
                   uC-zmflmo17329h09a1
5'-most EST
                   286511
Seq. No.
                   191569 1.R1011
Contig ID
                   uC-zmflmo17330c07a1
5'-most EST
                   286512
Seq. No.
                   191573 1.R1011
Contig ID
                   uC-zmf\overline{l}mo17330c11a1
5'-most EST
                   286513
Seq. No.
                   191647 1.R1011
Contig ID
                   uC-zmflmo17331d05a1
5'-most EST
                   286514
Seq. No.
                   191721 1.R1011
Contig ID
                   uC-zmfImo17332e02a1
5'-most EST
                   286515
Seq. No.
                   191736 1.R1011
Contig ID
                   uC-zmf\overline{1}mo17332f07a1
5'-most EST
                   BLASTX
Method
                   q3914486
NCBI GI
                   176
BLAST score
                   9.0e-13
E value
Match length
                   80
                   42
 % identity
NCBI Description PUTATIVE PSEUDOURIDYLATE SYNTHASE (PSEUDOURIDINE SYNTHASE)
                   >gi_2347206 (AC002338) pseudouridine synthase isolog
                    [Arabidopsis thaliana]
 Seq. No.
                    286516
                    191845 1.R1011
 Contig ID
                   uC-zmflmo17334c02a1
 5'-most EST
                    286517
 Seq. No.
                    191869 1.R1011
 Contig ID
                    uC-zmflmo17334e06a1
 5'-most EST
```

39893

286518

191956 1.R1011

Seq. No.

Contig ID



5'-most EST pmx700089967.h1

Method BLASTX
NCBI GI g228215
BLAST score 214
E value 2.0e-17
Match length 43
% identity 100

NCBI Description dihydrodipicolinate synthase [Zea mays]

Seq. No. 286519

Contig ID 192001_1.R1011 5'-most EST nbm700467537.h1

Seq. No. 286520

Contig ID 192037_1.R1011 5'-most EST uC-zmflmo17336f04a1

Seq. No. 286521

Contig ID 192055_1.R1011 5'-most EST uC-zmflmo17336g12a1

Seq. No. 286522

Contig ID 192075_1.R1011 5'-most EST uC-zmflmo17337b03a1

Seq. No. 286523

Contig ID 192155_1.R1011 5'-most EST uC-zmflmo17338c08b1

Seq. No. 286524

Contig ID 192171_1.R1011 5'-most EST uC-zmflmo17338g08b1

Seq. No. 286525

Contig ID 192207_1.R1011 5'-most EST uC-zmflmo17339d04a1

Seq. No. 286526

Contig ID 192212_1.R1011 5'-most EST uC-zmflmo17339d10a1

Seq. No. 286527

Contig ID 192216_1.R1011 5'-most EST uC-zmflmo17339e03a1

Seq. No. 286528

Contig ID 192237_1.R1011 5'-most EST uC-zmflmo17399b11a1

Method BLASTX
NCBI GI g1352469
BLAST score 522
E value 4.0e-53
Match length 105
% identity 97

NCBI Description BETA-FRUCTOFURANOSIDASE, CELL WALL ISOZYME PRECURSOR (SUCROSE-6-PHOSPHATE HYDROLASE) (INVERTASE) >gi 736359

(U17695) invertase [Zea mays] >gi_1582380_prf__2118364A



cell wall invertase [Zea mays]

uC-zmflmo17341g08a1

 Seq. No.
 286529

 Contig ID
 192244_1.R1011

 5'-most EST
 uC-zmrob73064d10a1

 Seq. No.
 286530

 Contig ID
 192393_1.R1011

 Seq. No.
 286531

 Contig ID
 192399_1.R1011

 5'-most EST
 uC-zmflmo17341h02a1

Method BLASTX
NCBI GI g3820648
BLAST score 147
E value 2.0e-09
Match length 48
% identity 58

5'-most EST

NCBI Description (Y12636) allene oxide synthase [Arabidopsis thaliana]

 Seq. No.
 286532

 Contig ID
 192424_1.R1011

 5'-most EST
 uC-zmflmo17342b09a1

 Seq. No.
 286533

 Contig ID
 192482_1.R1011

 5'-most EST
 nbm700475986.h1

 Seq. No.
 286535

 Contig ID
 192495_1.R1011

 5'-most EST
 uC-zmflmo17343c12a1

Seq. No. 286537
Contig ID 192664_1.R1011
5'-most EST uC-zmflmo17351e12a1
Method BLASTX

NCBI GI g2190419
BLAST score 803
E value 8.0e-86
Match length 179
% identity 82

NCBI Description (Y13632) dem [Lycopersicon esculentum]

 Seq. No.
 286538

 Contig ID
 192698_1.R1011

 5'-most EST
 uC-zmflmo17352c11a1

Seq. No. 286539



Contig ID 192706_1.R1011 5'-most EST uC-zmflmo17352f05a1

Method BLASTN
NCBI GI g3452302
BLAST score 41
E value 1.0e-13

E value 1.0e
Match length 189
% identity 82

NCBI Description Zea mays retrotransposon Milt 3' LTR, partial sequence

Seq. No. 286540

Contig ID 192736_1.R1011 5'-most EST uC-zmflmo17353e10a1

Seq. No. 286541

Contig ID 192770_1.R1011 5'-most EST uC-zmflmo17354b05a1

Seq. No. 286542

Contig ID 192812_1.R1011 5'-most EST uC-zmflmo17354f10a1

Seq. No. 286543

Contig ID 192833_1.R1011 5'-most EST uC-zmflmo17355a06a1

Seq. No. 286544

Contig ID 192840_1.R1011 5'-most EST uC-zmflmo17355b08a1

Method BLASTX
NCBI GI g2749982
BLAST score 263
E value 8.0e-23
Match length 155
% identity 40

NCBI Description (AF036705) Similar to phytoene desaturase; coded for by C.

elegans cDNA CEESX74F; coded for by C. elegans cDNA yk303f4.3; coded for by C. elegans cDNA yk257d4.3; coded for by C. elegans cDNA yk303f4.5; coded for by C. elegans

cDNA yk257d4.5;

Seq. No. 286545

Contig ID 192877_1.R1011 5'-most EST cyk700051284.f1

Method BLASTX
NCBI GI g2832661
BLAST score 279
E value 5.0e-25
Match length 89
% identity 70

NCBI Description (AL021710) pherophorin - like protein [Arabidopsis

thaliana]

Seq. No. 286546

Contig ID 192893_1.R1011 5'-most EST uC-zmflmo17355h11a1



Seq. No. 286547

Contig ID 192897_1.R1011 5'-most EST uC-zmflmo17356e02a1

Seq. No. 286548

Contig ID 192917 1.R1011 5'-most EST tfd700574462.h1

Seq. No. 286549

Contig ID 192990_1.R1011 5'-most EST uC-zmflmo17357d10a1

Seq. No. 286550

Contig ID 193010_1.R1011 5'-most EST hbs701185306.h1

Seq. No. 286551

Contig ID 193102 1.R1011 5'-most EST uC-zmflmo17360a09a1

Seq. No. 286552

Contig ID 193156_1.R1011 5'-most EST uC-zmflmo17366a02a1

Seq. No. 286553

Contig ID 193157_1.R1011 5'-most EST uC-zmromo17010b01a1

Method BLASTX
NCBI GI g2131352
BLAST score 197
E value 3.0e-24
Match length 168
% identity 37

NCBI Description hypothetical protein YDL166c - yeast (Saccharomyces

cerevisiae) >gi 1061273 emb CAA91580 (Z67750) putative

protein [Saccharomyces cerevisiae]

>gi_1431264_emb_CAA98740_ (Z74214) ORF YDL166c

[Saccharomyces cerevisiae]

Seq. No. 286554

Contig ID 193160_1.R1011 5'-most EST clt700043889.f1

Seq. No. 286555

Contig ID 193168_1.R1011 5'-most EST dyk700102661.h1

Seq. No. 286556

Contig ID 193203 1.R1011 5'-most EST ntr700075532.h1

Seq. No. 286557

Contig ID 193230_1.R1011 5'-most EST uC-zmflmo17363f08a1

Seq. No. 286558

Contig ID 193241 1.R1011



```
uC-zmflmo17363d05a1
5'-most EST
                   286559
Seq. No.
                   193340 1.R1011
Contig ID
                   uC-zmf\overline{l}mo17365b08a1
5'-most EST
                   286560
Seq. No.
                   193425_1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17366f12a1
                   286561
Seq. No.
                   193432 1.R1011
Contig ID
                   uC-zmflmo17366h04a1
5'-most EST
                   286562
Seq. No.
                   193464 1.R1011
Contig ID
                   wyr700239269.hl
5'-most EST
                   286563
Seq. No.
                   193484 1.R1011
Contig ID
                   uC-zmf\overline{1}mo17367f11a1
5'-most EST
                   BLASTN
Method
                   g2586142
NCBI GI
                   41
BLAST score
                   1.0e-13
E value
                   53
Match length
                   94
% identity
                   Musa acuminata ripening-associated protein mRNA, partial
NCBI Description
                   286564
Seq. No.
                   193522 1.R1011
Contig ID
                   uC-zmflmo17368b11a1
5'-most EST
                   286565
Seq. No.
                   193599 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17370e11a1
Seq. No.
                   286566
                   193640 1.R1011
Contig ID
5'-most EST
                   uC-zmfImo17371d04a1
                   286567
Seq. No.
                    193656 1.R1011
Contig ID
                   tzu700202783.hl
5'-most EST
Seq. No.
                    286568
                    193670 1.R1011
Contig ID
                    uC-zmfImo17374a08a1
 5'-most EST
                    286569
 Seq. No.
                    193678 1.R1011
 Contig ID
```

 $uC-zmf\overline{l}mo17376e11a1$ 5'-most EST

286570 Seq. No.

193728 1.R1011 Contig ID hvj700620123.hl 5'-most EST

Method BLASTX
NCBI GI g3875462
BLAST score 144
E value 5.0e-09
Match length 68
% identity 49

NCBI Description (Z68341) Similarity to Yeast antiviral protein SKI2

(SW:SKI2_YEAST); cDNA EST EMBL:D33772 comes from this gene; cDNA EST EMBL:D36688 comes from this gene; cDNA EST

yk272d3.3 comes from this gene; cDNA EST yk272d3.5 comes

from t

Seq. No. 286571

Contig ID 193737_1.R1011 5'-most EST uC-zmflmo17375b01a1

Seq. No. 286572

Contig ID 193748_1.R1011 5'-most EST uC-zmflmo17375c12a1

Seq. No. 286573

Contig ID 193754_1.R1011 5'-most EST uC-zmflmo17375d09a1

Seq. No. 286574

Contig ID 193782_1.R1011 5'-most EST uC-zmrob73049h07a1

Seq. No. 286575

Contig ID 193848_1.R1011 5'-most EST uC-zmflmo17376g12a1

Seq. No. 286576

Contig ID 193881 1.R1011 5'-most EST pmx700090328.h1

Seq. No. 286577

Contig ID 193884_1.R1011 5'-most EST gct701174344.h1

Seq. No. 286578

Contig ID 193895_1.R1011 5'-most EST uC-zmflmo17377e08a1

Seq. No. 286579

Contig ID 193946_1.R1011 5'-most EST uC-zmflmo17380d03a1

Seq. No. 286580

Contig ID 193996_1.R1011 5'-most EST uC-zmflmo17382e11a1

Seq. No. 286581

Contig ID 194025_1.R1011 5'-most EST xyt700342842.h1

Seq. No. 286582



194034 1.R1011 Contig ID uC-zmflmo17391c10a1 5'-most EST 286583 Seq. No. 194065 1.R1011 Contig ID uC-zmflmo17391h10a1 5'-most EST 286584 Seq. No. 194070 1.R1011 Contig ID uC-zmflmo17393a04a1 5'-most EST BLASTX Method q2655098 NCBI GI 211 BLAST score 7.0e-17 E value Match length 89 49 % identity (AF023472) peptide transporter [Hordeum vulgare] NCBI Description 286585 Seq. No. 194119 1.R1011 Contig ID uC-zmfImo17425e12a15'-most EST 286586 Seq. No. 194151 1.R1011 Contig ID gct701168693.h1 5'-most EST 286587 Seq. No. 194184 1.R1011 Contig ID uC-zmflmo17394e05a1 5'-most EST 286588 Seq. No. 194195 1.R1011 Contig ID $uC-zmf\overline{1}mo17394f06a1$ 5'-most EST 286589 Seq. No. 194245 1.R1011 Contig ID uC-zmflmo17395c12a1 5'-most EST 286590 Seq. No. 194273 1.R1011 Contig ID $uC-zmf\overline{1}mo17395f12a1$ 5'-most EST Method BLASTX NCBI GI g3169180 BLAST score 341 6.0e-32E value Match length 88 % identity 68 (AC004401) putative casein kinase II catalytic subunit NCBI Description

[Arabidopsis thaliana]

286591 Seq. No.

194274 1.R1011 Contig ID xdb700337628.h1 5'-most EST

286592 Seq. No.

194390 1.R1011 Contig ID uC-zmflmo17397c02a1 5'-most EST



```
Seq. No.
                  286593
                  194427 1.R1011
Contig ID
                  uC-zmflmo17397g03a1
5'-most EST
                  286594
Seq. No.
                  194430 1.R1011
Contig ID
                  uC-zmflmo17397g06a1
5'-most EST
                  286595
Seq. No.
Contig ID
                  194483 1.R1011
5'-most EST
                  cat700017104.rl
                  286596
Seq. No.
                  194488 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17398f02a1
                  BLASTX
Method
                  g1171814
NCBI GI
                  541
BLAST score
                  2.0e-55
E value
                  128
Match length
                   87
% identity
                  NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 4, CHLOROPLAST
NCBI Description
                   >gi_902285_emb_CAA60349_ (X86563) NADH dehydrogenase ND4
                   [Zea mays]
                   286597
Seq. No.
                   194509 1.R1011
Contig ID
                  rvt700549443.h1
5'-most EST
                   286598
Seq. No.
                   194526 1.R1011
Contig ID
                   uC-zmflmo17399b04a1
5'-most EST
                   286599
Seq. No.
                   194530 1.R1011
Contig ID
                   uC-zmflmo17399b08a1
5'-most EST
                   286600
Seq. No.
                   194622 1.R1011
Contig ID
                   uC-zmromo17008a03a1
5'-most EST
Method
                   BLASTN
                   g11957
NCBI GI
                   39
BLAST score
                   2.0e-12
E value
Match length
                   43
                   98
 % identity
NCBI Description Rice complete chloroplast genome
```

Contig ID 194646_1.R1011 5'-most EST uC-zmromo17010b02a1

Seq. No. 286602

Contig ID 194725_1.R1011 5'-most EST uC-zmflmo17404a01a1



286603 Seq. No. 194736 1.R1011 Contig ID $ceu700\overline{4}28932.h1$ 5'-most EST 286604 Seq. No. 194849 1.R1011 Contig ID uC-zmfImo17407h12a15'-most EST 286605 Seq. No. 194861 1.R1011 Contig ID $uC-zmf\overline{l}mo17408b03a1$ 5'-most EST 286606 Seq. No. 194875 1.R1011 Contig ID uC-zmflmo17408d04a1 5'-most EST 286607 Seq. No. 194941 1.R1011 Contig ID $uC-zmf\overline{l}mo17418e11a1$ 5'-most EST BLASTN Method g22243 NCBI GI 40 BLAST score 5.0e-13 E value 116 Match length 84 % identity Zea mays Cin1 repeat from Cin1 middle repetitive family NCBI Description 286608 Seq. No. 194945 1.R1011 Contig ID uC-zmrob73057h05a1 5'-most EST BLASTX Method q3641838 NCBI GI 370 BLAST score 2.0e-35 E value 133 Match length % identity (AL023094) putative protein (fragment) [Arabidopsis NCBI Description thaliana] 286609 Seq. No. 194962 1.R1011 Contig ID uC-zmfImo17417f10a15'-most EST 286610 Seq. No. 194971 1.R1011 Contig ID 5'-most EST uC-zmflmo17418g10a1 Seq. No. 286611

Contig ID 195031_1.R1011 5'-most EST uC-zmflmo17418f08a1

Seq. No. 286612

Contig ID 195089_1.R1011 5'-most EST gct701179008.h1

Seq. No. 286613

Contig ID 195147_1.R1011



5'-most EST uC-zmflmo17420e09a1

Seq. No. 286614

Contig ID 195223_1.R1011 5'-most EST uC-zmflmo17421e03a1

Seq. No. 286615

Contig ID 195224 1.R1011 5'-most EST wyr700239557.h1

Method BLASTX
NCBI GI g2582351
BLAST score 165
E value 3.0e-11
Match length 73
% identity 44

NCBI Description (AF018639) unknown [Dictyostelium discoideum]

Seq. No. 286616

Contig ID 195275_1.R1011 5'-most EST uC-zmflmo17424b08a1

Seq. No. 286617

Contig ID 195321_1.R1011 5'-most EST uC-zmflmo17424f08a1

Seq. No. 286618

Contig ID 195412_1.R1011 5'-most EST uC-zmrob73053g08a1

Seq. No. 286619

Contig ID 195427_1.R1011 5'-most EST uC-zmflmo17426a02a1

Seq. No. 286620

Contig ID 195431_1.R1011 5'-most EST uC-zmflmo17426a07a1

Seq. No. 286621

Contig ID 195483_1.R1011 5'-most EST uC-zmflmo17426f09a1

Method BLASTX
NCBI GI g2244989
BLAST score 170
E value 7.0e-13
Match length 65
% identity 53

NCBI Description (Z97340) strong similarity to naringenin 3-dioxygenase

[Arabidopsis thaliana]

Seq. No. 286622

Contig ID 195600_1.R1011 5'-most EST uC-zmflmo17428c06a1

Seq. No. 286623

Contig ID 195682_1.R1011 5'-most EST uC-zmromo17026e05a1



```
286624
Seq. No.
                  195709 1.R1011
Contig ID
                  uC-zmrob73002h03a1
5'-most EST
                  286625
Seq. No.
                   195733 1.R1011
Contig ID
                  uC-zmrob73006b09a1
5'-most EST
                   286626
Seq. No.
                   195737 1.R1011
Contig ID
                   uC-zmrob73006c01a1
5'-most EST
                   BLASTX
Method
                   g1732513
NCBI GI
BLAST score
                   167
                   1.0e-11
E value
Match length
                   39
                   77
% identity
                  (U62743) snapdragon myb protein 305 homolog [Arabidopsis
NCBI Description
                   thaliana]
                   286627
Seq. No.
                   195762 1.R1011
Contig ID
                   uC-zmrob73006e07a1
5'-most EST
                   286628
Seq. No.
                   195763 1.R1011
Contig ID
                   uC-zmrob73006f09a1
5'-most EST
                   286629
Seq. No.
                   195798 1.R1011
Contig ID
                   uC-zmrob73012e03b1
5'-most EST
                   BLASTX
Method
                   g3860263
NCBI GI
                   298
BLAST score
                   8.0e-27
E value
                   126
Match length
                   49
 % identity
                   (AC005824) putative cytochrome p450 protein [Arabidopsis
NCBI Description
                   thaliana]
                   286630
 Seq. No.
                   195821 1.R1011
 Contig ID
                   uC-zmrob73016h01a1
 5'-most EST
                    286631
 Seq. No.
                    195847 1.R1011
 Contig ID
 5'-most EST
                    ceu700\overline{431555.h1}
 Seq. No.
                    286632
                    195884 1.R1011
 Contig ID
                    uC-zmrob73022c03a1
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    q3258575
                    398
 BLAST score
```

1.0e-38

105

72

E value

Match length

% identity



NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]
Seq. No. 286633

Contig ID 195885_1.R1011 5'-most EST uC-zmromo17104c02a1

Seq. No. 286634

Contig ID 195889_1.R1011 5'-most EST uC-zmrob73022c10a1

Seq. No. 286635

Contig ID 195893_1.R1011 5'-most EST uC-zmrob73022d06a1

Method BLASTX
NCBI GI 94581139
BLAST score 379
E value 3.0e-36
Match length 145
% identity 46

NCBI Description (AC006919) putative ABC transporter [Arabidopsis thaliana]

Seq. No. 286636

Contig ID 195911 1.R1011 5'-most EST uwc700152738.h1

Seq. No. 286637

Contig ID 195928_1.R1011 5'-most EST uC-zmrob73052a10a1

Seq. No. 286638

Contig ID 195942_1.R1011 5'-most EST uC-zmrob73023c04a1

Seq. No. 286639

Contig ID 195954_1.R1011 5'-most EST uC-zmrob73023g10a1

Seq. No. 286640

Contig ID 195959_1.R1011 5'-most EST vux700156993.h1

Seq. No. 286641

Contig ID 195974_1.R1011 5'-most EST uC-zmromo17011d02a1

Seq. No. 286642

Contig ID 195986_1.R1011 5'-most EST uC-zmrob73035d07a1

Method BLASTX
NCBI GI g1402920
BLAST score 403
E value 3.0e-39
Match length 139
% identity 58

NCBI Description (X98321) peroxidase [Arabidopsis thaliana]

Seq. No. 286643



Contig ID 196003_1.R1011 5'-most EST uC-zmromo17111b10a1

Seq. No. 286644

Contig ID 196005_1.R1011 5'-most EST uC-zmrob73024g01a1

Seq. No. 286645

Contig ID 196026_2.R1011 5'-most EST tfd700575784.h1

Method BLASTX
NCBI GI g3641661
BLAST score 166
E value 9.0e-12
Match length 43
% identity 81

NCBI Description (AB008519) high affinity nitrate transporter [Oryza sativa]

Seq. No. 286646

Contig ID 196029_1.R1011 5'-most EST uC-zmrob73033c04a1

Seq. No. 286647

Contig ID 196049_1.R1011 5'-most EST uC-zmrob73033g11a1

Seq. No. 286648

Contig ID 196084_1.R1011 5'-most EST uC-zmrob73034f02a1

Seq. No. 286649

Contig ID 196087_1.R1011 5'-most EST uC-zmromo17066f11a1

Method BLASTX
NCBI GI g3335359
BLAST score 218
E value 3.0e-22
Match length 101
% identity 57

NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No. 286650

Contig ID 196094_1.R1011 5'-most EST uC-zmrob73034g03a1

Method BLASTX
NCBI GI g2920654
BLAST score 479
E value 6.0e-48
Match length 121
% identity 69

NCBI Description (AF047697) putative high-pI laccase [Oryza sativa]

Seq. No. 286651

Contig ID 196103_1.R1011 5'-most EST uC-zmrob73034h10a1

Seq. No. 286652



196107 1.R1011 Contig ID uC-zmrob73061g10a1 5'-most EST BLASTX Method q1890311 NCBI GI 220 BLAST score 7.0e-18 E value 69 Match length 67 % identity (Y11789) peroxidase ATP23b [Arabidopsis thaliana] NCBI Description 286653 Seq. No. 196109 1.R1011 Contig ID uC-zmrob73035a07a1 5'-most EST 286654 Seq. No. 196127 1.R1011 Contig ID $xdb700\overline{3}41995.h1$ 5'-most EST BLASTX Method q1064998 NCBI GI 142 BLAST score 8.0e-09 E value 27 Match length 100 % identity Nitrate Reductase (Cytochrome B Reductase Fragment) NCBI Description (E.C.1.6.6.1) Complexed With Fad And Adp >gi_1065382_pdb_2CND_ Nadh-Dependent Nitrate Reductase (Cytochrome B Reductase Fragment) (E.C.1.6.6.1) Complexed With Fad (Synchrotron X-Ray Diffraction) 286655 Seq. No. 196136 1.R1011 Contig ID uC-zmrob73035e01a1 5'-most EST BLASTX Method q3406742 NCBI GI 226 BLAST score 2.0e-18 E value 80 Match length 46 % identity (AF017990) Fkbp39p [Schizosaccharomyces pombe] NCBI Description >gi_4456817_emb_CAB37433.1_ (AL035548) Peptidyl Prolyl cis-trans isomerase [Schizosaccharomyces pombe] 286656 Seq. No. 196149 1.R1011 Contig ID uC-zmrob73035f07a1 5'-most EST 286657 Seq. No. 196156 1.R1011 Contig ID 5'-most EST uC-zmromo17088e01a1 286658 Seq. No. 196182 1.R1011 Contig ID

uC-zmromo17098g09a1 5'-most EST

286659 Seq. No.

196192 1.R1011 Contig ID uC-zmrob73037h10a1 5'-most EST



```
Method BLASTX
NCBI GI g4539383
BLAST score 514
E value 3.0e-52
Match length 155
% identity 65
```

NCBI Description (AL035526) putative protein (fragment) [Arabidopsis

thaliana]

Seq. No. 286660

Contig ID 196229_1.R1011 5'-most EST hvj700622322.h1

Seq. No. 286661

Contig ID 196239_1.R1011 5'-most EST uC-zmrob73039h09a1

Seq. No. 286662

Contig ID 196288_1.R1011 5'-most EST uC-zmrob73044g05a1

Seq. No. 286663

Contig ID 196303_1.R1011 5'-most EST uC-zmrob73045a05a1

Seq. No. 286664

Contig ID 196321_1.R1011 5'-most EST uC-zmrob73045d03a1

Seq. No. 286665

Contig ID 196348_1.R1011 5'-most EST dyk700103061.h1

Method BLASTX
NCBI GI g3258575
BLAST score 160
E value 1.0e-16
Match length 63
% identity 79

NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 286666

Contig ID 196355_1.R1011 5'-most EST uC-zmrob73057g08a1

Seq. No. 286667

Contig ID 196357_1.R1011 5'-most EST uC-zmrob73049a04a1

Seq. No. 286668

Contig ID 196359 1.R1011 5'-most EST uC-zmrob73049a06a1

Method BLASTX
NCBI GI g2208908
BLAST score 231
E value 7.0e-26
Match length 87
% identity 74



```
(AB004809) phosphate transporter [Catharanthus roseus]
NCBI Description
                   286669
Seq. No.
                   196370 1.R1011
Contig ID
                   uC-zmrob73049b10a1
5'-most EST
                   BLASTX
Method
                   g3860263
NCBI GI
                   252
BLAST score
                   8.0e-22
E value
                   113
Match length
                   47
% identity
                  (AC005824) putative cytochrome p450 protein [Arabidopsis
NCBI Description
                   thaliana]
                   286670
Seq. No.
                   196412 1.R1011
Contig ID
                   uC-zmrob73049g06a1
5'-most EST
                   BLASTX
Method
                   g4105125
NCBI GI
                   245
BLAST score
                   1.0e-20
E value
                   73
Match length
                   67
% identity
                   (AF043347) cell wall invertase; beta-fructosidase; Incw4
NCBI Description
                   [Zea mays]
                   286671
Seq. No.
                   196423 1.R1011
Contig ID
                   dyk700\overline{1}05171.h1
5'-most EST
                   286672
Seq. No.
                   196460 1.R1011
Contig ID
                   uC-zmrob73050d10a1
5'-most EST
                   BLASTX
Method
                   q2911073
NCBI GI
                   203
BLAST score
E value
                    7.0e-16
                   56
Match length
                    64
 % identity
                   (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                    286673
Seq. No.
                    196472 1.R1011
 Contig ID
                   uC-zmrob73050e11a1
 5'-most EST
                    286674
 Seq. No.
                    196493 1.R1011
 Contig ID
                    uC-zmromo17066a11a1
 5'-most EST
                    286675
 Seq. No.
                    196511 1.R1011
 Contig ID
                    tfd700572616.h1
 5'-most EST
```

286676

196572 1.R1011

uC-zmrob73051h01a1

Seq. No.

Contig ID 5'-most EST



Contig ID 196589_1.R1011 5'-most EST uC-zmrob73052b06a1

Method BLASTX
NCBI GI g2660670
BLAST score 413
E value 2.0e-40
Match length 113
% identity 73

NCBI Description (AC002342) putative Cu2+-transporting ATPase [Arabidopsis

thaliana]

Seq. No. 286678

Contig ID 196615_1.R1011 5'-most EST uC-zmrob73052e06a1

Method BLASTX
NCBI GI g3158476
BLAST score 348
E value 8.0e-33
Match length 77
% identity 82

NCBI Description (AF067185) aquaporin 2 [Samanea saman]

Seq. No. 286679

Contig ID 196617_1.R1011 5'-most EST uC-zmrob73052e09a1

Method BLASTX
NCBI GI g129806
BLAST score 150
E value 5.0e-15
Match length 124
% identity 39

NCBI Description PEROXIDASE 1 PRECURSOR >gi 22587 emb CAA41294 (X58396)

peroxidase [Hordeum vulgare]

Seq. No. 286680

Contig ID 196668_1.R1011 5'-most EST uC-zmrob73053d02a1

Seq. No. 286681

Contig ID 196679_1.R1011 5'-most EST uC-zmrob73053e03a1

Method BLASTX
NCBI GI g4539404
BLAST score 160
E value 6.0e-11
Match length 38
% identity 74

NCBI Description (AL049524) putative protein [Arabidopsis thaliana]

Seq. No. 286682

Contig ID 196694_1.R1011 5'-most EST uC-zmrob73053f10a1

Seq. No. 286683

Contig ID 196741_1.R1011 5'-most EST uC-zmrob73057d07a1



196756 1.R1011 Contig ID xsy700210455.hl 5'-most EST

286685 Seq. No.

196757 1.R1011 Contig ID $ceu700\overline{4}21902.h1$ 5'-most EST BLASTN

Method g3819236 NCBI GI 91 BLAST score 2.0e-43 E value 191

Match length 87 % identity

Hordeum vulgare partial mRNA; clone cMWG0784 NCBI Description

286686 Seq. No.

196777 1.R1011 Contig ID uC-zmrob73054g01a1 5'-most EST

286687 Seq. No.

196782_1.R1011 Contig ID uC-zmromo17011g02a1 5'-most EST

286688 Seq. No.

196783 1.R1011 Contig ID uC-zmrob73054g08a1 5'-most EST

286689 Seq. No.

196802 1.R1011 Contig ID 5'-most EST uC-zmrob73055a07a1

286690 Seq. No.

196835 1.R1011 Contig ID wyr700239876.h1 5'-most EST

Seq. No. 286691

196863 1.R1011 Contig ID uC-zmrob73055g06a1 5'-most EST

BLASTX Method g2129703 NCBI GI BLAST score 218 7.0e-29 E value 146 Match length 48 % identity

NCBI Description

receptor kinase - Arabidopsis thaliana >gi_2129704_pir__S71184 receptor kinase - Arabidopsis thaliana >gi_166692 (M80238) receptor kinase [Arabidopsis

thaliana] >gi_445123_prf__1908429A receptor kinase

[Arabidopsis thaliana]

286692 Seq. No.

196933 1.R1011 Contia ID uC-zmrob73056f10a1 5'-most EST

286693 Seq. No.

196950 1.R1011 Contig ID

286704



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uC-zmromo17009h11a1
5'-most EST
                  286694
Seq. No.
                  196953 1.R1011
Contig ID
                  ceu700\overline{4}26564.h1
5'-most EST
                  286695
Seq. No.
                  196991 1.R1011
Contig ID
                  uC-zmrob73057e05a1
5'-most EST
                  BLASTX
Method
                  g4454018
NCBI GI
                  143
BLAST score
                  7.0e-09
E value
                  81
Match length
                   42
% identity
                  (AL035396) SRG1-like protein [Arabidopsis thaliana]
NCBI Description
                   286696
Seq. No.
                   196995 1.R1011
Contig ID
                   uC-zmrob73057e09a1
5'-most EST
                   286697
Seq. No.
                   197051_1.R1011
Contig ID
                   tfd700575052.h1
5'-most EST
                   286698
Seq. No.
                   197061 1.R1011
Contig ID
                   uC-zmrob73058d05a1
5'-most EST
                   286699
Seq. No.
                   197089 1.R1011
Contig ID
                   uC-zmrob73058g09a1
5'-most EST
                   286700
Seq. No.
                   197096 1.R1011
Contig ID
5'-most EST
                   uC-zmromo17007a05a1
                   286701
Seq. No.
                   197106 1.R1011
Contig ID
5'-most EST
                   uC-zmrob73059a08a1
                   286702
Seq. No.
                   197143 1.R1011
Contig ID
                   dyk700104352.hl
5'-most EST
                   286703
Seq. No.
                   197149 1.R1011
Contig ID
                   uC-zmrob73059f04a1
 5'-most EST
Method
                   BLASTX
                   g3395429
NCBI GI
                   199
BLAST score
                   2.0e-15
 E value
                   97
Match length
 % identity
NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]
```



Contig ID 197167_1.R1011 5'-most EST uC-zmrob73059h05a1

Seq. No. 286705

Contig ID 197176_1.R1011 5'-most EST uC-zmrob73060a06a1

Seq. No. 286706

Contig ID 197208_1.R1011 5'-most EST uC-zmrob73060f11a1

Seq. No. 286707

Contig ID 197260_1.R1011 5'-most EST uC-zmrob73061b07a1

Seq. No. 286708

Contig ID 197291_1.R1011 5'-most EST uC-zmrob73061f06a1

Seq. No. 286709

Contig ID 197331_1.R1011 5'-most EST fxb700397562.h1

Seq. No. 286710

Contig ID 197415_1.R1011 5'-most EST xdb700339194.h1

Method BLASTX
NCBI GI 94455232
BLAST score 280
E value 9.0e-25
Match length 109
% identity 50

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 286711

Contig ID 197417_1.R1011 5'-most EST uC-zmromo17091d05a1

Seq. No. 286712

Contig ID 197457_1.R1011 5'-most EST uC-zmromo17006e02a1

Seq. No. 286713

Contig ID 197494_1.R1011 5'-most EST uC-zmromo17007b02a1

Seq. No. 286714

Contig ID 197520_1.R1011 5'-most EST uC-zmromo17007f09a1

Seq. No. 286715

Contig ID 197628_1.R1011 5'-most EST wty700166116.h1

Seq. No. 286716

Contig ID 197709_1.R1011 5'-most EST uC-zmromo17010g01a1

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286717
Seq. No.
                  197718 1.R1011
Contig ID
                  uC-zmromo17010g11a1
5'-most EST
                  286718
Seq. No.
                  197726 1.R1011
Contig ID
                  uC-zmromo17025c06a1
5'-most EST
                  286719
Seq. No.
                   197727_1.R1011
Contig ID
                   uC-zmromo17010h09a1
5'-most EST
                   BLASTX
Method
                   g4138679
NCBI GI
BLAST score
                   238
                   8.0e-20
E value
                   87
Match length
                   46
% identity
                   (Y09591) amino acid transporter [Vicia faba]
NCBI Description
                   286720
Seq. No.
                   197771 1.R1011
Contiq ID
                   yne700379004.h1
5'-most EST
                   286721
Seq. No.
                   197789_1.R1011
Contig ID
                   uC-zmromo17011g09a1
5'-most EST
                   BLASTX
Method
                   g1173309
NCBI GI
                   165
BLAST score
                   2.0e-11
E value
                   52
Match length
                   63
% identity
                   MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S10 PRECURSOR
NCBI Description
                   >gi_2119078_pir__S66361 ribosomal protein S10 precursor -
                   Arabidopsis thaliana >gi_517331_emb_CAA56711_ (X80694)
                   ribosomal protein S10 [Arabidopsis thaliana]
                   286722
 Seq. No.
                   197845 1.R1011
 Contig ID
                   uC-zmromo17017b01a1
 5'-most EST
                   286723
 Seq. No.
                   197870 1.R1011
 Contig ID
                   uC-zmromo17017d09a1
 5'-most EST
                   286724
 Seq. No.
                    197901_1.R1011
 Contig ID
 5'-most EST
                    uC-zmromo17017h03a1
                   BLASTX
 Method
                    q3127892
 NCBI GI
                    242
 BLAST score
                    1.0e-20
 E value
                    55
 Match length
                    80
 % identity
 NCBI Description (AJ006025) acyl-coA synthetase [Cicer arietinum]
```



286725 Seq. No. 197918 1.R1011 Contig ID uC-zmromo17023b10a1 5'-most EST Seq. No. 286726 197934 1.R1011 Contig ID uC-zmromo17023f10a1 5'-most EST 286727 Seq. No. 197937 1.R1011 Contig ID wyr700235975.hl 5'-most EST BLASTN Method q3925232 NCBI GI 130 BLAST score 6.0e-67 E value Match length 224 92 % identity NCBI Description Zea mays putative peroxidase P7X mRNA, partial cds 286728 Seq. No. 197959_1.R1011 Contig ID uC-zmromo17025c11a15'-most EST BLASTX Method q4544408 NCBI GI 415 BLAST score 1.0e-40 E value Match length 110 70 % identity (AC006955) unknown protein [Arabidopsis thaliana] NCBI Description 286729 Seq. No. 197998 1.R1011 Contig ID uC-zmromo17025h07a1 5'-most EST 286730 Seq. No. 198012 1.R1011 Contig ID 5'-most EST uer700583752.h1 286731 Seq. No. 198100 1.R1011 Contig ID uC-zmromo17027c06a1 5'-most EST 286732 Seq. No. 198101 1.R1011 Contig ID uC-zmromo17031d06a1 5'-most EST BLASTN Method

NCBI GI g3386564 BLAST score 36 1.0e-10 E value

Match length 44 95 % identity

Sorghum bicolor 1-aminocyclopropane-1-carboxylate oxidase NCBI Description

(ACO1) mRNA, complete cds

286733 Seq. No.

198106 1.R1011 Contig ID yyf700347733.h1 5'-most EST

E value

Match length

NCBI Description

% identity



```
286734
Seq. No.
                  198125 1.R1011
Contig ID
5'-most EST
                  uC-zmromo17027f06a1
                  286735
Seq. No.
                  198126 1.R1011
Contig ID
                  uC-zmromo17027f08a1
5'-most EST
                  286736
Seq. No.
Contig ID
                  198185 1.R1011
5'-most EST
                  xdb700337117.h1
                  286737
Seq. No.
Contig ID
                  198220_1.R1011
                  uC-zmromo17029d12a1
5'-most EST
Method
                  BLASTX
                  g3342798
NCBI GI
                  154
BLAST score
E value
                  4.0e-10
                  50
Match length
                   62
% identity
                  (AF061240) glutamine cyclotransferase precursor [Carica
NCBI Description
                  papaya]
                  286738
Seq. No.
                  198224 1.R1011
Contig ID
                  uC-zmromo17029e04a1
5'-most EST
                   286739
Seq. No.
Contig ID
                   198260 1.R1011
                  uC-zmromo17030a12a1
5'-most EST
                   BLASTX
Method
                   q2708749
NCBI GI
BLAST score
                   227
E value
                   2.0e-18
Match length
                   100
                   47
% identity
                  (AC003952) putative senescence-assoc. rhodanese-like
NCBI Description
                   protein [Arabidopsis thaliana]
                   286740
Seq. No.
                   198368 1.R1011
Contig ID
                   uC-zmromo17037a07a1
5'-most EST
Seq. No.
                   286741
                   198392 1.R1011
Contig ID
                   uC-zmromo17088b05a1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q5091496
BLAST score
                   69
```

39916

Oryza sativa genomic DNA, chromosome 6, clone P0680A03,

2.0e-30

complete sequence

136



```
286742
Seq. No.
                   198431_1.R1011
Contig ID
                  uer700583840.hl
5'-most EST
                  BLASTN
Method
                   g218203
NCBI GI
                   73
BLAST score
                   1.0e-32
E value
                   125
Match length
                   90
% identity
                  Rice mRNA for GTP binding protein
NCBI Description
                   286743
Seq. No.
                   198440 1.R1011
Contig ID
                   uC-zmromo17045g06a1
5'-most EST
                   BLASTX
Method
                   q112802
NCBI GI
                   310
BLAST score
                   2.0e-28
E value
                   90
Match length
                   73
% identity
                  4-COUMARATE--COA LIGASE >gi_82454_pir__JU0311
NCBI Description
                   4-coumarate--CoA ligase (EC 6.2.1.12) - rice
                   >gi 20161 emb_CAA36850_ (X52623) 4-coumarate-CoA ligase
                   [Oryza sativa]
                   286744
Seq. No.
Contig ID
                   198487 1.R1011
                   uwc700151427.h1
5'-most EST
                   286745
Seq. No.
                   198548 1.R1011
Contig ID
                   uC-zmromo17058c06a1
5'-most EST
                   286746
Seq. No.
                   198604_1.R1011
Contig ID
5'-most EST
                   uC-zmromo17066h08a1
Method
                   BLASTX
                   q401621
NCBI GI
                   249
BLAST score
                   7.0e-21
E value
Match length
                   187
                   36
% identity
                   HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION
NCBI Description
                   >gi 290561 (L10328) o188 [Escherichia coli] >gi 1790149
                   (AE000448) orf, hypothetical protein [Escherichia coli]
Seq. No.
                   286747
Contig ID
                   198604 2.R1011
5'-most EST
                   wyr700238032.h1
                   286748
Seq. No.
                   198623 1.R1011
Contig ID
                   ntr700\overline{0}77346.h1
5'-most EST
```

39917

286749

198695 1.R1011

uC-zmromo17068d12a1

Seq. No.

Contig ID

5'-most EST



Seq. No. 286750 Contig ID 198706

Contig ID 198706_1.R1011 5'-most EST uC-zmromo17068f04a1

Seq. No. 286751

Contig ID 198739_1.R1011 5'-most EST uC-zmromo17071b09a1

Seq. No. 286752

Contig ID 198822_1.R1011 5'-most EST uC-zmromo17080b03a1

Method BLASTX
NCBI GI g2660676
BLAST score 423
E value 1.0e-41
Match length 115
% identity 70

NCBI Description (AC002342) Dreg-2 like protein [Arabidopsis thaliana]

Seq. No. 286753

Contig ID 198834_1.R1011 5'-most EST uC-zmromo17080e04a1

Seq. No. 286754

Contig ID 198834_2.R1011 5'-most EST cyk700047867.f1

Seq. No. 286755

Contig ID 198875_1.R1011 5'-most EST uC-zmromo17085d06a1

Seq. No. 286756

Contig ID 198929_1.R1011 5'-most EST uC-zmromo17088e02a1

Seq. No. 286757

Contig ID 198944_1.R1011 5'-most EST uC-zmromo17089a02a1

Method BLASTX
NCBI GI g2191173
BLAST score 485
E value 2.0e-48
Match length 294
% identity 41

NCBI Description (AF007270) contains similarity to DNA polymerase III, alpha

chain (SP:P47277) [Arabidopsis thaliana]

Seq. No. 286758

Contig ID 198968_1.R1011 5'-most EST uC-zmromo17089d03a1

Seq. No. 286759

Contig ID 198975_1.R1011 5'-most EST uC-zmromo17089e01a1

Seq. No. 286760



199068 1.R1011 Contig ID amh700030452.f15'-most EST Seq. No. 286761 199089 1.R1011 Contig ID uC-zmromo17096f11a1 5'-most EST BLASTN Method q340933 NCBI GI BLAST score 38 7.0e-12 E value Match length 74 88 % identity Zea mays 10-kDa zein gene, complete cds NCBI Description Seq. No. 286762 199101 1.R1011 Contig ID 5'-most EST uC-zmromo17096g12a1 286763 Seq. No. Contig ID 199105 1.R1011 5'-most EST uC-zmromo17096h06a1 286764 Seq. No. 199115 1.R1011 Contig ID 5'-most EST uC-zmromo17098b02a1 286765 Seq. No. 199122 1.R1011 Contig ID 5'-most EST uC-zmromo17098b11a1 Seq. No. 286766 199131 1.R1011 Contig ID uC-zmromo17098d01a1 5'-most EST Seq. No. 286767 199150 1.R1011 Contig ID uC-zmromo17098g04a1 5'-most EST 286768 Seq. No. 199185 1.R1011 Contig ID uC-zmromo17100e05a1 5'-most EST 286769 Seq. No. 199227 1.R1011 Contig ID 5'-most EST wyr700237474.hl 286770 Seq. No. 199303 1.R1011 Contig ID

5'-most EST uC-zmromo17107b05a1

286771 Seq. No.

199326 1.R1011 Contig ID 5'-most EST hvj700621340.hl

Seq. No. 286772 Contig ID

199352_1.R1011 uC-zmromo17111c06a1 5'-most EST



Contig ID 199390_1.R1011 5'-most EST uC-zmromo17111h02a1

Seq. No. 286774

Contig ID 199518_1.R1011 5'-most EST uC-zmromo17114b04a1

Seq. No. 286775

Contig ID 199607_1.R1011 5'-most EST uC-zmromo17119g01a1

Method BLASTX
NCBI GI g2292978
BLAST score 225
E value 1.0e-18
Match length 56
% identity 80

NCBI Description (Y10253) pantoate--beta-alanine ligase [Oryza sativa]

Seq. No. 286776

Contig ID 199616_1.R1011 5'-most EST cat700018070.r1

Seq. No. 286777

Contig ID 199617_1.R1011 5'-most EST cat700016003.r1

Seq. No. 286778

Contig ID 199646 1.R1011 5'-most EST cat700021180.r1

Seq. No. 286779

Contig ID 199659_1.R1011 5'-most EST cat700016056.r1

Seq. No. 286780

Contig ID 199661_1.R1011 5'-most EST xsy700217972.h1

Seq. No. 286781

Contig ID 199697_1.R1011 5'-most EST xyt700343081.h1

Method BLASTX
NCBI GI g4337201
BLAST score 286
E value 2.0e-25
Match length 83
% identity 64

NCBI Description (AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No. 286782

Contig ID 199719_1.R1011 5'-most EST pmx700087863.h1

Method BLASTX
NCBI GI g2244965
BLAST score 286



E value 7.0e-26 Match length 126 % identity 48

NCBI Description (Z97340) unnamed protein product [Arabidopsis thaliana]

Seq. No. 286783

Contig ID 199737_1.R1011 5'-most EST cat700016156.r1

Seq. No. 286784

Contig ID 199772_1.R1011 5'-most EST cat700016192.r1

Method BLASTX
NCBI GI g2190259
BLAST score 364
E value 7.0e-35
Match length 119
% identity 56

NCBI Description (D86385) A-type cyclin [Catharanthus roseus]

Seq. No. 286785

Contig ID 199778_1.R1011 5'-most EST pmx700089927.h1

Method BLASTX
NCBI GI g3047064
BLAST score 466
E value 1.0e-46
Match length 145

% identity 63

NCBI Description (AF058825) contains similarity to peptidyl-prolyl cis-trans

isomerase (Pfam: pro_isomerase.hmm, score: 23.86 and 28.41

[Arabidopsis thaliana]

Seq. No. 286786

Contig ID 199781_1.R1011 5'-most EST tfd700569114.h1

Seq. No. 286787

Contig ID 199825_1.R1011 5'-most EST cat700016259.r1

Method BLASTN
NCBI GI g22320
BLAST score 75
E value 4.0e-34
Match length 281
% identity 87

NCBI Description Maize H1 mRNA for H1 histone

Seq. No. 286788

Contig ID 199854_1.R1011 5'-most EST cat700021484.r1

Seq. No. 286789

Contig ID 199872_1.R1011 5'-most EST tfd700573734.h1

Seq. No. 286790



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199897 1.R1011
Contig ID
5'-most EST
                   cat700016349.rl
                   286791
Seq. No.
                   199957 1.R1011
Contig ID
5'-most EST
                   tfd700570059.h1
Seq. No.
                   286792
Contig ID
                   199959 1.R1011
5'-most EST
                   cat700021162.rl
Seq. No.
                   286793
                   199963 1.R1011
Contig ID
5'-most EST
                   fdz701166555.h1
Seq. No.
                   286794
                   200029 1.R1011
Contig ID
5'-most EST
                   cat700017642.rl
Seq. No.
                   286795
                   200058 1.R1011
Contig ID
5'-most EST
                   cat700\overline{0}16556.r1
Method
                   BLASTX
NCBI GI
                   g2645168
BLAST score
                   148
E value
                   6.0e-10
Match length
                   40
% identity
NCBI Description (D50575) YY1 protein [Oryza sativa]
Seq. No.
                   286796
Contig ID
                   200096 1.R1011
5'-most EST
                   cat700\overline{0}16608.r1
Seq. No.
                   286797
                   200104 1.R1011
Contig ID
5'-most EST
                   cat700\overline{0}16617.r1
Method
                   BLASTX
NCBI GI
                   q2245054
BLAST score
                   184
E value
                   7.0e-14
                   77
Match length
% identity
NCBI Description (Z97342) protein kinase homolog [Arabidopsis thaliana]
Seq. No.
                   286798
                   200108 1.R1011
Contig ID
5'-most EST
                   fdz701166013.h1
Seq. No.
                   286799
                   200110 1.R1011
Contig ID
```

5'-most EST cat700016623.rl

BLASTX Method NCBI GI g223817 BLAST score 162 E value 3.0e-11Match length 35



% identity 83

NCBI Description ferredoxin II [Anabaena variabilis]

Seq. No. 286800

Contig ID 200113_1.R1011 5'-most EST gct701174734.h1

Seq. No. 286801

Contig ID 200114_1.R1011 5'-most EST cat700019921.r1

Method BLASTX
NCBI GI g2500378
BLAST score 268
E value 5.0e-24
Match length 56
% identity 84

NCBI Description 60S RIBOSOMAL PROTEIN L37

Seq. No. 286802

Contig ID 200126_1.R1011 5'-most EST ceu700425408.h1

Seq. No. 286803

Contig ID 200155_1.R1011 5'-most EST tfd700573185.h1

Method BLASTX
NCBI GI g3193287
BLAST score 511
E value 5.0e-52
Match length 100
% identity 91

NCBI Description (AF069298) Arabidopsis predicted protein of unknown function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]

Seq. No. 286804

Contig ID 200161_1.R1011 5'-most EST hbs701182831.h1

Seq. No. 286805

Contig ID 200169_1.R1011 5'-most EST gct701178306.h1

Seq. No. 286806

Contig ID 200174_1.R1011 5'-most EST cat700016704.r1

Seq. No. 286807

Contig ID 200193_1.R1011 5'-most EST pwr700449135.h1

Method BLASTX
NCBI GI g417570
BLAST score 435
E value 2.0e-43
Match length 92
% identity 90

NCBI Description DIHYDROOROTATE DEHYDROGENASE PRECURSOR (DIHYDROOROTATE

OXIDASE) (DHODEHASE) >gi 478676 pir S23762 dihydroorotate



oxidase (EC 1.3.3.1) - Arabidopsis thaliana >gi_16449_emb_CAA44695_ (X62909) dihydroorotate dehydrogenase [Arabidopsis thaliana]

Seq. No. 286808

Contig ID 200236_1.R1011 5'-most EST cat700016773.r1

Seq. No. 286809

Contig ID 200237_1.R1011 5'-most EST xjt700095139.h1

Method BLASTX
NCBI GI 94454012
BLAST score 972
E value 1.0e-105
Match length 284
% identity 64

NCBI Description (AL035396) Pollen-specific protein precursor like

[Arabidopsis thaliana]

Seq. No. 286810

Contig ID 200294 1.R1011 5'-most EST cat700016844.r2

Method BLASTX
NCBI GI g3335372
BLAST score 152
E value 2.0e-10
Match length 45
% identity 62

NCBI Description (AC003028) putative SRG1 protein [Arabidopsis thaliana]

Seq. No. 286811

Contig ID 200384_1.R1011 5'-most EST nwy700444247.h1

Method BLASTX
NCBI GI g4507669
BLAST score 440
E value 1.0e-43
Match length 86
% identity 100

NCBI Description tumor protein, translationally-controlled 1

>gi_136479_sp_P13693_TCTP_HUMAN_TRANSLATIONALLY_CONTROLLED

TUMOR PROTEIN (TCTP) (P23) >gi_88948_pir__S06590 IgE-dependent histamine-releasing factor - human

>gi_37496_emb_CAA34200 (X16064) tumor protein (AA 1 - 172)

[Homo sapiens]

Seq. No. 286812

Contig ID 200505_1.R1011 5'-most EST yyf700352352.h1

Method BLASTX
NCBI GI g108411
BLAST score 237
E value 2.0e-19
Match length 145
% identity 6

NCBI Description tenascin precursor - pig >gi 2125 emb CAA43796 (X61599)



Tenascin [Sus scrofa]

Seq. No. 286814

Contig ID 200584_1.R1011 5'-most EST cat700020145.r1

Seq. No. 286815

Contig ID 200597_1.R1011 5'-most EST tfd700576092.h1

Seq. No. 286816

Contig ID 200608_1.R1011 5'-most EST kyv700142469.h1

Seq. No. 286817

Contig ID 200641 1.R1011 5'-most EST cat700017283.r1

Seq. No. 286818

Contig ID 200726_1.R1011 5'-most EST cat700017450.r1

Seq. No. 286819

Contig ID 200859_1.R1011 5'-most EST cat700017651.r1

Seq. No. 286820

Contig ID 200869 1.R1011 5'-most EST cat700017664.r1

Seq. No. 286821

Contig ID 200873_1.R1011 5'-most EST cat700017668.r1

Seq. No. 286822

Contig ID 200882_1.R1011 5'-most EST ntr700072354.h1

Seq. No. 286823

Contig ID 200905_1.R1011 5'-most EST cat700017714.r1

Method BLASTX
NCBI GI g3150410
BLAST score 273
E value 3.0e-24
Match length 84
% identity 67

NCBI Description (AC004165) unknown protein [Arabidopsis thaliana]

Seq. No. 286824

Contig ID 200929_1.R1011 5'-most EST cat700017745.r1

Method BLASTX



NCBI GI q3402686 BLAST score 181 3.0e-13E value Match length 83 % identity 46 (AC004697) putative serine/threonine protein kinase NCBI Description [Arabidopsis thaliana] 286825 Seq. No. Contig ID 200932 1.R1011 5'-most EST qmh700028338.f1

Method BLASTX
NCBI GI g2842493
BLAST score 298
E value 2.0e-27
Match length 89
% identity 63

NCBI Description (AL021749) predicted protein [Arabidopsis thaliana]

Seq. No. 286826

Contig ID 200934_1.R1011 5'-most EST cat700017752.r1

Seq. No. 286827

Contig ID 200946_1.R1011 5'-most EST xmt700259167.h2

Seq. No. 286828

Contig ID 200982_1.R1011 5'-most EST xjt700093458.h1

Method BLASTX
NCBI GI g3551257
BLAST score 242
E value 2.0e-20
Match length 55
% identity 82

NCBI Description (AB012708) 98b [Daucus carota]

Seq. No. 286829

Contig ID 200991_1.R1011 5'-most EST pmx700084248.h1

Seq. No. 286830

Contig ID 201008_1.R1011 5'-most EST rvt700550772.h1

Seq. No. 286831

Contig ID 201017_1.R1011 5'-most EST mwy700440992.h1

Seq. No. 286832

Contig ID 201021_1.R1011 5'-most EST yyf700351533.h1

Seq. No. 286833

Contig ID 201089_1.R1011 5'-most EST cat700018020.r1



Contig ID

286834

201123 1.R1011

```
5'-most EST
                  xdb700\overline{3}37575.h1
Method
                  BLASTX
                  g1653033
NCBI GI
                   336
BLAST score
                   2.0e-31
E value
Match length
                   84
                   73
% identity
NCBI Description
                  (D90910) hypothetical protein [Synechocystis sp.]
                   286835
Seq. No.
                   201137 1.R1011
Contig ID
5'-most EST
                   cat700018085.r1
                  BLASTX
Method
NCBI GI
                   q2213600
BLAST score
                   228
                   9.0e-19
E value
Match length
                   94
% identity
                   45
                  (AC000348) T7N9.20 [Arabidopsis thaliana]
NCBI Description
                   286836
Seq. No.
                   201195 1.R1011
Contig ID
5'-most EST
                   hbs701181290.hl
Method
                   BLASTX
NCBI GI
                   q4454471
BLAST score
                   369
E value
                   1.0e - 35
Match length
                   90
                   74
% identity
                  (AC006234) putative G protein coupled receptor [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   286837
                   201258 1.R1011
Contig ID
5'-most EST
                   nbm700465215.h1
                   286838
Seq. No.
                   201261 1.R1011
Contig ID
                   vux700158396.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3169065
BLAST score
                   185
E value
                   4.0e-14
                   75
Match length
                   51
% identity
                  (AL023704) putative translocation elongation factor-Tu
NCBI Description
                   family [Schizosaccharomyces pombe]
Seq. No.
                   286839
                   201289 1.R1011
Contig ID
5'-most EST
                   cat700018279.rl
                   BLASTX
Method
NCBI GI
                   g2769566
                   202
BLAST score
```



```
E value 9.0e-16

Match length 59
% identity 59

NCBI Description (Y10477) chloroplast thylakoidal processing peptidase [Arabidopsis thaliana]

Seq. No. 286840

Contig ID 201361_1.R1011
5'-most EST xmt700260855.h1
```

 Seq. No.
 286842

 Contig ID
 201368_1.R1011

 5'-most EST
 dyk700105594.h1

 Method
 BLASTX

NCBI GI g1899025 BLAST score 278 E value 7.0e-29 Match length 143 % identity 51

NCBI Description (U28215) hexokinase 2 [Arabidopsis thaliana] >gi_3687232 (AC005169) hexokinase [Arabidopsis thaliana]

Seq. No. 286843 Contig ID 201382_1.R1011

5'-most EST cat700019790.r1

Seq. No. 286844

Contig ID 201469_1.R1011 5'-most EST cat700018512.r1

Seq. No. 286845

Contig ID 201484_1.R1011 5'-most EST cat700018528.r1

Seq. No. 286846

Contig ID 201503_1.R1011 5'-most EST vux700160936.h1 Method BLASTX

NCBI GI g4263795 BLAST score 336 E value 2.0e-31 Match length 138 % identity 48

NCBI Description (AC006068) putative glucosyltransferase [Arabidopsis thaliana]

Cliatiana

Seq. No. 286847

Contig ID 201505_1.R1011 5'-most EST wty700170062.h1

Seq. No. 286848

Contig ID 201511_1.R1011 5'-most EST rvt700553045.h1



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286849
Seq. No.
                   201534 1.R1011
Contig ID
                   ceu700432074.h1
5'-most EST
                   286850
Seq. No.
                   201555 1.R1011
Contig ID
5'-most EST
                   fdz701163008.h1
Seq. No.
                   286851
                   201624 1.R1011
Contig ID
                   pmx700091774.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                   q3046693
BLAST score
                   378
                   5.0e-74
E value
                   161
Match length
                   77
% identity
NCBI Description
                  (AL022140) receptor like protein (fragment) [Arabidopsis
                   thaliana]
Seq. No.
                   286852
                   201655 1.R1011
Contig ID
                   hbs701181235.h1
5'-most EST
                   286853
Seq. No.
                   201685 1.R1011
Contig ID
                   nwy700444480.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3152609
BLAST score
                   232
E value
                   2.0e-19
Match length
                   77
                   58
% identity
NCBI Description (AC004482) putative Su(var)3-9 protein [Arabidopsis
                   thaliana]
                   286854
Seq. No.
Contig ID
                   201745 1.R1011
                   cat700\overline{0}18858.r1
5'-most EST
                   286855
Seq. No.
Contig ID
                   201762 1.R1011
5'-most EST
                   xsy700208728.h1
Seq. No.
                   286856
                   201773 1.R1011
```

Contig ID 201773_1.R1011 5'-most EST tzu700201859.h1

Method BLASTX
NCBI GI g1708191
BLAST score 239
E value 2.0e-35
Match length 172
% identity 45

NCBI Description HEXOSE CARRIER PROTEIN HEX6 >gi_467319 (L08188) hexose

carrier protein [Ricinus communīs]



```
286857
Seq. No.
Contig ID
                   201799 1.R1011
                   cat700\overline{0}18923.r1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g3378526
BLAST score
                   155
E value
                   4.0e-82
Match length
                   191
% identity
                   95
NCBI Description Zea mays mRNA for anther specific protein (MZm3-3)
Seq. No.
                   286858
                   201866 1.R1011
Contig ID
5'-most EST
                   vux700162183.h1
                   BLASTX
Method
NCBI GI
                   g2252824
BLAST score
                   196
                   4.0e-15
E value
                   91
Match length
% identity
                   43
NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]
                   286859
Seq. No.
                   201957 1.R1011
Contig ID
                   cat700\overline{0}19161.r1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3242731
BLAST score
                   181
E value
                   2.0e-13
                   107
Match length
% identity
                   40
                   (AC003040) putative host response protein (Pir7)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   286860
                   201974 1.R1011
Contig ID
5'-most EST
                   cat700\overline{0}20604.r1
Seq. No.
                   286861
                   202000 1.R1011
Contig ID
5'-most EST
                   uwc700150976.h1
                   286862
Seq. No.
                   202055 1.R1011
Contig ID
5'-most EST
                   xjt700094957.h1
Seq. No.
                   286863
Contig ID
                   202064 1.R1011
5'-most EST
                   xsy700209481.hl
                   BLASTX
```

5'-most EST xsy70020948
Method BLASTX
NCBI GI g2583123
BLAST score 170
E value 6.0e-12
Match length 46

% identity

NCBI Description (AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]

Tallaj



Contig ID 202095_1.R1011 5'-most EST cat700019353.r1

Seq. No. 286865

Contig ID 202109_1.R1011 5'-most EST pmx700091160.h1

Method BLASTX
NCBI GI g3913437
BLAST score 541
E value 1.0e-55
Match length 105
% identity 97

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE >gi_1402875_emb_CAA66825_ (X98130) RNA helicase
[Arabidopsis thaliana] >gi_1495271_emb_CAA66613_ (X97970)

RNA helicase [Arabidopsis thaliana]

Seq. No. 286866

Contig ID 202121_1.R1011 5'-most EST gct701169158.h1

Seq. No. 286867

Contig ID 202129_1.R1011 5'-most EST wyr700240327.h1

Method BLASTX
NCBI GI g4218535
BLAST score 491
E value 1.0e-49
Match length 115
% identity 77

NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]

Seq. No. 286868

Contig ID 202253_1.R1011 5'-most EST wev700404903.h1

Seq. No. 286869

Contig ID 202293 1.R1011 5'-most EST cat700019609.r1

Seq. No. 286870

Contig ID 202312_1.R1011 5'-most EST cat700019636.r1

Seq. No. 286871

Contig ID 202363_1.R1011 5'-most EST cat700019695.r1

Seq. No. 286872

Contig ID 202416_1.R1011 5'-most EST hvj700623316.h1

Seq. No. 286873

Contig ID 202461 1.R1011 5'-most EST vux700162270.h1



Contig ID 202472_1.R1011 5'-most EST cat700022007.r1

Seq. No. 286875

Contig ID 202508_1.R1011 5'-most EST tbg700930354.h1

Method BLASTX
NCBI GI g2130082
BLAST score 274
E value 3.0e-24
Match length 143
% identity 41

NCBI Description protein kinase Xa21 (EC 2.7.1.-) - rice >gi_1122443

(U37133) receptor kinase-like protein [Oryza sativa] >gi_2586085 (U72723) receptor kinase-like protein [Oryza

longistaminata] >gi_1586408_prf__2203451A receptor

kinase-like protein [Oryza sativa]

Seq. No. 286876

Contig ID 202523_1.R1011 5'-most EST cat700021603.r1

Seq. No. 286877

Contig ID 202527_1.R1011 5'-most EST gct701168843.h1

Method BLASTX
NCBI GI g4115377
BLAST score 218
E value 1.0e-17
Match length 96
% identity 45

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 286878

Contig ID 202593_1.R1011 5'-most EST cat700019988.r1

Seq. No. 286879

Contig ID 202611_1.R1011 5'-most EST ymt700218808.h1

Seq. No. 286880

Contig ID 202703_1.R1011 5'-most EST xsy700212855.h1

Seq. No. 286881

Contig ID 202729_1.R1011 5'-most EST fdz701158923.h2

Method BLASTX
NCBI GI g2244910
BLAST score 171
E value 2.0e-12
Match length 45
% identity 76

NCBI Description (Z97339) unnamed protein product [Arabidopsis thaliana]



Contig ID 202730_1.R1011 5'-most EST gct701173687.h1

Seq. No. 286883

Contig ID 202733_1.R1011 5'-most EST xsy700211043.h1

Method BLASTX
NCBI GI g294845
BLAST score 296
E value 8.0e-27
Match length 124
% identity 46

NCBI Description (L13655) membrane protein [Saccharum hybrid cultivar

H65-7052]

Seq. No. 286884

Contig ID 202749_1.R1011 5'-most EST uer700580106.h1

Method BLASTX
NCBI GI g4336747
BLAST score 372
E value 1.0e-35
Match length 121
% identity 56

NCBI Description (AF104924) unconventional myosin heavy chain [Zea mays]

Seq. No. 286885

Contig ID 202750_1.R1011 5'-most EST cat700021613.r1

Seq. No. 286886

Contig ID 202797_1.R1011 5'-most EST cat700020257.r1

Seq. No. 286887

Contig ID 202818_1.R1011 5'-most EST cyk700047786.f1

Seq. No. 286888

Contig ID 202948_1.R1011 5'-most EST xmt700267607.h1

Seq. No. 286889

Contig ID 202949_1.R1011 5'-most EST cat700020454.r1

Seq. No. 286890

Contig ID 202958_1.R1011 5'-most EST cat700020469.r1

Method BLASTX
NCBI GI g3152568
BLAST score 315
E value 4.0e-29
Match length 123
% identity 52



NCBI Description (AC002986) Similar to hypothetical protein product

gb_Z97337 from A. thaliana. EST gb_H76597 comes from this

gene. [Arabidopsis thaliana]

Seq. No. 286891

Contig ID 202990_1.R1011 5'-most EST cat700020515.r1

Seq. No. 286892

Contig ID 203027_1.R1011 5'-most EST cat700020572.r1

Method BLASTX
NCBI GI g2244826
BLAST score 330
E value 4.0e-46
Match length 157
% identity 63

NCBI Description (Z97336) replication control protein homolog [Arabidopsis

thaliana]

Seq. No. 286893

Contig ID 203060_1.R1011 5'-most EST gct701172510.h1

Seq. No. 286894

Contig ID 203079_1.R1011 5'-most EST cat700021754.r1

Seq. No. 286895

Contig ID 203104_1.R1011 5'-most EST hvj700624428.h1 Method BLASTX

NCBI GI g2464866
BLAST score 191
E value 2.0e-14
Match length 88
% identity 48

NCBI Description (Z99707) hydroxynitrile lyase like protein [Arabidopsis

thaliana]

Seq. No. 286896

Contig ID 203123_1.R1011 5'-most EST yyf700350001.h1

Seq. No. 286897

Contig ID 203155_1.R1011 5'-most EST ceu700432511.h1

Seq. No. 286898

Contig ID 203165_1.R1011 5'-most EST cat700020756.r1

Seq. No. 286899

Contig ID 203187_1.R1011 5'-most EST cat700020785.r1 Method BLASTX

NCBI GI g3047125



BLAST score 250 E value 2.0e-21 Match length 83 % identity 51

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 286900

Contig ID 203236_1.R1011 5'-most EST pmx700084134.h1

Seq. No. 286901

Contig ID 203242_1.R1011 5'-most EST cat700021828.r1

Seq. No. 286902

Contig ID 203286_1.R1011 5'-most EST cat700020906.r1

Seq. No. 286903

Contig ID 203292_1.R1011 5'-most EST xsy700210213.h1

Seq. No. 286904

Contig ID 203297_1.R1011 5'-most EST pmx700090181.h1

Seq. No. 286905

Contig ID 203341_1.R1011 5'-most EST cat700020970.r1

Seq. No. 286906

Contig ID 203375_1.R1011 5'-most EST xsy700214553.h1

Seq. No. 286907

Contig ID 203421_1.R1011 5'-most EST uwn700281613.h1

Seq. No. 286908

Contig ID 203448_1.R1011 5'-most EST clt700043437.f1

Seq. No. 286909

Contig ID 203461_2.R1011 5'-most EST fdz701158793.h1

Seq. No. 286910

Contig ID 203466_1.R1011 5'-most EST nwy700447794.h1

Seq. No. 286911

Contig ID 203506_1.R1011 5'-most EST xsy700211805.h1

Seq. No. 286912

Contig ID 203536_1.R1011 5'-most EST cat700021324.r1



Contig ID 203592_1.R1011 5'-most EST cat700021391.r1

Seq. No. 286914

Contig ID 203613_1.R1011 5'-most EST cat700021419.r1

Seq. No. 286915

Contig ID 203620_1.R1011 5'-most EST pmx700085707.h1

Method BLASTX
NCBI GI g3287696
BLAST score 453
E value 2.0e-45
Match length 116
% identity 73

NCBI Description (AC003979) Strong similarity to phosphoribosylanthranilate transferase gb_D86180 from Pisum sativum. This ORF may be

part of a larger gene that lies in the overlapping region.

[Arabidopsis thaliana]

Seq. No. 286916

Contig ID 203650_1.R1011 5'-most EST cat700021463.r1

Method BLASTN
NCBI GI g575959
BLAST score 261
E value 1.0e-145
Match length 277
% identity 99

NCBI Description Z.mays (Black Mexican Sweet) mRNA for

1-acyl-glycerol-3-phosphate acyltransferase (putative)

Seq. No. 286917

Contig ID 203657_1.R1011 5'-most EST cat700021471.r1

Seq. No. 286918

Contig ID 203670_1.R1011 5'-most EST cat700021489.r1

Method BLASTX
NCBI GI g2642448
BLAST score 259
E value 1.0e-22
Match length 102
% identity 53

NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana]

>qi 3169187 (AC004401) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 286919

Contig ID 203690_1.R1011 5'-most EST cjh700192923.h1

Seq. No. 286920



203734 1.R1011 Contig ID wty700164137.h1 5'-most EST Seq. No. 286921 203740 1.R1011 Contig ID 5'-most EST $hvj700\overline{6}21247.h1$ Method BLASTX NCBI GI q4539603 BLAST score 199 2.0e-15 E value Match length 100 47 % identity NCBI Description (AL049522) putative dolichol kinase [Schizosaccharomyces pombe] Seq. No. 286922 203804 1.R1011 Contig ID 5'-most EST gwl700612374.h1 Seq. No. 286923 203813 1.R1011 Contig ID 5'-most EST nbm700474036.h1 Seq. No. 286924 203820 1.R1011 Contig ID 5'-most EST $cat700\overline{0}21727.r1$ 286925 Seq. No. 203843 1.R1011 Contig ID 5'-most EST xsy700212305.h1 BLASTX Method NCBI GI g4309698 BLAST score 334 E value 1.0e-31 Match length 70 % identity 87 NCBI Description (AC006266) putative glucosyltransferase [Arabidopsis thaliana] 286926 Seq. No. 203888 1.R1011 Contig ID 5'-most EST vux700158414.h1 Seq. No. 286927 Contig ID 203895 1.R1011 5'-most EST $xmt700\overline{2}62571.h1$ Seq. No. 286928 Contig ID 203895 2.R1011 5'-most EST $xdb700\overline{3}39551.h1$

Seq. No. 286929

Contig ID 203915_1.R1011 5'-most EST ymt700219956.h1

Method BLASTX NCBI GI g3687240 BLAST score 359



E value 6.0e-34 Match length 182 % identity 24

NCBI Description (AC005169) extensin-like protein [Arabidopsis thaliana]

Seq. No. 286930

Contig ID 203928 1.R1011 5'-most EST cat700021878.r1

Seq. No. 286931

Contig ID 203977_1.R1011 5'-most EST cat700021942.r1

Seq. No. 286932

Contig ID 204218_1.R1011 5'-most EST cyk700047306.f1

Seq. No. 286933

Contig ID 204222_1.R1011 5'-most EST zuv700356104.h1

Method BLASTX
NCBI GI g3249105
BLAST score 374
E value 1.0e-45
Match length 141
% identity 66

NCBI Description (AC003114) Contains similarity to protein phosphatase 2C (ABI1) qb X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 286934

Contig ID 204223_1.R1011 5'-most EST cyk700047312.f1

Method BLASTX
NCBI GI g4467126
BLAST score 332
E value 3.0e-32
Match length 102
% identity 71

NCBI Description (AL035538) guanine nucleotide-exchange protein-like

[Arabidopsis thaliana]

Seq. No. 286935

Contig ID 204225_1.R1011 5'-most EST uwc700152776.h1

Method BLASTX
NCBI GI g3953463
BLAST score 228
E value 8.0e-19
Match length 82
% identity 52

NCBI Description (AC002328) F20N2.8 [Arabidopsis thaliana]

Seq. No. 286936

Contig ID 204295_1.R1011 5'-most EST hvj700619969.h1

Seq. No. 286937



Contig ID 204296_1.R1011 5'-most EST cyk700047407.f1

Seq. No. 286938

Contig ID 204353_1.R1011 5'-most EST dyk700106859.h1

Seq. No. 286939

Contig ID 204430_1.R1011 5'-most EST cyk700047587.f1

Seq. No. 286940

Contig ID 204486_1.R1011 5'-most EST tfd700571453.h1

Method BLASTX
NCBI GI g1209756
BLAST score 258
E value 1.0e-26
Match length 102
% identity 67

NCBI Description (U43629) integral membrane protein [Beta vulgaris]

Seq. No. 286941

Contig ID 204497_1.R1011 5'-most EST cyk700047681.f1

Seq. No. 286942

Contig ID 204499_1.R1011 5'-most EST cyk700047684.f1

Seq. No. 286943

Contig ID 204514_1.R1011 5'-most EST wyr700243526.h1

Method BLASTX
NCBI GI g2826786
BLAST score 363
E value 9.0e-35
Match length 100
% identity 78

NCBI Description (Y10905) RAPB protein [Oryza sativa]

Seq. No. 286944

Contig ID 204517_1.R1011 5'-most EST wyr700241609.h1

Method BLASTX
NCBI GI g4580398
BLAST score 475
E value 1.0e-75
Match length 200
% identity 70

NCBI Description (AC007171) putative protein kinase APK1A [Arabidopsis

thaliana]

Seq. No. 286945

Contig ID 204560_1.R1011 5'-most EST dyk700102272.h1



```
286946
Seq. No.
                  204585 1.R1011
Contig ID
5'-most EST
                  fwa700099846.hl
                  BLASTX
Method
                  q3393062
NCBI GI
                  256
BLAST score
                  4.0e-28
E value
                  88
Match length
                  66
% identity
                  (Y17386) putative In2.1 protein [Triticum aestivum]
NCBI Description
                  286947
Seq. No.
                  204654 1.R1011
Contig ID
                  pmx700087557.hl
5'-most EST
Method
                  BLASTX
                  g3395431
NCBI GI
                  326
BLAST score
                  3.0e - 30
E value
                  124
Match length
                   49
% identity
                  (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                   286948
Seq. No.
                   204654 2.R1011
Contig ID
5'-most EST
                   cyk700047895.f1
                  BLASTX
Method
                   g3395431
NCBI GI
BLAST score
                   169
                   5.0e-12
E value
                   53
Match length
                   58
% identity
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
                   286949
Seq. No.
                   204701 1.R1011
Contig ID
5'-most EST
                   cyk700047967.f1
Seq. No.
                   286950
                   204713 1.R1011
Contig ID
                   rvt700551762.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1653655
BLAST score
                   238
E value
                   6.0e-20
Match length
                   125
                   39
% identity
                   (D90915) ATP-dependent Clp protease proteolytic subunit
NCBI Description
                   [Synechocystis sp.]
                   286951
Seq. No.
                   204725 1.R1011
Contig ID
                   yne700378964.h1
5'-most EST
                   BLASTX
Method
```

g3024552 NCBI GI 393 BLAST score

E value 3.0e-38 95 Match length



% identity 82

NCBI Description RAS-RELATED PROTEIN RGP2 (GTP-BINDING REGULATORY PROTEIN RGP2) >gi_419797_pir__S30273 GTP-binding protein rgp2 - rice >gi_218204_dbj_BAA02437_ (D13152) GTP binding protein [Oryza sativa] >gi_446772_prf__1912297A rgp2 gene [Oryza sativa]

Seq. No. 286952

Contig ID 204734_2.R1011 5'-most EST uer700577250.h1

Seq. No. 286953

Contig ID 204734_3.R1011 5'-most EST yyf700350890.h1

Seq. No. 286954

Contig ID 204762_1.R1011 5'-most EST qmh700028684.f1

Seq. No. 286955

Contig ID 204767_1.R1011 5'-most EST tzu700207012.h1

Method BLASTX
NCBI GI g3355473
BLAST score 179
E value 3.0e-13
Match length 74
% identity 53

NCBI Description (AC004218) hypothetical protein [Arabidopsis thaliana]

Seq. No. 286956

Contig ID 204820_1.R1011 5'-most EST cyk700048152.f1

Seq. No. 286957

Contig ID 204825_1.R1011 5'-most EST cyk700051417.f1

Seq. No. 286958

Contig ID 204838_1.R1011 5'-most EST uwc700150185.h1

Method BLASTX
NCBI GI g4115379
BLAST score 142
E value 3.0e-20
Match length 90
% identity 52

NCBI Description (AC005967) putative carbonyl reductase [Arabidopsis

thaliana]

Seq. No. 286959

Contig ID 204845_1.R1011 5'-most EST pwr700448918.h1

Method BLASTX
NCBI GI g2842481
BLAST score 338
E value 1.0e-31



Match length 96 % identity 66

NCBI Description (AL021749) extensin-like protein [Arabidopsis thaliana]

Seq. No. 286960

Contig ID 204850_1.R1011 5'-most EST qmh700026194.f1

Seq. No. 286961

Contig ID 204885_1.R1011 5'-most EST cyk700048244.f1

Method BLASTX
NCBI GI g2498329
BLAST score 462
E value 2.0e-46
Match length 125
% identity 72

NCBI Description PATTERN FORMATION PROTEIN EMB30 >gi_2129665_pir__S65571 pattern-formation protein GNOM - Arabidopsis thaliana

>gi_1209633 (U36433) GNOM gene product [Arabidopsis

thaliana] >gi_1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi_1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession

Number J03918 [Arabidopsis thaliana]

Seq. No. 286962

Contig ID 204888_1.R1011 5'-most EST cyk700048247.f1

Seq. No. 286963

Contig ID 204903_1.R1011 5'-most EST wyr700240222.h1

Seq. No. 286964

Contig ID 204911_1.R1011 5'-most EST wen700332944.h1

Seq. No. 286965

Contig ID 204911_2.R1011 5'-most EST qmh700029985.f1

Seq. No. 286966

Contig ID 204925_1.R1011 5'-most EST hbs701181182.h1

Method BLASTX
NCBI GI g4218537
BLAST score 155
E value 2.0e-10
Match length 64
% identity 52

NCBI Description (AJ010830) GRAB2 protein [Triticum sp.]

Seq. No. 286967

Contig ID 204925_2.R1011 5'-most EST cyk700048290.f1

Method BLASTN



g4218536 NCBI GI 34 BLAST score E value 1.0e-09 66 Match length 88 % identity NCBI Description Triticum sp. mRNA for GRAB2 protein 286968 Seq. No. 204936 1.R1011 Contig ID uwc700152583.h1 5'-most EST 286969 Seq. No. 204966 1.R1011 Contig ID afb700381542.h1 5'-most EST BLASTX Method q4503511 NCBI GI 146 BLAST score 4.0e-09 E value 102 Match length 36 % identity UNKNOWN >gi 3264861 (U97670) eukaryotic translation NCBI Description initiation factor eIF3, p35 subunit [Homo sapiens] 286970 Seq. No. 205040_1.R1011 Contig ID 5'-most EST wty700166419.h1 BLASTX Method g2262173 NCBI GI 860 BLAST score 1.0e-92 E value Match length 194 % identity (AC002329) NADPH thioredoxin reductase [Arabidopsis NCBI Description thaliana]

286971 Seq. No.

205043 1.R1011 Contig ID 5'-most EST vux700160678.h1

286972 Seq. No.

205077 1.R1011 Contig ID tzu700201325.hl 5'-most EST

BLASTX Method NCBI GI g1353193 BLAST score 248 2.0e-21 E value Match length 77 % identity 69

O-METHYLTRANSFERASE ZRP4 (OMT) >gi 542186 pir__JQ2268 NCBI Description O-methyltransferase (EC 2.1.1.-) - maize >gi 404070

(L14063) O-methyltransferase [Zea mays]

286973 Seq. No.

205136 1.R1011 Contig ID $xmt700\overline{2}65976.h1$ 5'-most EST

BLASTX Method NCBI GI g228058



BLAST score 143 5.0e-09 E value Match length 69 49 % identity

protein kinase C I [Aplysia californica] NCBI Description

286974 Seq. No.

205163 1.R1011 Contig ID ymt700224259.h1 5'-most EST

BLASTX Method g1174740 NCBI GI 739 BLAST score 2.0e-78 E value 203 Match length 69 % identity

DNA TOPOISOMERASE II >gi_2129576_pir__S53599 DNA NCBI Description

topoisomerase II - Arabidopsis thaliana >gi 474890 (L21015)

topoisomerase II [Arabidopsis thaliana]

Seq. No. 286975

205212 1.R1011 Contig ID dyk700105835.h1 5'-most EST

Method BLASTX NCBI GI g4371296 BLAST score 279 8.0e-25 E value 139 Match length 47 % identity

(AC006260) putative receptor protein kinase [Arabidopsis NCBI Description

thaliana]

286976 Seq. No.

205236 1.R1011 Contig ID ntr700072140.h1 5'-most EST

286977 Seq. No.

205243 1.R1011 Contig ID 5'-most EST xsy700213356.hl

286978 Seq. No.

205264 1.R1011 Contig ID 5'-most EST $wen700\overline{3}33809.h1$

286979 Seq. No.

205267 1.R1011 Contig ID cyk700048802.f1 5'-most EST

Method BLASTX NCBI GI q4503325 BLAST score 334 2.0e-31 E value 96 Match length 67 % identity

NCBI Description

deoxyhypusine synthase >gi_1352267_sp_P49366_DHYS_HUMAN DEOXYHYPUSINE SYNTHASE >gi_994715 (L39068) deoxyhypusine synthase [Homo sapiens] >gi_1710220 (U79262) deoxyhypusine synthase [Homo sapiens] >gi_3021398_emb_CAA04940_

(AJ001701) deoxyhypusine synthase [Homo sapiens]



Seq. No. 286980

Contig ID 205268_1.R1011 5'-most EST nbm700477519.h1

Seq. No. 286981

Contig ID 205272_1.R1011 5'-most EST cyk700048807.f1

Method BLASTX
NCBI GI g4314388
BLAST score 182
E value 5.0e-14
Match length 57
% identity 54

NCBI Description (AC006232) hypothetical protein [Arabidopsis thaliana]

Seq. No. 286982

Contig ID 205306_1.R1011 5'-most EST qmh700029188.f1

Seq. No. 286983

Contig ID 205326_1.R1011 5'-most EST ntr700075076.h1

Seq. No. 286984

Contig ID 205403_1.R1011 5'-most EST cyk700048975.f1

Method BLASTX
NCBI GI g4587610
BLAST score 196
E value 3.0e-15
Match length 68
% identity 62

NCBI Description (AC006951) putative indole-3-glycerol phosphate synthase

precursor [Arabidopsis thaliana]

Seq. No. 286985

Contig ID 205410_1.R1011 5'-most EST ypc700806158.h1

Method BLASTX
NCBI GI g2736147
BLAST score 339
E value 1.0e-31
Match length 91
% identity 64

NCBI Description (AF021804) fatty acid hydroxylase Fahlp [Arabidopsis

thaliana] >gi_3132481 (AC003096) fatty acid hydroxylase,

FAH1 [Arabidopsis thaliana]

Seq. No. 286986

Contig ID 205434_1.R1011 5'-most EST cyk700049021.f1

Seq. No. 286987

Contig ID 205444_1.R1011 5'-most EST ymt700223916.h1

Method BLASTX



NCBI GI g2842481 BLAST score 182 E value 5.0e-13 Match length 127 % identity 35

NCBI Description (AL021749) extensin-like protein [Arabidopsis thaliana]

Seq. No. 286988

Contig ID 205477_1.R1011 5'-most EST cyk700049874.f1

Method BLASTX
NCBI GI g4512659
BLAST score 521
E value 2.0e-53
Match length 113
% identity 86

NCBI Description (AC006931) putative protein kinase [Arabidopsis thaliana] >gi_4544465 gb AAD22372.1 AC006580 4 (AC006580) putative

protein kinase [Arabidopsis thaliana]

Seq. No. 286989

Contig ID 205489 1.R1011 5'-most EST cyk700049088.f1

Seq. No. 286990

Contig ID 205539_1.R1011 5'-most EST cyk700049154.f1

Method BLASTN
NCBI GI g3925218
BLAST score 167
E value 5.0e-89
Match length 199
% identity 96

NCBI Description Zea mays peroxidase R15 mRNA, partial cds

Seq. No. 286991

Contig ID 205541_1.R1011 5'-most EST pmx700083774.h1

Method BLASTX
NCBI GI g1346809
BLAST score 625
E value 3.0e-65
Match length 150
% identity 77

NCBI Description PATHOGEN-RELATED PROTEIN >gi_499074_emb_CAA34641_ (X16648)

pathogenesis related protein [Hordeum vulgare]

Seq. No. 286992

Contig ID 205576_1.R1011 5'-most EST cyk700049208.f1

Seq. No. 286993

Contig ID 205595_1.R1011 5'-most EST cyk700049235.f1

Method BLASTX
NCBI GI g3914365
BLAST score 616



E value 2.0e-64 Match length 130 % identity 88

NCBI Description PHOSPHOLIPASE D 2 PRECURSOR (PLD 2) (CHOLINE PHOSPHATASE 2)

(PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D 2)

>gi_1902901_dbj_BAA19466_ (AB001919) phospholipase D [Oryza

satīva]

Seq. No. 286994

Contig ID 205614_1.R1011 5'-most EST wty700171725.h1

Seq. No. 286995

Contig ID 205630 1.R1011 5'-most EST ymy700282472.h2

Seq. No. 286996

Contig ID 205649_1.R1011 5'-most EST cyk700049304.f1

Method BLASTX
NCBI GI g4154352
BLAST score 242
E value 2.0e-20
Match length 132
% identity 42

NCBI Description (AF110333) PrMC3 [Pinus radiata]

Seq. No. 286997

Contig ID 205660_1.R1011 5'-most EST cyk700049321.f1

Method BLASTX
NCBI GI g3063471
BLAST score 194
E value 6.0e-15
Match length 54
% identity 67

NCBI Description (AC003981) F22013.33 [Arabidopsis thaliana]

Seq. No. 286998

Contig ID 205672_1.R1011 5'-most EST cyk700049335.f1

Seq. No. 286999

Contig ID 205696_1.R1011 5'-most EST wen700336650.h1

Method BLASTX
NCBI GI g3334756
BLAST score 409
E value 4.0e-40
Match length 108
% identity 69

NCBI Description (Y16672) putative arginine/serine-rich splicing factor

[Medicago sativa]

Seq. No. 287000

Contig ID 205701_1.R1011 5'-most EST tzu700203920.h1



BLASTX Method g3402699 NCBI GI 184 BLAST score 7.0e-22 E value 158 Match length 39 % identity (AC004261) unknown protein [Arabidopsis thaliana] NCBI Description 287001 Seq. No. 205728 1.R1011 Contig ID 5'-most EST dyk700106650.hl BLASTX Method q4586053 NCBI GI 397 BLAST score 2.0e-39 E value 127 Match length 63 % identity (AC007020) putative lacasse [Arabidopsis thaliana] NCBI Description 287002 Seq. No. 205734 1.R1011 Contig ID fwa700099454.hl 5'-most EST BLASTX Method q4138724 NCBI GI 476 BLAST score 6.0e-48 E value 125 Match length 74 % identity (AJ001061) hexose transporter [Vitis vinifera] NCBI Description 287003 Seq. No. 205737 1.R1011 Contig ID 5'-most EST xjt700094866.h1 287004 Seq. No. Contig ID 205744 1.R1011 dyk700105542.h1 5'-most EST BLASTX Method NCBI GI q1711355 BLAST score 187 E value 9.0e-16 103 Match length 50 % identity SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE NCBI Description >gi_421786_pir__S34678 short-chain alcohol dehydrogenase -Norway spruce >gi_395223_emb_CAA52213_ (X74115) short-chain alcohol dehydrogenase [Picea abies] 287005 Seq. No. 205786 1.R1011 Contig ID

cyk700049491.fl 5'-most EST

287006 Seq. No.

205795 1.R1011 Contig ID $wyr700\overline{2}37164.h1$ 5'-most EST

BLASTX Method g4336747 NCBI GI



BLAST score 273 7.0e-24 E value Match length 164 42 % identity (AF104924) unconventional myosin heavy chain [Zea mays] NCBI Description 287007 Seq. No. 205804 1.R1011 Contig ID $cyk700\overline{0}49519.f1$ 5'-most EST BLASTX Method g2191187 NCBI GI BLAST score 281 1.0e-24 E value Match length 212 30 % identity (AF007271) contains similarity to a DNAJ-like domain NCBI Description [Arabidopsis thaliana] 287008 Seq. No. 205810 1.R1011 Contig ID gct701180422.hl 5'-most EST 287009 Seq. No. 205821 1.R1011 Contig ID cyk700051346.fl 5'-most EST BLASTX Method g1418331 NCBI GI BLAST score 292 1.0e-26 E value 94 Match length 60 % identity (X95909) receptor like protein kinase [Arabidopsis NCBI Description thaliana] 287010 Seq. No. 205822 1.R1011 Contig ID ntr700075082.h1 5'-most EST BLASTX Method q3461817 NCBI GI 169 BLAST score 5.0e-23E value 107 Match length 56 % identity (AC004138) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 287011

Contig ID 205880_1.R1011 5'-most EST cyk700049622.f1

Seq. No. 287012

Contig ID 205887 1.R1011 5'-most EST gct701176976.h1

Method BLASTX
NCBI GI g4115379
BLAST score 352
E value 5.0e-33
Match length 172

Match length

% identity

161

81



% identity (AC005967) putative carbonyl reductase [Arabidopsis NCBI Description thalianal 287013 Seq. No. Contig ID 205891_1.R1011 $wyr700\overline{2}36233.h1$ 5'-most EST BLASTX Method NCBI GI q3075398 BLAST score 642 E value 3.0e-67 Match length 172 % identity 66 NCBI Description (AC004484) unknown protein [Arabidopsis thaliana] 287014 Seq. No. Contig ID 205919 1.R1011 5'-most EST cyk700049674.f1 Seq. No. 287015 Contig ID 205925 1.R1011 5'-most EST xsy700214873.h1 Method BLASTX NCBI GI q4103959 BLAST score 258 E value 1.0e-22 Match length 75 37 % identity (AF030033) calmodulin [Phaseolus vulgaris] NCBI Description Seq. No. 287016 205965 1.R1011 Contig ID 5'-most EST cyk700049737.f1 Method BLASTX NCBI GI g3482979 BLAST score 208 E value 2.0e-16 Match length 46 78 % identity NCBI Description (AL031369) putative protein [Arabidopsis thaliana] >gi_4567258_gb_AAD23672.1_AC007070_21 (AC007070) hypothetical protein [Arabidopsis thaliana] 287017 Seq. No. Contig ID 206031 1.R1011 $cyk700\overline{0}49830.f1$ 5'-most EST 287018 Seq. No. 206050 1.R1011 Contig ID wyr700236972.h1 5'-most EST BLASTN Method NCBI GI q2342495 BLAST score 41 E value 9.0e-14

39950

NCBI Description Ananas comosus mRNA for bromelain, complete cds



Seq. No.

Contig ID 5'-most EST

287019

206117 1.R1011

rvt700552169.h1

```
BLASTX
Method
NCBI GI
                   q4510375
BLAST score
                   460
                   8.0e-46
E value
Match length
                   184
                   49
% identity
NCBI Description
                   (AC007017) putative homeotic protein BEL1 [Arabidopsis
                   thaliana]
                   287020
Seq. No.
Contig ID
                   206125 1.R1011
5'-most EST
                   cyk700049959.f1
                   BLASTX
Method
NCBI GI
                   q2281111
BLAST score
                   223
E value
                   3.0e-38
Match length
                   135
% identity
                   56
NCBI Description
                   (AC002333) endochitinase isolog [Arabidopsis thaliana]
                   >gi 2288991 (AC002335) endochitinase isolog [Arabidopsis
                   thaliana]
                   287021
Seq. No.
                   206132 1.R1011
Contig ID
                   hbs701185950.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4001663
BLAST score
                   222
E value
                   1.0e-24
Match length
                   82
% identity
                   78
NCBI Description
                  (AB015207) ribosomal protein CRP7 [Neurospora crassa]
                   287022
Seq. No.
                   206137 1.R1011
Contig ID
5'-most EST
                   cyk700049976.f1
                   287023
Seq. No.
                   206176 1.R1011
Contig ID
                   ymt700\overline{2}22659.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4240207
BLAST score
                   149
                   1.0e-09
E value
                   62
Match length
                   42
% identity
NCBI Description
                   (AB020666) KIAA0859 protein [Homo sapiens]
                   287024
Seq. No.
                   206177 1.R1011
Contig ID
5'-most EST
                   cyk700\overline{0}50025.f1
Seq. No.
                   287025
```



Contig ID 206187 1.R1011 5'-most EST wyr700239973.h1

Seq. No. 287026

Contig ID 206205_1.R1011 5'-most EST gct701180484.h1

Seq. No. 287027

Contig ID 206214_1.R1011 5'-most EST tfd700574877.h1

Seq. No. 287028

Contig ID 206217_1.R1011 5'-most EST cyk700050090.f1

Method BLASTX
NCBI GI g2464865
BLAST score 250
E value 2.0e-21
Match length 103
% identity 51

NCBI Description (Z99707) pectinesterase like protein [Arabidopsis thaliana]

Seq. No. 287029

Contig ID 206231_1.R1011 5'-most EST wyr700240311.h1

Method BLASTX
NCBI GI g493947
BLAST score 164
E value 1.0e-11
Match length 58
% identity 53

NCBI Description Chymotrypsin Inhibitor 2 (Ci2) Mutant With Ile 76 Replaced

By Val (I76v)

Seq. No. 287030

Contig ID 206239_1.R1011 5'-most EST qmh700027418.f1

Method BLASTX
NCBI GI 94455302
BLAST score 318
E value 5.0e-43
Match length 126
% identity 70

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 287031

Contig ID 206286_1.R1011 5'-most EST ymt700223048.h1

Seq. No. 287032

Contig ID 206290_1.R1011 5'-most EST wty700168533.h1

Seq. No. 287033

Contig ID 206306 1.R1011 5'-most EST xsy700210616.h1

Method BLASTX



```
q3687223
NCBI GI
                   354
BLAST score
                   2.0e-33
E value
Match length
                   171
% identity
                   47
                   (AC005169) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   287034
Seq. No.
                   206325_1.R1011
Contig ID
                   uwc700149980.h1
5'-most EST
Method
                   BLASTX
                   q1707657
NCBI GI
BLAST score
                   262
E value
                   4.0e-23
Match length
                   96
% identity
                   56
NCBI Description
                   (Z71640) DnaJ homologue [Pisum sativum]
                   287035
Seq. No.
Contig ID
                   206328 1.R1011
5'-most EST
                   xsy700213024.h1
                   287036
Seq. No.
Contig ID
                   206333 1.R1011
                   ntr700077395.h1
5'-most EST
                   287037
Seq. No.
                   206425 1.R1011
Contig ID
5'-most EST
                   cyk700\overline{0}50379.f1
Seq. No.
                   287038
                   206426 1.R1011
Contig ID
5'-most EST
                   qmh700027435.f1
Seq. No.
                   287039
Contig ID
                   206446 1.R1011
5'-most EST
                   cyk700050406.f1
                   287040
Seq. No.
                   206448 1.R1011
Contig ID
5'-most EST
                   cyk700050521.f1
Seq. No.
                   287041
                   206485 1.R1011
Contig ID
                   qmh700\overline{0}30458.f1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4454010
BLAST score
                   366
                   4.0e-35
E value
Match length
                   123
                   55
% identity
                  (AL035396) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No.

206487 1.R1011 Contig ID 5'-most EST cyk700050455.f1



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287043
Seq. No.
                   206495 1.R1011
Contig ID
5'-most EST
                   hbs701181048.h1
Method
                   BLASTX
                   q4585142
NCBI GI
                   312
BLAST score
                   7.0e-29
E value
                   104
Match length
                   60
% identity
                   (AF088276) NADPH oxidase; gp91; phox homolog [Lycopersicon
NCBI Description
                   287044
Seq. No.
Contig ID
                   206515 1.R1011
5'-most EST
                   qmh700025762.f1
                   287045
Seq. No.
                   206522 1.R1011
Contig ID
                   wty700163006.h1
5'-most EST
Method
                   BLASTX
                   g2911073
NCBI GI
                   153
BLAST score
E value
                   4.0e-10
Match length
                   48
                   54
% identity
NCBI Description
                  (AL021960) putative protein [Arabidopsis thaliana]
                   287046
Seq. No.
                   206522 2.R1011
Contiq ID
5'-most EST
                   fdz701164813.hl
                   287047
Seq. No.
                   206527 1.R1011
Contig ID
5'-most EST
                   cyk700050507.f1
Seq. No.
                   287048
                   206534 1.R1011
Contig ID
                   cyk700050514.f1
5'-most EST
                   287049
Seq. No.
                   206569 1.R1011
Contig ID
                   qmh700\overline{0}28914.f1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1077551
BLAST score
                   216
E value
                   2.0e-17
Match length
                   115
                   41
% identity
                   probable membrane protein YDR049w - yeast (Saccharomyces
NCBI Description
                   cerevisiae) >gi_798901_emb_CAA89079 (Z49209) unknown
                   [Saccharomyces cerevisiae]
                   287050
Seq. No.
```

206598 1.R1011 Contig ID 5'-most EST $qmh700\overline{0}27329.f1$

BLASTX Method NCBI GI g868154



BLAST score 507 E value 1.0e-51 Match length 135 % identity 73

NCBI Description (U26537) similar to mipB gene product in Mesembryanthemum crystallinum, encoded by Genbank Accession Number L36097; MIP homolog; Method: conceptual translation supplied by

author [Mesembryanthemum crystallinum]

Seq. No. 287051

Contig ID 206604_1.R1011 5'-most EST pmx700090051.h1

Method BLASTN
NCBI GI g1747293
BLAST score 49
E value 1.0e-18
Match length 81
% identity 90

NCBI Description Oryza sativa mRNA for vacuolar H+-pyrophosphatase, complete

cds

Seq. No. 287052

Contig ID 206607_1.R1011 5'-most EST ntr700073545.h1

Method BLASTX
NCBI GI g4218535
BLAST score 208
E value 1.0e-16
Match length 50
% identity 78

NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]

Seq. No. 287053

Contig ID 206623_1.R1011 5'-most EST tzu700204267.h1

Seq. No. 287054

Contig ID 206628_1.R1011 5'-most EST wyr700241877.h1

Method BLASTX
NCBI GI g4559371
BLAST score 161
E value 8.0e-11
Match length 76
% identity 42

NCBI Description (AC006585) putative peroxidase [Arabidopsis thaliana]

Seq. No. 287055

Contig ID 206638_1.R1011 5'-most EST cyk700050643.f1

Seq. No. 287056

Contig ID 206644_1.R1011 5'-most EST xjt700095393.h1

Seq. No. 287057

Contig ID 206725 1.R1011



5'-most EST

cyk700050924.f1

```
287058
Seq. No.
                   206732 1.R1011
Contig ID
5'-most EST
                   cjh700196639.hl
                   BLASTX
Method
                   g2696225
NCBI GI
                   333
BLAST score
                   4.0e-31
E value
Match length
                   133
                   58
% identity
                  (D55710) chitinase [Oryza sativa]
NCBI Description
                   287059
Seq. No.
                   206805 1.R1011
Contig ID
5'-most EST
                   cyk700050847.f1
                   BLASTX
Method
                   q3763940
NCBI GI
                   157
BLAST score
                   2.0e-10
E value
Match length
                   54
% identity
                   61
                   (AC004450) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   287060
Seq. No.
                   206819 1.R1011
Contig ID
                   cyk700\overline{0}52438.f1
5'-most EST
Method
                   BLASTX
                   g2702268
NCBI GI
BLAST score
                   195
                   3.0e-20
E value
                   95
Match length
                   54
% identity
                  (AC003033) putative cellulase [Arabidopsis thaliana]
NCBI Description
                   287061
Seq. No.
Contig ID
                   206823 1.R1011
                   cyk700050868.f1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4469022
                   366
BLAST score
E value
                   8.0e-46
Match length
                   233
                   47
% identity
                   (AL035602) cytochrome P450-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   287062
                   206941 1.R1011
Contig ID
                   wyr700242337.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1922242
BLAST score
                   198
                   3.0e-15
E value
                   57
Match length
% identity
                  (Y10084) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```



Seq. No.	287063
Contig ID	206965_1.R1011
5'-most EST	cyk700051050.f1
	007064

 Seq. No.
 287064

 Contig ID
 206966_1.R1011

 5'-most EST
 qmh700026415.f1

 Seq. No.
 287067

 Contig ID
 206997_2.R1011

 5'-most EST
 xmt700258394.h1

 Method
 BLASTX

 NCBI GI
 g4519673

BLAST score 670
E value 2.0e-70
Match length 206
% identity 60

NCBI Description (AB017694) WREBP-2 [Nicotiana tabacum]

 Seq. No.
 287069

 Contig ID
 207025_1.R1011

 5'-most EST
 cyk700051167.f1

Seq. No. 287071 Contig ID 207049_1.R1011 5'-most EST hvj700622442.h1

 Seq. No.
 287072

 Contig ID
 207059_1.R1011

 5'-most EST
 cyk700051232.f1

Method BLASTX
NCBI GI 94432860
BLAST score 165
E value 2.0e-11
Match length 105
% identity 38

NCBI Description (AC006300) putative glucose-induced repressor protein

[Arabidopsis thaliana]

Seq. No. 287073



207069 1.R1011 Contig ID rvt700552622.h1 5'-most EST BLASTX Method NCBI GI q3885342 BLAST score 410 1.0e-79 E value 163 Match length 82 % identity (ACO05623) putative DNA polymerase [Arabidopsis thaliana] NCBI Description 287074 Seq. No. 207092 1.R1011 Contig ID $cyk700\overline{0}51932.f1$ 5'-most EST BLASTX Method g2618721 NCBI GI BLAST score 211 8.0e-17 E value 46 Match length 78 % identity (U49072) IAA16 [Arabidopsis thaliana] NCBI Description 287075 Seq. No. 207105 1.R1011 Contig ID 5'-most EST qmh700029082.f1 287076 Seq. No. 207126 1.R1011 Contig ID cyk700051328.f1 5'-most EST 287077 Seq. No. 207163 1.R1011 Contig ID $cyk700\overline{0}51377.f1$ 5'-most EST BLASTX Method g2696221 NCBI GI 219 BLAST score E value 3.0e-18 75 Match length 56 % identity (D55708) chitinase [Oryza sativa] NCBI Description Seq. No. 287078 207176 1.R1011 Contig ID tzu700206523.h1 5'-most EST Method BLASTX g3925233 NCBI GI BLAST score 592 E value 2.0e-61 118 Match length 97 % identity NCBI Description (AF037034) putative peroxidase P7X [Zea mays] Seq. No. 287079 207207 1.R1011 Contig ID

39958

cyk700051447.f1

BLASTX

g3420801 239

5'-most EST

BLAST score

Method NCBI GI



E value 4.0e-20 Match length 111 48

NCBI Description (AF081066) IAA-amino acid hydrolase homolog ILL3

[Arabidopsis thaliana]

Seq. No. 287080

Contig ID 207225_1.R1011 5'-most EST hvj700621605.h1

Method BLASTX
NCBI GI g1174783
BLAST score 299
E value 3.0e-44
Match length 130
% identity 75

NCBI Description TRYPTOPHAN SYNTHASE ALPHA CHAIN PRECURSOR

>gi_1362207_pir__S56665 tryptophan synthase (EC 4.2.1.20)
alpha chain - maize >gi_440171_emb_CAA54131_ (X76713)

tryptophan synthase, alpha subunit [Zea mays]

Seq. No. 287081

Contig ID 207248_1.R1011 5'-most EST cyk700051512.f1

Seq. No. 287082

Contig ID 207260_1.R1011 5'-most EST pmx700081935.h1

Method BLASTX
NCBI GI 94220477
BLAST score 159
E value 1.0e-13
Match length 59
% identity 59

NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 287083

Contig ID 207262_1.R1011 5'-most EST wyr700241752.h1

Method BLASTX
NCBI GI g2618699
BLAST score 490
E value 2.0e-49
Match length 126
% identity 69

NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No. 287084

Contig ID 207268_1.R1011 5'-most EST clt700045353.f1

Seq. No. 287085

Contig ID 207302_1.R1011 5'-most EST gct701170866.h1

Method BLASTX
NCBI GI g4539009
BLAST score 309
E value 4.0e-54



```
157
Match length
% identity
                   (ALO49481) putative protein [Arabidopsis thaliana]
NCBI Description
                  287086
Seq. No.
                  207337 1.R1011
Contig ID
                  xsy700210944.hl
5'-most EST
                  287087
Seq. No.
                  207404 1.R1011
Contig ID
                  xtd700282392.h2
5'-most EST
                  BLASTX
Method
                  g2695861
NCBI GI
                   226
BLAST score
                   9.0e-19
E value
Match length
                   56
                   75
% identity
                  (Y14272) 3-deoxy-D-manno-2-octulosonate-8-phosphate
NCBI Description
                   synthase [Pisum sativum] >gi_2695863_emb_CAA74645_ (Y14273)
                   3-deoxy-D-manno-2-octulosonate-8-phosphate synthase [Pisum
                   sativum]
                   287088
Seq. No.
                   207406 1.R1011
Contig ID
                   wyr700240224.h1
5'-most EST
                   BLASTX
Method
                   q2642158
NCBI GI
                   150
BLAST score
                   6.0e-10
E value
                   92
Match length
                   34
% identity
                  (AC003000) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   287089
Seq. No.
                   207421 1.R1011
Contig ID
5'-most EST
                   xdq700405225.h1
Method
                   BLASTX
NCBI GI
                   q2842493
BLAST score
                   337
                   7.0e-32
E value
Match length
                   74
% identity
NCBI Description (AL021749) predicted protein [Arabidopsis thaliana]
                   287090
Seq. No.
                   207456 1.R1011
Contig ID
5'-most EST
                   gct701169302.h1
Method
                   BLASTX
NCBI GI
                   g2558660
BLAST score
                   260
                   2.0e-22
E value
Match length
                   156
                   40
% identity
                   (ACO02354) No definition line found [Arabidopsis thaliana]
NCBI Description
```

39960

287091

207461 1.R1011

Seq. No.

Contig ID



```
5'-most EST
                   yyf700349308.h1
                   287092
Seq. No.
                   207497 1.R1011
Contig ID
                   yyf700349016.h1
5'-most EST
                   287093
Seq. No.
                   207498 1.R1011
Contig ID
                   cyk700051884.fl
5'-most EST
                   BLASTX
Method
                   g3925231
NCBI GI
BLAST score
                   428
                   1.0e-42
E value
                   80
Match length
                   96
% identity
                  (AF037033) anionic peroxidase H [Zea mays]
NCBI Description
Seq. No.
                   287094
                   207505 1.R1011
Contig ID
                   cyk700051891.f1
5'-most EST
Seq. No.
                   287095
                   207517 1.R1011
Contig ID
                   cyk700\overline{0}51909.f1
5'-most EST
Seq. No.
                   287096
                   207562 1.R1011
Contig ID
5'-most EST
                   ceu700422826.h1
                   287097
Seq. No.
                   207580 1.R1011
Contig ID
                   xmt700\overline{2}59152.h2
5'-most EST
                   BLASTX
Method
                   g3327150
NCBI GI
                   179
BLAST score
                   8.0e-13
E value
                   194
Match length
% identity
NCBI Description (AB014568) KIAA0668 protein [Homo sapiens]
                   287098
Seq. No.
                   207592 1.R1011
Contig ID
                   ceu700424791.h1
5'-most EST
                   BLASTX
Method
                    q4432821
NCBI GI
                    507
BLAST score
                    2.0e-51
E value
Match length
                   147
                    69
% identity
                    (AC006593) putative transmembrane protein [Arabidopsis
NCBI Description
                    thaliana]
                    287099
```

Seq. No. 207596 1.R1011 Contig ID $qmh700\overline{0}26031.f1$ 5'-most EST

Seq. No. 287100



Contig ID 207611_1.R1011
5'-most EST xyt700345995.h1

Seq. No. 287101
Contig ID 207621_1.R1011
5'-most EST cyk700052065.f1
Method BLASTX

NCBI GI g3559807
BLAST score 154
E value 2.0e-12
Match length 102
% identity 42

NCBI Description (Y15628) HCF136 protein [Arabidopsis thaliana]

Seq. No. 287102

Contig ID 207638_1.R1011 5'-most EST cyk700052083.f1

Seq. No. 287103

Contig ID 207646_1.R1011 5'-most EST cyk700052091.f1

Seq. No. 287104

Contig ID 207667_1.R1011 5'-most EST cyk700052125.f1

Seq. No. 287105

Contig ID 207687_1.R1011 5'-most EST cyk700052149.f1

Seq. No. 287106

Contig ID 207710_1.R1011 5'-most EST ymt700219335.h1

Seq. No. 287107

Contig ID 207741_1.R1011 5'-most EST tzu700203939.h1

Method BLASTX
NCBI GI g3128168
BLAST score 147
E value 2.0e-09
Match length 54
% identity 46

NCBI Description (AC004521) putative carboxyl-terminal peptidase

[Arabidopsis thaliana]

Seq. No. 287108

Contig ID 207746_1.R1011 5'-most EST gct701180577.h1

Seq. No. 287109

Contig ID 207775_1.R1011 5'-most EST cyk700052283.f1

Method BLASTX
NCBI GI g4512685
BLAST score 162
E value 4.0e-11



Match length 84 % identity 42

NCBI Description (AC006931) hypothetical protein [Arabidopsis thaliana]

>gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No. 287110

Contig ID 207784_1.R1011 5'-most EST cyk700052293.f1

Seq. No. 287111

Contig ID 207816_1.R1011 5'-most EST tzu700201987.h1

Seq. No. 287112

Contig ID 207862_1.R1011 5'-most EST cyk700052439.f1

Method BLASTX
NCBI GI g1314711
BLAST score 438
E value 1.0e-43
Match length 97
% identity 84

NCBI Description (U54615) calcium-dependent protein kinase [Arabidopsis

thaliana] >gi_3068712 (AF049236) calcium dependent protein

kinase [Arabidopsis thaliana]

Seq. No. 287113

Contig ID 207897_1.R1011 5'-most EST pmx700087010.h1

Seq. No. 287114

Contig ID 207907_1.R1011 5'-most EST qmh700026731.f1

Method BLASTX
NCBI GI g2506931
BLAST score 290
E value 6.0e-26
Match length 114
% identity 50

NCBI Description APYRASE PRECURSOR (ATP-DIPHOSPHATASE) (ADENOSINE DIPHOSPHATASE) (ADPASE) (ATP-DIPHOSPHOHYDROLASE)

>gi_2129977_pir__JC4616 apyrase (EC 3.6.1.5) - potato
>gi_1381633 (U58597) ATP-diphosphohydrolase [Solanum

tuberosum]

Seq. No. 287115

Contig ID 207908_1.R1011 5'-most EST qmh700030004.f1

Method BLASTX
NCBI GI g1353516
BLAST score 471
E value 3.0e-47
Match length 132
% identity 71

NCBI Description (U38651) sugar transporter [Medicago truncatula]



```
287116
Seq. No.
                   207925 1.R1011
Contig ID
                   qmh700\overline{0}25712.f1
5'-most EST
                   287117
Seq. No.
                   207965 1.R1011
Contig ID
                   qmh700025758.fl
5'-most EST
                   BLASTX
Method
                   g2655031
NCBI GI
BLAST score
                   499
                   6.0e-51
E value
                   93
Match length
                   100
% identity
                  (AF019297) starch synthase isoform zSTSII-2 [Zea mays]
NCBI Description
                   287118
Seq. No.
                   207966 1.R1011
Contig ID
                   qmh700\overline{0}25759.f1
5'-most EST
                   BLASTX
Method
                   g4240269
NCBI GI
                   207
BLAST score
                   2.0e-16
E value
                   113
Match length
                   42
% identity
                  (AB020697) KIAA0890 protein [Homo sapiens]
NCBI Description
Seq. No.
                   287119
                   207977 1.R1011
Contig ID
5'-most EST
                   qmh700025771.f1
                   287120
Seq. No.
                   207983 1.R1011
Contig ID
                   qmh700025778.f1
5'-most EST
                   BLASTX
Method
                   q4006878
NCBI GI
BLAST score
                   210
E value
                   3.0e-17
                   54
Match length
% identity
NCBI Description (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
Seq. No.
                   287121
                   207988 1.R1011
Contig ID
                   pmx700086720.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4309759
BLAST score
                   733
                   9.0e-78
E value
Match length
                   205
% identity
                   71
                   (AC006217) unknown protein with Src homology 3 (SH3) domain
NCBI Description
                   profile (PDOC50002) [Arabidopsis thaliana]
```

287122

208057 1.R1011

qmh700030633.f1

Seq. No.

Contig ID 5'-most EST



Seq. No. 287123

Contig ID 208080_1.R1011 5'-most EST wyr700235894.h1

Method BLASTX
NCBI GI 94512659
BLAST score 170
E value 4.0e-12
Match length 113
% identity 37

NCBI Description (AC006931) putative protein kinase [Arabidopsis thaliana] >gi_4544465_gb_AAD22372.1_AC006580_4 (AC006580) putative

protein kinase [Arabidopsis thaliana]

Seq. No. 287124

Contig ID 208113_1.R1011 5'-most EST qmh700025939.f1

Seq. No. 287125

Contig ID 208119_1.R1011 5'-most EST qmh700025946.f1

Seq. No. 287126

Contig ID 208120_1.R1011 5'-most EST qmh700025947.f1

Seq. No. 287127

Contig ID 208130_1.R1011 5'-most EST qmh700025958.f1

Method BLASTX
NCBI GI g586477
BLAST score 398
E value 1.0e-38
Match length 151
% identity 52

NCBI Description HYPOTHETICAL 44.2 KD GTP-BINDING PROTEIN IN SCO2-MRF1 INTERGENIC REGION >gi_626828_pir__S45881 probable purine

nucleotide-binding protein YBR025c - yeast (Saccharomyces cerevisiae) >gi_498754 emb_CAA53682_ (X76078) YBR0309 [Saccharomyces cerevisiae] >gi_536234_emb_CAA84967_ (Z35894) ORF YBR025c [Saccharomyces cerevisiae] >gi_1587583_prf__2206497F ORF YBR0309 [Saccharomyces

cerevisiae]

Seq. No. 287128

Contig ID 208139_1.R1011 5'-most EST wyr700240840.h1

Method BLASTN
NCBI GI g4115614
BLAST score 345
E value 0.0e+00
Match length 455
% identity 94

NCBI Description Zea mays mRNA for root cap-specific glycine-rich protein,

complete cds

Seq. No. 287129

Contig ID 208141_1.R1011



tzu700205806.h1 5'-most EST 287130 Seq. No. 208141 2.R1011 Contig ID 5'-most EST qmh700025971.f1 287131 Seq. No. 208143_1.R1011 Contig ID 5'-most EST tzu700205957.h1 BLASTX Method g4493908 NCBI GI BLAST score 163 3.0e-11 E value 66 Match length 42 % identity (AL034558) predicted using hexExon; MAL3P2.30 (PFC0305w), NCBI Description Putative homologue of Human EB1, len: 511 aa; Similarity to Human EB1 protein. H.sapiens EB1 protein (TR:Q156910) BLAST Score: 325, sum P(2) = 6.2e-35; 46% identity in 287132 Seq. No. 208164_1.R1011 Contig ID 5'-most EST wyr700237936.hl 287133 Seq. No. 208179 1.R1011 Contig ID fdz701159841.h1 5'-most EST 287134 Seq. No. 208200 1.R1011 Contig ID 5'-most EST ntr700073581.hl Method BLASTX q481815 NCBI GI 189 BLAST score 3.0e-14E value Match length 82 % identity 44 vegetative storage protein - western balsam poplar \mathbf{x} NCBI Description cottonwood >gi 309839 (L20233) vegetative storage protein [Populus trichocarpa x Populus deltoides] Seq. No. 287135 208262 1.R1011 Contig ID $ceu700\overline{4}21660.h1$ 5'-most EST 287136 Seq. No. 208264 1.R1011 Contig ID tzu700205488.h1 5'-most EST

Seq. No. 287137

Contig ID 208284_1.R1011 5'-most EST tzu700201150.h1

Seq. No. 287138

Contig ID 208289_1.R1011 5'-most EST qmh700026168.f1

Method BLASTX



```
g2253010
NCBI GI
BLAST score
                  371
                  2.0e-58
E value
Match length
                  141
                   78
% identity
                   (Y14199) MAP3K delta-1 protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  287139
Seq. No.
                   208293 1.R1011
Contig ID
5'-most EST
                  wyr700237076.h1
Method
                  BLASTX
                   q2498731
NCBI GI
                   169
BLAST score
E value
                   4.0e-12
                   53
Match length
                   60
% identity
                  PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
NCBI Description
                   >gi_1362013_pir__S57611 zeta-crystallin homolog -
                   Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768)
                   zeta-crystallin homologue [Arabidopsis thaliana]
Seq. No.
                   287140
Contig ID
                   208349 1.R1011
                   dyk700106519.h1
5'-most EST
                   287141
Seq. No.
                   208351 1.R1011
Contig ID
                   xjt700095529.h1
5'-most EST
Seq. No.
                   287142
                   208360 1.R1011
Contig ID
                   wyr700235330.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2598575
BLAST score
                   526
                   1.0e-53
E value
                   130
Match length
% identity
                   76
                  (Y15293) MtN21 [Medicago truncatula]
NCBI Description
Seq. No.
                   287143
                   208386_1.R1011
Contig ID
                   qmh700026306.f1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2493318
                   200
BLAST score
                   1.0e-15
E value
                   61
Match length
                   61
% identity
                   BLUE COPPER PROTEIN PRECURSOR >gi 562779 emb CAA80963
NCBI Description
                   (Z25471) blue copper protein [Pisum sativum]
                   >gi 1098264 prf 2115352A blue Cu protein [Pisum sativum]
```

Seq. No. 287144

Contig ID 208387_1.R1011 5'-most EST wty700167587.h1



115

thaliana]

40

Match length

NCBI Description

% identity

287145 Seq. No. 208403 1.R1011 Contig ID dyk700103204.hl 5'-most EST BLASTX Method g2801803 NCBI GI 392 BLAST score 1.0e-65 E value 164 Match length 80 % identity (AF042489) germin-like protein 16 [Oryza sativa] NCBI Description 287146 Seq. No. 208403 2.R1011 Contig ID $dyk700\overline{1}02774.h1$ 5'-most EST BLASTX Method q1070358 NCBI GI 212 BLAST score 4.0e-17 E value 50 Match length 82 % identity (X93171) oxalate oxidase-like protein or germin-like NCBI Description protein [Hordeum vulgare] 287147 Seq. No. 208406_1.R1011 Contig ID 5'-most EST xsy700214357.h1 BLASTX Method g548702 NCBI GI 332 BLAST score 6.0e-31 E value 94 Match length 60 % identity DNA-DIRECTED RNA POLYMERASE II 14.5 KD POLYPEPTIDE (RPB9) NCBI Description (RPB14.5) >gi_543001_pir__S41621 DNA-directed RNA polymerase (EC 2.7.7.6) II 14.5K chain - human >gi_397150_emb_CAA80649_ (Z23102) RNA Polymerase II subunit 14.5 kD [Homo sapiens] >gi_1905901 (AD001527) HUMAN DNA-DIRECTED RNA POLYMERASE II 14.5 KD SUBUNIT [Homo sapiens] Seq. No. 287148 208427 1.R1011 Contig ID xjt700094231.h1 5'-most EST 287149 Seq. No. 208446 1.R1011 Contig ID qmh700026378.f15'-most EST BLASTX Method q4115379 NCBI GI BLAST score 201 E value 1.0e-15

39968

(AC005967) putative carbonyl reductase [Arabidopsis



Seq. No.

287150

208452 1.R1011

```
Contig ID
                   nbm700\overline{4}65296.h1
5'-most EST
                   BLASTX
Method
                   q3096935
NCBI GI
                   656
BLAST score
                   9.0e-69
E value
Match length
                   172
                   75
% identity
                   (AL023094) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    287151
                    208469 1.R1011
Contig ID
                   wyr700238547.h1
5'-most EST
                    287152
Seq. No.
                    208477 1.R1011
Contig ID
                    qmh700026421.f1
5'-most EST
                    287153
Seq. No.
                    208480 1.R1011
Contig ID
                    hbs701185662.h1
5'-most EST
                    BLASTX
Method
                    g3056592
NCBI GI
                    239
BLAST score
                    5.0e-20
E value
                    154
Match length
                    38
% identity
                   (AC004255) T1F9.13 [Arabidopsis thaliana]
NCBI Description
                    287154
Seq. No.
                    208499 1.R1011
Contig ID
                    gct701168423.h1
5'-most EST
                    BLASTX
Method
                    g112802
NCBI GI
                    192
BLAST score
                    8.0e-15
E value
Match length
                    52
                    71
% identity
                   4-COUMARATE--COA LIGASE >gi_82454_pir__JU0311
4-coumarate--CoA ligase (EC 6.2.1.12) - rice
NCBI Description
                    >gi 20161_emb_CAA36850_ (X52623) 4-coumarate-CoA ligase
                    [Oryza sativa]
                    287155
Seq. No.
                    208526 1.R1011
Contig ID
 5'-most EST
                    dyk700102288.h1
                    BLASTX
Method
NCBI GI
                    g2735502
                    329
BLAST score
                    1.0e-30
E value
                    126
Match length
                    57
 % identity
NCBI Description (U96096) endo-1,3-beta-glucanase [Hordeum vulgare]
                     287156
 Seq. No.
                     208598_1.R1011
 Contig ID
```

E value

2.0e-29



```
uer700577252.h1
5'-most EST
                   287157
Seq. No.
                   208626 1.R1011
Contig ID
                   dyk700\overline{1}05591.h1
5'-most EST
                   BLASTX
Method
                   g2252634
NCBI GI
                   332
BLAST score
                   9.0e-34
E value
                   145
Match length
                   50
% identity
                   (U95973) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   287158
Seq. No.
                   208633 1.R1011
Contig ID
                   qmh700027745.f1
5'-most EST
                   287159
Seq. No.
                   208699 1.R1011
Contig ID
                   dyk700105904.h1
5'-most EST
                   BLASTX
Method
                   g4006918
NCBI GI
                   280
BLAST score
                   1.0e-24
E value
                   129
Match length
                   47
% identity
                   (Z99708) peroxidase like protein [Arabidopsis thaliana]
NCBI Description
                   287160
Seq. No.
                   208703 1.R1011
Contig ID
                   qmh700026722.f1
5'-most EST
                   BLASTX
Method
                   g2342724
NCBI GI
BLAST score
                   416
                   9.0e-41
E value
Match length
                   121
% identity
                   65
                   (AC002341) unknown protein [Arabidopsis thaliana]
NCBI Description
                   287161
Seq. No.
                   208717 1.R1011
Contig ID
                   qmh700\overline{0}26738.f1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2244839
                   379
BLAST score
                   3.0e-36
E value
Match length
                   188
% identity
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    287162
                   208723 1.R1011
Contig ID
                    qmh700026744.fl
5'-most EST
Method
                   BLASTN
NCBI GI
                    g726475
BLAST score
                    67
```



119 Match length 89 % identity NCBI Description

Avena fatua nondormancy-associated clone AFN2 putative ORF1 mRNA, partial cds

287163

Seq. No. 208730 1.R1011 Contig ID wyr700243086.hl 5'-most EST

Method BLASTX q1546692 NCBI GI BLAST score 209 1.0e-16 E value 58 Match length 64 % identity

(X98805) peroxidase ATP19a [Arabidopsis thaliana] NCBI Description

287164 Seq. No.

208756 1.R1011 Contig ID dyk700105701.h1 5'-most EST

BLASTX Method q1279654 NCBI GI 143 BLAST score 4.0e-09 E value Match length 50 % identity 54

(X97351) peroxidase [Populus balsamifera subsp. NCBI Description

trichocarpa]

287165 Seq. No.

208760 1.R1011 Contig ID uwc700150074.h1 5'-most EST

BLASTX Method NCBI GI g2492782 BLAST score 377 E value 2.0e-36 Match length 117 % identity 63

ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE) NCBI Description

(ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi_504489 (L27992)

alpha-galactosidase [Coffea arabica]

287166 Seq. No.

208791 1.R1011 Contig ID $qmh700\overline{0}26843.f1$ 5'-most EST

Seq. No. 287167

208819 2.R1011 Contig ID fdz701163191.hl 5'-most EST

287168 Seq. No.

208819 3.R1011 Contig ID uer700576791.h1 5'-most EST

287169 Seq. No.

208848 1.R1011 Contig ID 5'-most EST qmh700026930.f1

BLASTX Method



```
g4558550
NCBI GI
                   473
BLAST score
                   1.0e-47
E value
Match length
                   112
                   74
% identity
                   (AC007138) putative protein transport factor [Arabidopsis
NCBI Description
                   thaliana]
                   287170
Seq. No.
                   208857 1.R1011
Contig ID
                   fdz701158593.h1
5'-most EST
                   287171
Seq. No.
                   208903 1.R1011
Contig ID
                   dyk700103281.hl
5'-most EST
                   287172
Seq. No.
                   208913 1.R1011
Contig ID
                   qmh700\overline{0}27009.f1
5'-most EST
                   BLASTX
Method
                   g3093294
NCBI GI
                   334
BLAST score
                   3.0e-31
E value
                   116
Match length
                   59
% identity
                   (Y12782) putative villin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   287173
                   208950 1.R1011
Contig ID
                   qmh700027058.fl
5'-most EST
                   287174
Seq. No.
                   208978 1.R1011
Contig ID
                   xjt700\overline{0}92325.h1
5'-most EST
                   BLASTN
Method
                   g4159707
NCBI GI
BLAST score
                   36
E value
                   1.0e-10
                   100
Match length
                   84
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MJK13, complete sequence [Arabidopsis thaliana]
                   287175
Seq. No.
                   209009 1.R1011
Contig ID
                   clt700043821.f1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4127348
BLAST score
                    403
                    2.0e-39
E value
                   117
Match length
% identity
                   (AJ010449) glutathione transferase [Alopecurus myosuroides]
NCBI Description
```

Seq. No. 287176

Contig ID 209011_1.R1011 5'-most EST hbs701186269.h1



```
287177
Seq. No.
Contig ID
                   209031 1.R1011
5'-most EST
                   qmh700027162.f1
                   287178
Seq. No.
                   209033 1.R1011
Contig ID
5'-most EST
                   qmh700\overline{0}27164.f1
                   BLASTX
Method
                   q4220462
NCBI GI
                   359
BLAST score
                   6.0e-40
E value
Match length
                   114
                   64
% identity
                  (AC006216) Strong similarity to gb_Z50851 HD-zip (athb-8)
NCBI Description
                   gene from Arabidopsis thaliana containing Homeobox PF_00046
                   and bZIP PF 00170 domains. [Arabidopsis thaliana]
                   287179
Seq. No.
Contig ID
                   209054 1.R1011
                   rv1700454826.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1707642
BLAST score
                   501
E value
                   1.0e-50
Match length
                   143
% identity
                   70
NCBI Description (Y07748) TMK [Oryza sativa]
Seq. No.
                   287180
                   209069 1.R1011
Contig ID
5'-most EST
                   qmh700\overline{0}27211.f1
Method
                   BLASTX
                   g418777
NCBI GI
BLAST score
                   302
E value
                   7.0e-28
                   58
Match length
% identity
NCBI Description phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic
                   chain (clone EP7) - Arabidopsis thaliana (fragment)
Seq. No.
                   287181
Contig ID
                   209071 1.R1011
                   qmh700027213.f1
5'-most EST
Seq. No.
                   287182
                   209132 1.R1011
Contig ID
5'-most EST
                   mwy700440537.h1
```

Method BLASTX
NCBI GI g2760333
BLAST score 191
E value 1.0e-14
Match length 98
% identity 42

NCBI Description (AC002130) F1N21.18 [Arabidopsis thaliana]

Seq. No. 287183



209137 1.R1011 Contig ID qmh700027304.f1 5'-most EST 287184 Seq. No. 209140 1.R1011 Contig ID qmh700027309.f15'-most EST BLASTX Method g294845 NCBI GI 193 BLAST score 5.0e-15 E value 77 Match length 53 % identity (L13655) membrane protein [Saccharum hybrid cultivar NCBI Description H65-7052] 287185 Seq. No. 209168 1.R1011 Contig ID $qmh700\overline{0}27560.f1$ 5'-most EST 287186 Seq. No. 209207 1.R1011 Contig ID $qmh700\overline{0}27401.f1$ 5'-most EST BLASTX Method g860676 NCBI GI BLAST score 212 E value 6.0e-17 Match length 50 74 % identity (U24188) calcium/calmodulin-dependent protein kinase NCBI Description [Lilium longiflorum] >gi_1097385_prf__2113422A Ca/calmodulin-dependent protein kinase [Lilium longiflorum] 287187 Seq. No. 209231 1.R1011 Contig ID $qmh700\overline{0}27427.f1$ 5'-most EST Seq. No. 287188 Contig ID 209306 1.R1011 5'-most EST wyr700236274.hl 287189 Seq. No. 209306 2.R1011 Contig ID 5'-most EST wty700162982.hl 287190 Seq. No. 209341_1.R1011 Contig ID 5'-most EST gct701175455.h1 Seq. No. 287191 209352 1.R1011 Contig ID $ntr700\overline{0}73929.h1$ 5'-most EST Method BLASTX

Method BLASTX
NCBI GI g1743354
BLAST score 284
E value 2.0e-29
Match length 101
% identity 64



(Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum] NCBI Description 287192 Seq. No. 209369 1.R1011 Contig ID qmh700027593.f15'-most EST 287193 Seq. No. 209378 1.R1011 Contig ID 5'-most EST $qmh700\overline{0}27607.f1$ Method BLASTX NCBI GI q2459446 BLAST score 401 7.0e-39 E value 183 Match length 42 % identity (ACO02332) putative cinnamoyl-CoA reductase [Arabidopsis NCBI Description thaliana] 287194 Seq. No. 209386 1.R1011 Contig ID qmh700027615.f15'-most EST 287195 Seq. No. 209402 1.R1011 Contig ID 5'-most EST tzu700201760.hl Method BLASTX a1350951 NCBI GI BLAST score 411 2.0e-40 E value 103 Match length 79 % identity 40S RIBOSOMAL PROTEIN S18E >gi_1071977_pir__S50886 NCBI Description ribosomal protein S18.e, cytosolic - yeast (Saccharomyces cerevisiae) >gi_575693 emb CAA86629 (Z46659) 40S ribosomal protein gene, len: 146, CAI: 0.74 [Saccharomyces cerevisiae] >qi 927725 (U33007) Ydr450wp [Saccharomyces cerevisiae] 287196 Seq. No.

Contig ID 209442_1.R1011 5'-most EST qmh700027687.f1

Seq. No. 287197

Contig ID 209459_1.R1011 5'-most EST qmh700029630.f1

Seq. No. 287198

Contig ID 209513_1.R1011 5'-most EST uwc700152213.h1

Seq. No. 287199

Contig ID 209532_1.R1011 5'-most EST qmh700027809.f1

Seq. No. 287200

Contig ID 209540_1.R1011 5'-most EST vux700158261.h1



Contig ID 209542_1.R1011 5'-most EST pmx700082536.h1

Method BLASTX
NCBI GI g4544399
BLAST score 672
E value 1.0e-86
Match length 197
% identity 83

NCBI Description (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana]

Seq. No. 287202

Contig ID 209552_1.R1011 5'-most EST qmh700028317.f1

Seq. No. 287203

Contig ID 209575_1.R1011 5'-most EST qmh700027867.f1

Method BLASTX
NCBI GI g3193300
BLAST score 179
E value 2.0e-13
Match length 94
% identity 48

NCBI Description (AF069298) No definition line found [Arabidopsis thaliana]

Seq. No. 287204

Contig ID 209595_1.R1011 5'-most EST qmh700027896.f1

Seq. No. 287205

Contig ID 209612_1.R1011 5'-most EST xsy700211916.h1

Seq. No. 287206

Contig ID 209629_1.R1011 5'-most EST qmh700027937.f1

Seq. No. 287207

Contig ID 209645_1.R1011 5'-most EST qmh700027953.f1

Seq. No. 287208

Contig ID 209647_1.R1011 5'-most EST qmh700027955.f1

Seq. No. 287209

Contig ID 209685_1.R1011 5'-most EST ymt700220024.h1

Method BLASTX
NCBI GI g2708532
BLAST score 485
E value 3.0e-50
Match length 140
% identity 69



```
(AF029351) putative RNA binding protein [Nicotiana tabacum]
NCBI Description
                  287210
Seq. No.
                  209730 1.R1011
Contig ID
                  qmh700028063.fl
5'-most EST
                  BLASTX
Method
                  g2498098
NCBI GI
                  235
BLAST score
E value
                  6.0e-20
                  80
Match length
% identity
                  60
                  A3 PROTEIN >gi_2129909_pir__S58310 gene A3 protein - cowpea
NCBI Description
                  >gi_938300_emb_CAA62086_ (X90487) unknown [Vigna
                  unguiculata]
                  287211
Seq. No.
                  209730 2.R1011
Contig ID
                  vux700159036.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2498098
                  166
BLAST score
E value
                   5.0e-12
Match length
                   58
                   59
% identity
                  A3 PROTEIN >gi 2129909 pir S58310 gene A3 protein - cowpea
NCBI Description
                   >gi 938300_emb_CAA62086_ (X90487) unknown [Vigna
                   unguiculata]
                   287212
Seq. No.
                   209731 1.R1011
Contig ID
5'-most EST
                   qmh700028064.f1
                   287213
Seq. No.
                   209743_1.R1011
Contig ID
5'-most EST
                   wyr700235714.h1
                   287214
Seq. No.
                   209763 1.R1011
Contig ID
5'-most EST
                   pmx700088856.h1
                   287215
Seq. No.
                   209785 1.R1011
Contig ID
                   qmh700028143.f1
5'-most EST
                   287216
Seq. No.
Contig ID
                   209852 1.R1011
                   xsy700217531.h1
5'-most EST
                   BLASTX
Method
                   g1353193
NCBI GI
BLAST score
                   175
                   8.0e-24
E value
                   119
Match length
                   50
% identity
                   O-METHYLTRANSFERASE ZRP4 (OMT) >gi 542186_pir__JQ2268
NCBI Description
```

(L14063) O-methyltransferase [Zea mays]

O-methyltransferase (EC 2.1.1.-) - maize >gi 404070

Contig ID 5'-most EST



```
287217
Seq. No.
                   209875 1.R1011
Contig ID
                   xjt700094048.h1
5'-most EST
Method
                   BLASTX
                   g1151134
NCBI GI
                   263
BLAST score
                   3.0e-23
E value
                   50
Match length
                   98
% identity
                   (U43034) permease 1 [Zea mays]
NCBI Description
                   287218
Seq. No.
                   209893 1.R1011
Contig ID
                   amh700028282.f1
5'-most EST
                   BLASTX
Method
                   g3047318
NCBI GI
BLAST score
                   393
                   6.0e-40
E value
                   106
Match length
                   19
% identity
                   (AF056625) poly-ubiquitin [Magnaporthe grisea]
NCBI Description
Seq. No.
                   287219
                   209927_1.R1011
Contig ID
5'-most EST
                   qmh700\overline{0}28327.f1
                   BLASTN
Method
                   q1946264
NCBI GI
BLAST score
                   36
                   6.0e-11
E value
                   48
Match length
% identity
                   94
NCBI Description O.sativa mRNA for myb factor, 1202 bp
                   287220
Seq. No.
Contig ID
                   209934 1.R1011
5'-most EST
                   qmh700028336.f1
                   287221
Seq. No.
                   210033 1.R1011
Contig ID
                    qmh700028480.f1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1742959
BLAST score
                   272
                    2.0e-24
E value
                   73
Match length
% identity
                    70
                    (Z71450) CLC-d chloride channel protein [Arabidopsis
NCBI Description
                    thaliana]
                    287222
Seq. No.
                    210073 1.R1011
Contig ID
                    ceu700\overline{4}33205.h1
5'-most EST
                    287223
Seq. No.
```

210073 2.R1011

yyf700351796.h1



```
287224
Seq. No.
                  210078 1.R1011
Contig ID
5'-most EST
                  amh700028547.f1
                  287225
Seq. No.
                  210085 1.R1011
Contig ID
5'-most EST
                  qmh700028555.fl
                  287226
Seq. No.
                  210101_1.R1011
Contig ID
5'-most EST
                  nbm700477603.hl
                  BLASTN
Method
                  q5091496
NCBI GI
                  56
BLAST score
E value
                  7.0e-23
                  124
Match length
                   86
% identity
                  Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
NCBI Description
                   complete sequence
                   287227
Seq. No.
                   210101_2.R1011
Contig ID
5'-most EST
                   qmh700028572.f1
Method
                   BLASTN
                   q5091496
NCBI GI
BLAST score
                   62
                   2.0e-26
E value
Match length
                   142
                   86
% identity
                   Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
NCBI Description
                   complete sequence
                   287228
Seq. No.
                   210104 1.R1011
Contig ID
5'-most EST
                   qmh700028576.f1
                   287229
Seq. No.
                   210109 1.R1011
Contig ID
5'-most EST
                   ymt700219253.h1
                   287230
Seq. No.
                   210119 1.R1011
Contig ID
                   hbs701182570.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4539314
BLAST score
                   211
                   8.0e-17
E value
```

123 Match length 38 % identity

(AL035679) kinesin like protein [Arabidopsis thaliana] NCBI Description

287231 Seq. No.

210129 1.R1011 Contig ID $qmh700\overline{0}28610.f1$ 5'-most EST

Seq. No. 287232

210132_1.R1011 Contig ID

Contig ID 5'-most EST

287242

210435 1.R1011

uwc700155042.h1



5'-most EST qmh700028613.f1 287233 Seq. No. Contig ID 210136 1.R1011 5'-most EST nbm700470847.h1 287234 Seq. No. 210150 1.R1011 Contig ID 5'-most EST $qmh700\overline{0}28633.f1$ Seq. No. 287235 210271 1.R1011 Contig ID tzu700206624.hl 5'-most EST BLASTX Method NCBI GI a3850584 BLAST score 262 6.0e-23E value Match length 86 63 % identity (AC005278) ESTs gb H37641 and gb AA651422 come from this NCBI Description gene. [Arabidopsis thaliana] Seq. No. 287236 210336 1.R1011 Contig ID 5'-most EST dyk700106496.h1 Method BLASTX NCBI GI q3249105 BLAST score 599 E value 3.0e-62 Match length 138 % identity 80 (AC003114) Contains similarity to protein phosphatase 2C NCBI Description (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana] Seq. No. 287237 210366 1.R1011 Contig ID 5'-most EST wty700171572.h1 287238 Seq. No. 210372 1.R1011 Contig ID $xdb700\overline{3}37382.h1$ 5'-most EST 287239 Seq. No. 210394 1.R1011 Contig ID 5'-most EST rvt700553302.hl 287240 Seq. No. 210401 1.R1011 Contig ID 5'-most EST wyr700237869.hl 287241 Seq. No. 210412 1.R1011 Contig ID 5'-most EST xyt700344475.h1



Method BLASTX
NCBI GI g4063747
BLAST score 172
E value 3.0e-12
Match length 61
% identity 57

NCBI Description (AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No. 287243

Contig ID 210488_1.R1011 5'-most EST gct701168969.h1

Method BLASTX
NCBI GI g1123105
BLAST score 194
E value 9.0e-15
Match length 152
% identity 31

NCBI Description (U42438) similar to S. cerevisiae longevity-assurance

protein 1 (SP:P38703) [Caenorhabditis elegans]

Seq. No. 287244

Contig ID 210517 1.R1011 5'-most EST ymt700219938.h1

Seq. No. 287245

Contig ID 210520_1.R1011 5'-most EST vux700162211.h1

Method BLASTX
NCBI GI 94154283
BLAST score 224
E value 3.0e-18
Match length 171
% identity 38

NCBI Description (AF089744) xenotropic and polytropic murine leukemia virus

receptor X3 [Homo sapiens] >gi 4324975 gb AAD17211_

(AF115389) SYG1 protein [Homo sapiens]

Seq. No. 287246

Contig ID 210526_1.R1011 5'-most EST qmh700029132.f1

Seq. No. 287247

Contig ID 210532_1.R1011 5'-most EST qmh700029139.f1

Seq. No. 287248

Contig ID 210545_1.R1011 5'-most EST xsy700208776.h1

Seq. No. 287249

Contig ID 210549_1.R1011 5'-most EST qmh700029160.f1

Seq. No. 287250

Contig ID 210587_1.R1011 5'-most EST qmh700029208.f1



```
287251
Seq. No.
                   210629 1.R1011
Contig ID
                   pmx700085864.h1
5'-most EST
                   287252
Seq. No.
                   210641 2.R1011
Contig ID
                   vux700159574.h1
5'-most EST
                   287253
Seq. No.
                   210663 1.R1011
Contig ID
5'-most EST
                   qmh700029537.f1
                   287254
Seq. No.
                   210670 1.R1011
Contig ID
5'-most EST
                   sz1700184958.h1
                   287255
Seq. No.
                   210674 1.R1011
Contig ID
                   qmh700029353.f1
5'-most EST
                   BLASTX
Method
                   g4586053
NCBI GI
                   388
BLAST score
                   7.0e - 38
E value
                   94
Match length
                   67
% identity
                  (AC007020) putative lacasse [Arabidopsis thaliana]
NCBI Description
                   287256
Seq. No.
                   210676 1.R1011
Contig ID
                   nbm700469088.h1
5'-most EST
                   BLASTX
Method
                   q4309741
NCBI GI
                   240
BLAST score
E value
                   2.0e-20
                   80
Match length
% identity
                   61
                  (AC006439) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   287257
Seq. No.
                   210681 1.R1011
Contiq ID
5'-most EST
                   ntr700073081.h1
Method
                   BLASTX
NCBI GI
                   g2160169
BLAST score
                   202
E value
                   9.0e-16
Match length
                   81
% identity
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.
                   287258
                   210689 1.R1011
Contig ID
                   xmt700\overline{2}66470.h1
5'-most EST
```

BLASTX Method g3253159 NCBI GI

314 BLAST score 9.0e-29 E value 170 Match length



% identity 44

NCBI Description (AF005355) translation initiation factor eIF2C [Oryctolagus

cuniculus]

Seq. No. 287259

Contig ID 210709_1.R1011 5'-most EST tzu700205523.h1

Seq. No. 287260

Contig ID 210744_1.R1011 5'-most EST ymt700221419.h1

Seq. No. 287261

Contig ID 210748_1.R1011 5'-most EST dyk700106333.h1

Method BLASTX
NCBI GI g3831440
BLAST score 351
E value 2.0e-33
Match length 96
% identity 69

NCBI Description (AC005819) putative cytochrome P450 [Arabidopsis thaliana]

>gi_4415946_gb_AAD20176_ (AC006418) putative cytochrome

P450 [Arabidopsis thaliana]

Seq. No. 287262

Contig ID 210824 1.R1011 5'-most EST rvt700551777.h1

Seq. No. 287263

Contig ID 210866_1.R1011 5'-most EST qmh700029601.f1

Seq. No. 287264

Contig ID 210884_1.R1011 5'-most EST pmx700090914.h1

Seq. No. 287265

Contig ID 210887_1.R1011 5'-most EST qmh700029628.f1

Seq. No. 287266

Contig ID 210916_1.R1011 5'-most EST qmh700029665.f1

Method BLASTX
NCBI GI g4220480
BLAST score 311
E value 2.0e-28
Match length 147
% identity 24

NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 287267

Contig ID 210921_1.R1011 5'-most EST dyk700103391.h1

Method BLASTX NCBI GI g2244876



426 BLAST score 5.0e-42 E value Match length 139 % identity 59

(Z97338) hypothetical protein [Arabidopsis thaliana] NCBI Description

287268 Seq. No.

Contig ID 210924 1.R1011 5'-most EST qmh700029675.f1

Seq. No. 287269

210926 1.R1011 Contig ID tzu700204786.h1 5'-most EST

Seq. No. 287270

210949 1.R1011 Contig ID 5'-most EST xjt700096434.h1

287271 Seq. No.

Contig ID 210951 1.R1011 5'-most EST qmh700029709.f1

Seq. No. 287272

210967 1.R1011 Contig ID 5'-most EST vux700156928.h1

287273 Seq. No.

Contig ID 210980 1.R1011 qmh700029740.f15'-most EST

287274 Seq. No.

211018 1.R1011 Contig ID $qmh700\overline{0}29782.f1$ 5'-most EST

Method BLASTX NCBI GI g2191140 BLAST score 192 6.0e-15 E value 69 Match length

54 % identity

(AF007269) contains weak similarity to MYB-related proteins NCBI Description

[Arabidopsis thaliana]

287275 Seq. No.

211021 1.R1011 Contig ID rvt700549912.h1 5'-most EST

BLASTX Method NCBI GI g4249382 BLAST score 209 7.0e-17 E value Match length 47 79 % identity

(AC005966) Strong similarity to gi_3337350 F13P17.3 NCBI Description

putative permease from Arabidopsis thaliana BAC

gb AC004481. [Arabidopsis thaliana]

Seq. No. 287276

Contig ID 211067 1.R1011

Method

NCBI GI

BLASTX

g3184283



```
5'-most EST
                   qmh700029844.fl
                   287277
Seq. No.
Contig ID
                   211089 1.R1011
                   fwa700100882.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3928084
BLAST score
                   142
E value
                   7.0e-09
Match length
                   106
                   39
% identity
                   (AC005770) retrotransposon-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   287278
                   211090 1.R1011
Contig ID
                   qmh700\overline{0}29869.f1
5'-most EST
                   287279
Seq. No.
Contig ID
                   211116 1.R1011
5'-most EST
                   wyr700237651.h1
                   287280
Seq. No.
Contig ID
                   211122 1.R1011
5'-most EST
                   qmh700029913.fl
                   287281
Seq. No.
                   211136_1.R1011
Contig ID
                   qmh700029930.f1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3367571
BLAST score
                   216
E value
                   6.0e-18
Match length
                   75
% identity
                  (AL031135) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   287282
                   211217 1.R1011
Contig ID
5'-most EST
                   wyr700242045.h1
Seq. No.
                   287283
                   211243 1.R1011
Contig ID
                   xdg700405178.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4455309
BLAST score
                   394
E value
                   2.0e-38
                   130
Match length
                   62
% identity
NCBI Description (AL035528) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   287284
                   211246 1.R1011
Contig ID
5'-most EST
                   xjt700\overline{0}96282.h1
```



600 BLAST score E value 2.0e-62 Match length 135 85 % identity (AC004136) putative TBP-binding protein [Arabidopsis NCBI Description thaliana] 287285 Seq. No. Contig ID 211270 1.R1011 ntr700073662.h1 5'-most EST Method BLASTX g3954807 NCBI GI 232 BLAST score 3.0e-19 E value Match length 114 % identity 40 (AJ011862) flavonoid 3',5'-hydroxylase [Catharanthus NCBI Description roseus] 287286 Seq. No. 211273 1.R1011 Contig ID qmh700030124.f1 5'-most EST Method BLASTX NCBI GI q2760830 588 BLAST score E value 5.0e-61 137 Match length % identity 81 (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis NCBI Description thaliana] 287287 Seq. No. 211327 1.R1011 Contig ID 5'-most EST qmh700030194.f1 Seq. No. 287288 211341 1.R1011 Contig ID amh700030212.f15'-most EST BLASTX Method NCBI GI g4581150 BLAST score 411 4.0e-40 E value 166 Match length 56 % identity (AC006919) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 287289 211399 1.R1011 Contig ID 5'-most EST qmh700030277.f1 Seq. No. 287290 211404 1.R1011 Contig ID

Contig ID 211404_1.R1011 5'-most EST qmh700030282.f1

Method BLASTX
NCBI GI g3292824
BLAST score 565
E value 3.0e-58



Match length 167 % identity 67

NCBI Description

(AL031018) putative protein [Arabidopsis thaliana]

Seq. No. Contig ID 287291 211417 1.R1011

5'-most EST qmh700 $\overline{0}$ 30304.f1

287292

287293

Seq. No.

Contig ID 211454_1.R1011 5'-most EST qmh700030348.f1

Method BLASTX
NCBI GI g2642165
BLAST score 237
E value 9.0e-20
Match length 142
% identity 37

NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.

Contig ID 211457_1.R1011 5'-most EST qmh700030351.f1

Seq. No. 287294

Contig ID 211477_1.R1011 5'-most EST uwc700156155.h1

Seq. No. 287295

Contig ID 211505_1.R1011 5'-most EST ypc700805420.h1

Method BLASTN
NCBI GI g288611
BLAST score 106
E value 2.0e-52
Match length 305
% identity 85

NCBI Description Z.mays PG gene for polygalacturonase

Seq. No. 287296

Contig ID 211538_1.R1011 5'-most EST qmh700030457.f1

Seq. No. 287297

Contig ID 211571_1.R1011 5'-most EST vux700157020.h1

Method BLASTX
NCBI GI g1872521
BLAST score 226
E value 1.0e-18
Match length 93
% identity 53

NCBI Description (U87833) zinc-finger protein Lsdl [Arabidopsis thaliana]

>gi_1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis

thaliana]

Seq. No. 287298

Contig ID 211588 1.R1011



```
qmh700030523.f1
5'-most EST
                   287299
Seq. No.
                   211590 1.R1011
Contig ID
                   tzu700205168.hl
5'-most EST
                   287300
Seq. No.
                   211642 1.R1011
Contig ID
5'-most EST
                   qmh700\overline{0}30603.f1
                   BLASTX
Method
NCBI GI
                   q3482916
                   264
BLAST score
                   3.0e-23
E value
Match length
                   115
% identity
                   49
                  (AC003970) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   287301
Seq. No.
                   211644 1.R1011
Contig ID
                   uwc700150743.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2760830
BLAST score
                   232
E value
                   2.0e-19
Match length
                   65
% identity
                   65
                   (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
                   287302
Seq. No.
                   211657 1.R1011
Contig ID
                   xjt700\overline{0}95811.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4056421
BLAST score
                   252
E value
                   1.0e-21
                   73
Match length
                   66
% identity
                   (AC005322) Similar to gb_Z30094 basic transcripion factor
NCBI Description
                   2, 44 kD subunit from Homo sapiens. EST gb_W43325 comes
                   from this gene. [Arabidopsis thaliana]
                   287303
Seq. No.
                   211660 1.R1011
Contig ID
5'-most EST
                   qmh700030624.f1
Method
                   BLASTX
                   g3482933
NCBI GI
                   499
BLAST score
                   1.0e-50
E value
                   137
Match length
% identity
                   69
                   (AC003970) Similar to cdc2 protein kinases [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   287304
```

39988

211664 1.R1011

tzu700204530.h1

Contig ID

5'-most EST



Contig ID 211677_1.R1011 5'-most EST fwa700101003.h1

Method BLASTX
NCBI GI g4585975
BLAST score 206
E value 3.0e-16
Match length 81
% identity 48

NCBI Description (AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 287306

Contig ID 211713_1.R1011 5'-most EST wen700335459.h1

Seq. No. 287307

Contig ID 211722_1.R1011 5'-most EST tzu700204460.h1

Method BLASTX
NCBI GI g1143381
BLAST score 204
E value 1.0e-24
Match length 116
% identity 52

NCBI Description (Z49063) polygalacturonase inhibitor [Actinidia deliciosa]

Seq. No. 287308

Contig ID 211734_1.R1011 5'-most EST pmx700086191.h1

Seq. No. 287309

Contig ID 211734_2.R1011 5'-most EST tym700023125.f1

Seq. No. 287310

Contig ID 211755_1.R1011 5'-most EST tzu700201791.h1

Seq. No. 287311

Contig ID 211757_2.R1011 5'-most EST tzu700201123.h1

Method BLASTX
NCBI GI g4204695
BLAST score 369
E value 1.0e-35
Match length 104
% identity 61

NCBI Description (AF117062) putative inositol polyphosphate 5-phosphatase

At5P1 [Arabidopsis thaliana]

Seq. No. 287312

Contig ID 211770_1.R1011 5'-most EST tzu700201143.h1

Seq. No. 287313

Contig ID 211786_1.R1011

Contig ID

5'-most EST

287321

211952_2.R1011 pmx700087337.h1



```
5'-most EST
                  xsy700214634.hl
Seq. No.
                  287314
                  211836 1.R1011
Contig ID
5'-most EST
                  wty700167763.hl
Seq. No.
                  287315
Contig ID
                  211865 1.R1011
5'-most EST
                  uwc700154114.hl
Seq. No.
                  287316
                  211868 1.R1011
Contig ID
                  tzu700201269.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1621465
BLAST score
                  511
E value
                   7.0e-52
Match length
                  172
% identity
                   54
NCBI Description (U73105) laccase [Liriodendron tulipifera]
                  287317
Seq. No.
                  211921 1.R1011
Contig ID
5'-most EST
                  hbs701182446.h1
Method
                  BLASTX
NCBI GI
                   q1620753
BLAST score
                  209
E value
                   1.0e-16
                  78
Match length
% identity
                   53
                  (U72942) proteinase inhibitor [Oryza sativa]
NCBI Description
                  >gi_2829212_gb_AAC00503_ (AF044059) proteinase inhibitor
                   [Oryza sativa]
Seq. No.
                   287318
                   211945 1.R1011
Contig ID
5'-most EST
                   gw1700614545.hl
Method
                  BLASTX
NCBI GI
                  q2323410
BLAST score
                   151
E value
                   5.0e-10
                  59
Match length
                   51
% identity
NCBI Description (AF015913) Skb1Hs [Homo sapiens]
Seq. No.
                   287319
                   211946 1.R1011
Contig ID
5'-most EST
                  hvj700620725.h1
Seq. No.
                   287320
                   211952 1.R1011
Contig ID
5'-most EST
                  ymt700223669.hl
```



287322 Seq. No. 211961 1.R1011 Contig ID ceu700429539.h1 5'-most EST 287323 Seq. No. 211967 1.R1011 Contig ID pmx700082010.h1 5'-most EST BLASTXMethod g2832700 NCBI GI 213 BLAST score 1.0e-16 E value 78 Match length 54 % identity (AL021713) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 287324 212016 1.R1011 Contig ID hvj700622558.h1 5'-most EST BLASTN Method q3819466 NCBI GI 35 BLAST score 3.0e-10 E value 91 Match length 85 % identity Hordeum vulgare genomic DNA fragment; clone MWG0967.uni NCBI Description 287325 Seq. No. Contig ID 212039 1.R1011 tzu700203709.h1 5'-most EST 287326 Seq. No. 212118 1.R1011 Contig ID 5'-most EST tzu700201631.h1 BLASTX Method g4115946 NCBI GI 198 BLAST score E value 3.0e-15 83 Match length 45 % identity (AF118223) contains similarity to Ipomoea nil leaf protein NCBI Description (GB: D85101) [Arabidopsis thaliana] 287327 Seq. No. 212136 1.R1011 Contig ID 5'-most EST $cjh700\overline{1}96881.h1$ Seq. No. 287328

Contig ID 212155_1.R1011 5'-most EST fdz701165645.h1

Method BLASTX
NCBI GI g2654559
BLAST score 191
E value 1.0e-14
Match length 107
% identity 34

NCBI Description (AF006621) embryonic lung protein [Homo sapiens]



212241 1.R1011 Contig ID fdz701162956.h1 5'-most EST

BLASTX Method g2959767 NCBI GI 343 BLAST score 2.0e-32 E value 109 Match length 60 % identity

(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 NCBI Description

(AC005309) glutathione-conjugate transporter AtMRP4

[Arabidopsis thaliana]

287330 Seq. No.

212243 1.R1011 Contig ID tzu700201786.hl 5'-most EST

287331 Seq. No.

212261 1.R1011 Contig ID fdz701164659.h1 5'-most EST

287332 Seq. No.

212282 1.R1011 Contig ID ymt700220722.h1 5'-most EST

287333 Seq. No.

Contig ID 212362 1.R1011 tzu700201948.h1 5'-most EST

BLASTX Method q1731101 NCBI GI BLAST score 314 6.0e-29 E value 127 Match length

54 % identity

HYPOTHETICAL 29.7 KD PROTEIN IN FOLD-AHRC INTERGENIC REGION NCBI Description

>gi_1303921_dbj_BAA12577_ (D84432) YqiF [Bacillus subtilis] >gi_2634860_emb_CAB14357_ (Z99116) alternate gene name: yqiF; similar to hemolysin-like [Bacillus subtilis]

287334 Seq. No.

212398 1.R1011 Contig ID tzu700201995.h1 5'-most EST

BLASTX Method NCBI GI g3522943 BLAST score 433 5.0e-43E value Match length 115 % identity

NCBI Description (AC004411) putative p-glycoprotein [Arabidopsis thaliana]

287335 Seq. No.

212401 1.R1011 Contig ID tzu700204996.h1 5'-most EST

287336 Seq. No.

212548 1.R1011 Contig ID $tzu700\overline{2}02288.h1$ 5'-most EST



Method BLASTX
NCBI GI g4417304
BLAST score 262
E value 3.0e-25
Match length 97
% identity 56

NCBI Description (AC006446) putative beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis

thaliana]

Seq. No. 287337

Contig ID 212580_1.R1011 5'-most EST xsy700217731.h1

Seq. No. 287338

Contig ID 212607_1.R1011 5'-most EST xyt700343509.h1

Method BLASTX
NCBI GI g3006088
BLAST score 248
E value 7.0e-21
Match length 177
% identity 38

NCBI Description (AJ222724) SGT protein [Rattus norvegicus]

Seq. No. 287339

Contig ID 212666_1.R1011 5'-most EST tzu700202469.h1

Seq. No. 287340

Contig ID 212668_1.R1011 5'-most EST tzu700202473.h1

Method BLASTX
NCBI GI g3522946
BLAST score 268
E value 5.0e-24
Match length 75
% identity 68

NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 287341

Contig ID 212695_1.R1011 5'-most EST nwy700445036.h1

Seq. No. 287342

Contig ID 212737 1.R1011 5'-most EST tzu700202578.h1

Method BLASTX
NCBI GI g2213882
BLAST score 391
E value 1.0e-46
Match length 141
% identity 73

NCBI Description (AF004165) 2-isopropylmalate synthase [Lycopersicon

pennellii]

Seq. No. 287343



Contig ID 212742_1.R1011 5'-most EST xsy700213424.h1

Seq. No. 287344

Contig ID 212743_1.R1011 5'-most EST tzu700205607.h1

Seq. No. 287345

Contig ID 212744 1.R1011 5'-most EST ceu700421957.h1

Seq. No. 287346

Contig ID 212772_1.R1011 5'-most EST tzu700202638.h1

Method BLASTX
NCBI GI g3212870
BLAST score 331
E value 4.0e-31
Match length 107
% identity 61

NCBI Description (AC004005) putative N-myristoyltransferase [Arabidopsis

thaliana]

Seq. No. 287347

Contig ID 212805_1.R1011 5'-most EST tzu700202740.h1

Method BLASTX
NCBI GI g4103635
BLAST score 157
E value 1.0e-10
Match length 79
% identity 39

NCBI Description (AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No. 287348

Contig ID 212869_1.R1011 5'-most EST tzu700202839.h1

Method BLASTX
NCBI GI g124131
BLAST score 184
E value 1.0e-13
Match length 63
% identity 57

NCBI Description SUBTILISIN INHIBITOR >gi 100106 pir A21463 subtilisin

inhibitor - fava bean (fragment)

Seq. No. 287349

Contig ID 212934_1.R1011 5'-most EST tfd700569758.h1

Seq. No. 287350

Contig ID 213013_1.R1011 5'-most EST wyr700238191.h1

Seq. No. 287351

Contig ID 213079_1.R1011 5'-most EST uwc700154807.h1

287356



```
BLASTN
Method
NCBI GI
                  g3821780
                   36
BLAST score
                   9.0e-11
E value
                   48
Match length
                   67
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   287352
Seq. No.
                   213121 1.R1011
Contig ID
                  tzu700203253.h1
5'-most EST
                  BLASTX
Method
                   q1805254
NCBI GI
                   152
BLAST score
                   5.0e-11
E value
Match length
                   66
                   59
% identity
                   (U62622) monogalactosyldiacylglycerol synthase [Cucumis
NCBI Description
                   sativus]
                   287353
Seq. No.
                   213136 1.R1011
Contig ID
                   ypc700803973.h1
5'-most EST
                   BLASTX
Method
                   q4512659
NCBI GI
                   384
BLAST score
                   2.0e-37
E value
                   90
Match length
                   78
% identity
                   (AC006931) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   >gi_4544465_gb_AAD22372.1_AC006580_4 (AC006580) putative
                   protein kinase [Arabidopsis thaliana]
                   287354
Seq. No.
                   213157 1.R1011
Contig ID
5'-most EST
                   qct701177930.hl
Method
                   BLASTX
NCBI GI
                   q1362064
BLAST score
                   293
                   1.0e-26
E value
                   77
Match length
                   69
% identity
                   small G protein - garden pea >gi 871514 emb_CAA90079_
NCBI Description
                   (Z49899) small G protein [Pisum sativum]
                   287355
Seq. No.
                   213187 1.R1011
Contig ID
5'-most EST
                   ntr700071826.hl
Method
                   BLASTX
                   q2827659
NCBI GI
                   416
BLAST score
                   6.0e-41
E value
Match length
                   118
% identity
                   (AL021637) putative protein [Arabidopsis thaliana]
NCBI Description
```



```
213216_1.R1011
Contig ID
                   wty700\overline{1}71825.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g3821780
BLAST score
                   36
                   9.0e-11
E value
                   48
Match length
                   67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   287357
                   213227 1.R1011
Contig ID
5'-most EST
                   wyr700239935.h1
                   287358
Seq. No.
                   213254 1.R1011
Contig ID
                   tzu700203458.h1
5'-most EST
                   287359
Seq. No.
                   213277 1.R1011
Contig ID
5'-most EST
                   wyr700241830.h1
                   287360
Seq. No.
                   213307 1.R1011
Contig ID
5'-most EST
                   tzu700203551.h1
Method
                   BLASTX
NCBI GI
                   q4454011
BLAST score
                   157
                   1.0e-19
E value
Match length
                   73
                   63
% identity
NCBI Description (AL035396) putative protein [Arabidopsis thaliana]
                   287361
Seq. No.
Contig ID
                   213337_1.R1011
5'-most EST
                   vux700157639.h1
Method
                   BLASTX
                   q4539304
NCBI GI
BLAST score
                   140
                   9.0e-09
E value
Match length
                   81
% identity
NCBI Description (AL049480) putative protein [Arabidopsis thaliana]
                   287362
Seq. No.
                   213338 1.R1011
Contig ID
5'-most EST
                   tzu700203589.h1
Method
                   BLASTX
NCBI GI
                   q3341686
BLAST score
                   365
E value
                   4.0e-35
Match length
                   91
% identity
```

thaliana]

287363

NCBI Description

Seq. No.

39996

(AC003672) putative glycosyl transferase [Arabidopsis



213342 1.R1011 Contig ID 5'-most EST wyr700243442.h1 Method BLASTX g3249071 NCBI GI BLAST score 144 7.0e-09E value Match length 150 % identity 28 NCBI Description (AC004473) Contains similarity to protein-tyrosine phosphatase 2 gb_L15420 from Dictyostelium discoideum. EST gb N38718 comes from this g [Arabidopsis thaliana] 287364 Seq. No. 213401 1.R1011 Contig ID $wen700\overline{3}33276.h1$ 5'-most EST

Seq. No. 287365

Contig ID 213418_1.R1011 5'-most EST nwy700445714.h1

Seq. No. 287366

Contig ID 213432_1.R1011 5'-most EST hvj700623981.h1

Method BLASTX
NCBI GI g3935181
BLAST score 150
E value 3.0e-10
Match length 41
% identity 66

NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana]

Seq. No. 287367

Contig ID 213453_1.R1011 5'-most EST gct701173447.h2

Seq. No. 287368

Contig ID 213459_1.R1011 5'-most EST fwa700100685.h1

Method BLASTX
NCBI GI g1707657
BLAST score 418
E value 3.0e-41
Match length 119
% identity 66

NCBI Description (Z71640) DnaJ homologue [Pisum sativum]

Seq. No. 287369

Contig ID 213465_1.R1011 5'-most EST nwy700443715.h1

Method BLĀSTX
NCBI GI g310940
BLAST score 146
E value 2.0e-09
Match length 62
% identity 45

NCBI Description (L20756) ABA- and ripening-induced protein [Solanum

lycopersicum]

Method

Contig ID

5'-most EST

287379

BLASTX

213656_1.R1011 uwc700153422.h1



```
287370
Seq. No.
                   213466 1.R1011
Contig ID
                   ntr700076323.hl
5'-most EST
                   287371
Seq. No.
                   213470 1.R1011
Contig ID
                   xsy700\overline{2}14453.h1
5'-most EST
Seq. No.
                   287372
                   213487 1.R1011
Contig ID
                   dyk700105086.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2827528
BLAST score
                   218
                   2.0e-17
E value
Match length
                   81
                   47
% identity
NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]
Seq. No.
                   287373
                   213527 1.R1011
Contig ID
                   nbm700474069.h1
5'-most EST
Seq. No.
                   287374
                   213571 1.R1011
Contiq ID
5'-most EST
                   ntr700075348.h1
                   287375
Seq. No.
                   213599 1.R1011
Contig ID
5'-most EST
                   wyr700242962.h1
Seq. No.
                   287376
                   213614 1.R1011
Contig ID
5'-most EST
                   tzu700204045.h1
                   287377
Seq. No.
                   213637 1.R1011
Contig ID
                   tzu700204074.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2501423
BLAST score
                   229
                   3.0e-19
E value
Match length
                   42
% identity
                   100
                   TUBULIN GAMMA CHAIN >gi_629842_pir S44193 tubulin gamma
NCBI Description
                   chain - maize >gi_47440\overline{6}_{emb}C\overline{A}A55\overline{48}8_{(X78891)}
                   gamma-tubulin [Zea mays]
Seq. No.
                   287378
                   213641 1.R1011
Contig ID
5'-most EST
                   ntr700072411.h2
```



NCBI GI g1872521 BLAST score 261 E value 9.0e-23 Match length 69 % identity 35

NCBI Description (U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi 1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis

thaliana]

Seq. No. 287380

Contig ID 213689_1.R1011 5'-most EST xmt700258384.h1

Method BLASTN
NCBI GI 94206305
BLAST score 212
E value 1.0e-116
Match length 300
% identity 93

NCBI Description Zea mays retrotransposon Cinful-1, complete sequence

Seq. No. 287381

Contig ID 213697_1.R1011 5'-most EST tzu700204162.h1

Seq. No. 287382

Contig ID 213723_1.R1011 5'-most EST zvd700460642.h1

Seq. No. 287383

Contig ID 213730_1.R1011 5'-most EST tzu700204206.h1

Seq. No. 287384

Contig ID 213782_1.R1011 5'-most EST uwc700152053.h1

Seq. No. 287385

Contig ID 213801 1.R1011 5'-most EST tzu700204307.h1

Method BLASTX
NCBI GI g3399777
BLAST score 225
E value 4.0e-22
Match length 114
% identity 57

NCBI Description (AF069738) symbiotic ammonium transporter; nodulin [Glycine

max]

Seq. No. 287386

Contig ID 213823 1.R1011 5'-most EST uwc700156176.h1

Seq. No. 287387

Contig ID 213862_1.R1011 5'-most EST pmx700087285.h1

Method BLASTX NCBI GI g4539437



428 BLAST score E value 2.0e-42101 Match length 75 % identity

(AL049523) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. Contig ID 5'-most EST 287388 213885 1.R1011 $nbm700\overline{4}68881.h1$

Seq. No.

287389 Contig ID 213898 1.R1011 uer700580227.hl 5'-most EST

Seq. No. Contig ID 5'-most EST 287390 213908 1.R1011 tzu700204449.h1

Seq. No. Contig ID 5'-most EST

287391 213933 1.R1011 tzu700204480.h1

Seq. No. Contig ID 5'-most EST

287392 213990 1.R1011 tzu700204547.h1

Seq. No. Contig ID 5'-most EST

287393 214029 1.R1011 ntr700074552.h1

Seq. No. Contig ID 5'-most EST

287394 214043 1.R1011 xjt700096003.hl BLASTX

Method NCBI GI BLAST score E value Match length

q3927838 214 3.0e-1746

89

% identity

NCBI Description (AC005727) unknown protein [Arabidopsis thaliana]

Seq. No. Contig ID 5'-most EST

287395 214064 1.R1011 tzu700204641.h1

Seq. No. Contig ID 5'-most EST

287396 214070_1.R1011 rv1700458628.h1

Seq. No. Contig ID

5'-most EST

287397 214077 1.R1011 tzu700204654.h1

 ${\tt BLASTX}$ Method g3075399 NCBI GI BLAST score 156 E value 4.0e-15 Match length 84



```
% identity
                  (AC004484) SF16-like protein [Arabidopsis thaliana]
NCBI Description
                  287398
Seq. No.
                  214100 1.R1011
Contig ID
                  tzu700204680.hl
5'-most EST
Method
                  BLASTN
                  q3821780
NCBI GI
BLAST score
                  36
                  8.0e-11
E value
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  287399
Seq. No.
Contig ID
                  214106 1.R1011
                  uwc700151880.h1
5'-most EST
Method
                  BLASTX
                  g3360289
NCBI GI
BLAST score
                  341
                  4.0e-32
E value
Match length
                  78
                  83
% identity
NCBI Description
                  (AF023164) leucine-rich repeat transmembrane protein kinase
                  1 [Zea mays]
                  287400
Seq. No.
Contig ID
                  214148 1.R1011
5'-most EST
                  fwa700101472.h1
                  287401
Seq. No.
                  214151 1.R1011
Contig ID
5'-most EST
                  tzu700204742.h1
Method
                  BLASTX
NCBI GI
                  q4567315
BLAST score
                  345
E value
                  1.0e-32
Match length
                  80
% identity
                  78
                 (AC005956) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  287402
Seq. No.
                  214182 1.R1011
Contig ID
5'-most EST
                  tzu700204779.h1
Method
                  BLASTX
                  q112994
NCBI GI
BLAST score
                  189
                  7.0e-23
E value
                  69
Match length
% identity
                  71
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >gi 82685 pir S04536 embryonic abundant protein,
                  glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
```

40001

>gi_226091_prf__1410284A abscisic acid inducible gene [Zea

ABA-inducible gene protein [Zea mays]

mays]



Seq. No. 287403 Contig ID 214184_1.R1011

5'-most EST tzu700204781.h1
Method BLASTX
NCBI GI g3367638

NCBI GI g3367638 BLAST score 368 E value 3.0e-35 Match length 126 % identity 60

NCBI Description (AJ000331) monogalactosyldiacylglycerol synthase

[Arabidopsis thaliana]

Seq. No. 287404

Contig ID 214238_1.R1011 5'-most EST tfd700572748.h1

Method BLASTX
NCBI GI g3688808
BLAST score 174
E value 2.0e-12
Match length 98
% identity 41

NCBI Description (AF084104) AcsA [Bacillus firmus]

Seq. No. 287405

Contig ID 214272_1.R1011 5'-most EST tzu700204893.h1

Seq. No. 287406

Contig ID 214273_1.R1011 5'-most EST tzu700204901.h1

Seq. No. 287407

Contig ID 214314_1.R1011 5'-most EST ntr700072258.h1

Method BLASTN
NCBI GI g2944039
BLAST score 270
E value 1.0e-150
Match length 281
% identity 99

NCBI Description Zea mays indeterminate spikelet 1 (ids1) mRNA, complete cds

Seq. No. 287408

Contig ID 214318_1.R1011 5'-most EST tzu700204961.h1

Method BLASTX
NCBI GI g3927831
BLAST score 171
E value 1.0e-16
Match length 71
% identity 68

NCBI Description (AC005727) similar to mouse ankyrin 3 [Arabidopsis

thaliana]

Seq. No. 287409

Contig ID 214345_1.R1011 5'-most EST tzu700205002.h1



Contig ID 214354_1.R1011 5'-most EST pmx700085333.h1

Method BLASTX
NCBI GI g3169174
BLAST score 343
E value 3.0e-32
Match length 123
% identity 53

NCBI Description (AC004401) putative serine carboxypeptidase I [Arabidopsis

thaliana]

Seq. No. 287411

Contig ID 214384 1.R1011 5'-most EST tzu700205048.h1

Method BLASTX
NCBI GI g4049410
BLAST score 461
E value 3.0e-46
Match length 102
% identity 74

NCBI Description (Y10225) L-ascorbate oxidase [Cucumis melo]

Seq. No. 287412

Contig ID 214386_1.R1011 5'-most EST tzu700205050.h1

Seq. No. 287413

Contig ID 214408_1.R1011 5'-most EST fwa700097093.h1

Seq. No. 287414

Contig ID 214414 1.R1011 5'-most EST zuv700354840.h1

Seq. No. 287415

Contig ID 214437_1.R1011 5'-most EST pmx700085463.h1

Method BLASTX
NCBI GI g2244807
BLAST score 365
E value 7.0e-35
Match length 126
% identity 53

NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 287416

Contig ID 214478_1.R1011 5'-most EST xsy700208319.h1

Seq. No. 287417

Contig ID 214480_1.R1011 5'-most EST tzu700205166.h1

Seq. No. 287418

Contig ID 214487 1.R1011



```
ymt700221087.h1
5'-most EST
                   287419
Seq. No.
                   214507 1.R1011
Contig ID
                   cjh700195750.h1
5'-most EST
Seq. No.
                   287420
                   214543 1.R1011
Contig ID
                   tzu700205315.h1
5'-most EST
Seq. No.
                   287421
                   214555 1.R1011
Contig ID
5'-most EST
                   wty700170468.h1
                   287422
Seq. No.
                   214573 1.R1011
Contig ID
                   wyr700\overline{2}35149.h1
5'-most EST
Seq. No.
                   287423
                   214579 1.R1011
Contig ID
                   tzu700205372.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2696229
BLAST score
                   186
E value
                   9.0e-25
Match length
                   131
% identity
                   48
NCBI Description (D55712) chitinase [Oryza sativa]
                   287424
Seq. No.
                   214583 1.R1011
Contig ID
5'-most EST
                   tzu700205376.h1
Seq. No.
                   287425
                   214620 1.R1011
Contig ID
                   clt700044380.f1
5'-most EST
                   287426
Seq. No.
                   214638 1.R1011
Contig ID
                   tzu700205463.h1
5'-most EST
                   BLASTX
Method
                   g3402711
NCBI GI
BLAST score
                   285
                   3.0e-25
E value
Match length
                   84
                   62
% identity
                   (AC004261) putative RNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
```

Contig ID 214651_1.R1011 5'-most EST ymt700221370.h1

Method BLASTX
NCBI GI g431164
BLAST score 417
E value 3.0e-41

Match length 98



```
% identity
                  (D21823) ORF [Lilium longiflorum]
NCBI Description
Seq. No.
                  287428
                  214666 1.R1011
Contig ID
5'-most EST
                  xsy700211776.h1
Method
                  BLASTX
NCBI GI
                  q4587525
BLAST score
                  156
E value
                  1.0e-10
Match length
                  80
% identity
                  44
NCBI Description
                  (AC007060) Contains the PF 00650 CRAL/TRIO
                  phosphatidyl-inositol-transfer protein domain. ESTs
                  gb T76582, gb N06574 and gb Z25700 come from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  287429
Contig ID
                  214705 1.R1011
5'-most EST
                  wty700169529.hl
Seq. No.
                  287430
Contig ID
                  214709 1.R1011
5'-most EST
                  tzu700205559.h1
Method
                  BLASTX
NCBI GI
                  q1619602
BLAST score
                  207
E value
                  4.0e-16
Match length
                  166
% identity
                  28
NCBI Description
                  (Y08726) MtN3 [Medicago truncatula]
Seq. No.
                  287431
                  214728 1.R1011
Contig ID
5'-most EST
                  tzu700205589.h1
                  287432
Seq. No.
                  214738 1.R1011
Contig ID
5'-most EST
                  uwc700154983.h1
Method
                  BLASTX
NCBI GI
                  q2429290
BLAST score
                  406
                  7.0e-40
E value
Match length
                  110
% identity
                  67
NCBI Description
                  (AF014469) peroxidase [Oryza sativa]
Seq. No.
                  287433
                  214741 1.R1011
Contig ID
                  wyr700239493.h1
5'-most EST
                  BLASTX
Method
```

Method BLASTX
NCBI GI g2129550
BLAST score 677
E value 2.0e-71
Match length 171
% identity 74

NCBI Description calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -



Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi_836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No. 287434

Contig ID 214858_1.R1011 5'-most EST tzu700205759.h1

Seq. No. 287435

Contig ID 214859_1.R1011 5'-most EST tbg700930387.h1

Seq. No. 287436

Contig ID 214880 1.R1011 5'-most EST tzu700205787.h1

Method BLASTX
NCBI GI g3252807
BLAST score 324
E value 6.0e-30
Match length 106
% identity 61

NCBI Description (AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No. 287437

Contig ID 214905_1.R1011 5'-most EST tzu700205820.h1

Seq. No. 287438

Contig ID 214906 1.R1011 5'-most EST xmt700260124.h1

Method BLASTX
NCBI GI g1706551
BLAST score 672
E value 9.0e-71
Match length 164
% identity 77

NCBI Description GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR

((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)

(BETA-1,3-ENDOGLUCANASE) >gi_924953 (U30323) beta

1,3-glucanase [Triticum aestivum]

Seq. No. 287439

Contig ID 214912_1.R1011 5'-most EST tzu700205827.h1

Seq. No. 287440

Contig ID 214913_1.R1011 5'-most EST tzu700205828.h1

Seq. No. 287441

Contig ID 214936_1.R1011 5'-most EST afb700381953.h1 Method BLASTX



NCBI GI g478409 BLAST score 177 E value 6.0e-13 Match length 54 % identity 61

NCBI Description peroxidase (EC 1.11.1.7), cationic - adzuki bean

>gi_218328_dbj_BAA01950_ (D11337) peroxidase [Vigna

angularis]

Seq. No. 287442

Contig ID 214936_2.R1011 5'-most EST uwc700152006.h1

Seq. No. 287443

Contig ID 214947_1.R1011 5'-most EST tzu700205875.h1

Seq. No. 287444

Contig ID 214974_1.R1011 5'-most EST tzu700205918.h1

Method BLASTX
NCBI GI g4325282
BLAST score 149
E value 9.0e-10
Match length 36
% identity 75

NCBI Description (AF123310) NAC domain protein NAM [Arabidopsis thaliana]

>gi 4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM

[Arabidopsis thaliana]

Seq. No. 287445

Contig ID 215030_1.R1011 5'-most EST tzu700205996.h1

Method BLASTX
NCBI GI g3913425
BLAST score 183
E value 1.0e-13
Match length 69
% identity 52

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE >gi 2275203 (AC002337) RNA helicase isolog

[Arabidopsis thaliana]

Seq. No. 287446

Contig ID 215060_1.R1011 5'-most EST tzu700206057.h1

Method BLASTX
NCBI GI g1946366
BLAST score 254
E value 8.0e-22
Match length 121
% identity 50

NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 287447

Contig ID 215067 1.R1011 5'-most EST ymt700220680.h1



BLASTX Method NCBI GI q1665777 BLAST score 254 E value 1.0e-21 152 Match length % identity 38

NCBI Description (D87444) Similar to S.cerevisiae EMP70 protein precursor

(S25110) [Homo sapiens]

Seq. No. 287448

Contig ID 215075 1.R1011 5'-most EST tzu700206073.h1

Method BLASTX q1706551 NCBI GI 651 BLAST score 4.0e-68 E value 172 Match length % identity 70

GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR NCBI Description

((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)

(BETA-1,3-ENDOGLUCANASE) >gi_924953 (U30323) beta

1,3-glucanase [Triticum aestivum]

Seq. No. 287449

215097 1.R1011 Contig ID xyt700342483.h1 5'-most EST

Method BLASTX a732174 NCBI GI BLAST score 761 E value 4.0e-81 Match length 201 69 % identity

NCBI Description

PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE K03H1.2 >gi_3878176_emb_CAA82662_ (Z29560) similar to DEAH subfamily RNA helicases, especially yeast pre-mRNA splicing factors 22 and 16; cDNA EST EMBL:D27770 comes from this gene; cDNA EST EMBL:D27769 comes from this gene; cDNA

EST EMBL: D36247 comes from this ...

>gi_4249768_gb_AAD13795_ (AF120269) sex determination

protein MOG-1 [Caenorhabditis elegans]

287450 Seq. No.

215124 1.R1011 Contig ID tzu700206141.h1 5'-most EST

Method BLASTX NCBI GI q2760839 BLAST score 166 8.0e-12 E value Match length 70 % identity 46

(AC003105) putative receptor kinase [Arabidopsis thaliana] NCBI Description

Seq. No.

287451 215137 1.R1011 Contig ID 5'-most EST ceu700422569.hl

Seq. No. 287452

Match length

% identity

54

```
215158 1.R1011
Contig ID
5'-most EST
                   xyt700346558.h1
                   BLASTX
Method
                   g3819164
NCBI GI
BLAST score
                   418
E value
                   2.0e-41
Match length
                   98
% identity
                   83
                   (AJ012318) cytosolic chaperonin, delta-subunit [Glycine
NCBI Description
Seq. No.
                   287453
                   215163 1.R1011
Contig ID
5'-most EST
                   tzu700206187.h1
Seq. No.
                   287454
Contig ID
                   215198 1.R1011
5'-most EST
                   tzu700206242.h1
Seq. No.
                   287455
                   215202 1.R1011
Contig ID
5'-most EST
                   wyr700240826.h1
Method
                   BLASTX
NCBI GI
                   g2443348
BLAST score
                   207
E value
                   6.0e-18
Match length
                   90
                   54
% identity
NCBI Description (AB001379) cytochrome P450 [Glycyrrhiza echinata]
Seq. No.
Contig ID
                   215219 1.R1011
5'-most EST
                   tzu700206270.h1
Seq. No.
                   287457
Contig ID
                   215286 1.R1011
5'-most EST
                   pmx700086579.h1
Seq. No.
                   287458
                   215330 1.R1011
Contig ID
5'-most EST
                   wyr700235940.h1
Seq. No.
                   287459
                   215343 1.R1011
Contig ID
5'-most EST
                   wyr700\overline{2}38970.h1
Seq. No.
                   287460
                   215361 1.R1011
Contig ID
5'-most EST
                   fdz701159017.h1
Method
                   BLASTX
                   q3738331
NCBI GI
BLAST score
                   165
E value
                   1.0e-11
```

42

40009

NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]



Seq. No. 215394 1.R1011 Contig ID tzu700206490.h1 5'-most EST BLASTN Method g4140643 NCBI GI BLAST score 278 E value 1.0e-155 Match length 325 % identity 97

NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

complete sequence

Seq. No. 287462

Contig ID 215399_1.R1011 5'-most EST tzu700206496.h1

Seq. No. 287463

Contig ID 215444_1.R1011 5'-most EST tzu700206558.h1

Seq. No. 287464

Contig ID 215480 1.R1011 5'-most EST pmx700086089.h1

Method BLASTX
NCBI GI g3033393
BLAST score 207
E value 2.0e-16
Match length 43
% identity 91

NCBI Description (AC004238) putative phosphatidylinositol-glycan-class C

(PIGC) [Arabidopsis thaliana]

Seq. No. 287465

Contig ID 215545_1.R1011 5'-most EST tzu700206695.h1

Seq. No. 287466

Contig ID 215560 1.R1011 5'-most EST xsy700210486.h1

Seq. No. 287467

Contig ID 215808_1.R1011 5'-most EST dyk700105456.h1 Method BLASTN

Method BLASTN
NCBI GI g4115614
BLAST score 104
E value 2.0e-51
Match length 272
% identity 85

NCBI Description Zea mays mRNA for root cap-specific glycine-rich protein,

complete cds

Seq. No. 287468

Contig ID 215846 1.R1011 5'-most EST gwl700613708.h1

Method BLASTX NCBI GI g4126471



BLAST score 178 E value 1.0e-15 Match length 118 % identity 45

NCBI Description (AB014722) rSALT-1(806) [Rattus norvegicus]

Seq. No. 287469

Contig ID 215859 1.R1011 5'-most EST fwa700101806.h1

Method BLASTX
NCBI GI g2499535
BLAST score 280
E value 4.0e-40
Match length 159
% identity 54

NCBI Description 2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi_595681

(U13238) 2-oxoglutarate/malate translocator [Spinacia

oleracea]

Seq. No. 287470

Contig ID 215882 1.R1011 5'-most EST clt700041575.f1

Seq. No. 287471

Contig ID 215889 1.R1011 5'-most EST clt700045275.f1

Method BLASTX
NCBI GI g2738996
BLAST score 255
E value 3.0e-22
Match length 96
% identity 53

NCBI Description (AF022457) CYP97B2p [Glycine max]

Seq. No. 287472

Contig ID 215892_1.R1011 5'-most EST vux700158526.h1

Seq. No. 287473

Contig ID 215907_1.R1011 5'-most EST clt700041621.f1

Seq. No. 287474

Contig ID 215998 1.R1011 5'-most EST clt700041758.f1

Seq. No. 287475

Contig ID 216001_1.R1011 5'-most EST xsy700209989.h1

Method BLASTX
NCBI GI g115815
BLAST score 301
E value 1.0e-27
Match length 72
% identity 79

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-M9) (LHCP) >gi_100866_pir__S13098 chlorophyll



a/b-binding protein precursor - maize >gi_22355_emb_CAA39376_ (X55892) light-harvesting chlorophyll a/b binding protein [Zea mays]

287476 Seq. No. 216019 1.R1011 Contig ID 5'-most EST clt700041786.f1 Method BLASTX g1001478 NCBI GI BLAST score 218 5.0e-18 E value Match length 81 52 % identity (D63999) hypothetical protein [Synechocystis sp.] NCBI Description 287477 Seq. No. 216039 1.R1011 Contig ID 5'-most EST pmx700090265.h1 Method BLASTX g4469011 NCBI GI BLAST score 420 2.0e-41 E value 107 Match length 72 % identity

NCBI Description (AL035602) carbohydrate kinase-like protein [Arabidopsis

thaliana]

Seq. No. 287478

Contig ID 216090_1.R1011 5'-most EST clt700044523.f1

Seq. No. 287479

Contig ID 216121_1.R1011 5'-most EST fwa700098182.h1

Method BLASTX
NCBI GI g1707657
BLAST score 266
E value 4.0e-23
Match length 136
% identity 44

NCBI Description (Z71640) DnaJ homologue [Pisum sativum]

Seq. No. 287480

Contig ID 216131_1.R1011 5'-most EST clt700041939.f1

Method BLASTX
NCBI GI g587566
BLAST score 192
E value 2.0e-16
Match length 83
% identity 53

NCBI Description (X80237) mitochondrial processing peptidase [Solanum

tuberosum]

Seq. No. 287481

Contig ID 216162_1.R1011 5'-most EST fwa700100996.h1



Seq. No. Contig ID 5'-most EST	287482 216192 1.R1011 clt700042034.f1
Seq. No. Contig ID 5'-most EST	287483 216194_1.R1011 clt700042040.f1
Seq. No. Contig ID 5'-most EST	287484 216202_1.R1011 ymt700223506.h1
Seq. No. Contig ID 5'-most EST	287485 216220_1.R1011 clt700042076.f1
Seq. No. Contig ID 5'-most EST	287486 216260_1.R1011 ceu700423529.h1
Seq. No. Contig ID 5'-most EST	287487 216301_1.R1011 clt700043243.f1
5'-most EST Method NCBI GI BLAST score E value Match length % identity	287488 216345_1.R1011 gwl700613258.h1 BLASTX g1652057 228 2.0e-18 154 38 (D90902) hypothetical protein [Synechocystis sp.]
Seq. No. Contig ID 5'-most EST	287489 216358_1.R1011 xyt700345296.h1
Seq. No. Contig ID 5'-most EST	287490 216387 1.R1011 xmt700262119.h1
Seq. No. Contig ID 5'-most EST	287491 216443_1.R1011 ceu700429410.h1
Seq. No. Contig ID 5'-most EST Method NCBI GI	287492 216452_1.R1011 clt700042481.f1 BLASTX g4519936

g4519936 453 4.0e-45 NCBI GI BLAST score E value Match length % identity 149 60



```
NCBI Description
                   (AB019186) RPR1 [Oryza sativa]
                    287493
Seq. No.
Contig ID
                    216481 1.R1011
5'-most EST
                    pmx700086945.h1
Seq. No.
                    287494
Contig ID
                    216496 1.R1011
5'-most EST
                    clt700042553.f1
Seq. No.
                    287495
Contig ID
                    216560 1.R1011
5'-most EST
                    pmx700081938.h1
Method
                    BLASTX
NCBI GI
                    q3559807
BLAST score
                    443
                    3.0e-44
E value
Match length
                    96
% identity
                    86
NCBI Description
                   (Y15628) HCF136 protein [Arabidopsis thaliana]
                    287496
Seq. No.
Contig ID
                    216647 1.R1011
                    clt700\overline{0}42820.f1
5'-most EST
Method
                    BLASTX
NCBI GI
                    q121446
BLAST score
                    794
E value
                    4.0e-85
Match length
                    154
% identity
                    99
NCBI Description
                    FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE PRECURSOR
                    (FD-GOGAT) >gi_100877_pir__A38596 glutamate synthase (ferredoxin) (EC 1.4.7.1) - maize >gi_168477 (M59190)
                    ferredoxin-dependent glutamate synthase [Zea mays]
Seq. No.
                    287497
Contig ID
                    216715 1.R1011
5'-most EST
                    clt700042936.f1
                    287498
Seq. No.
Contig ID
                    216772 1.R1011
5'-most EST
                    rvt700553403.h1
Seq. No.
                    287499
                    216794 1.R1011
5'-most EST
                    rv1700454356.h1
Method
                    BLASTX
                    q2065531
                    236
```

Contig ID

NCBI GI BLAST score E value Match length 89

5.0e-20

% identity NCBI Description

56 (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No.

287500

Contig ID 5'-most EST

216822 1.R1011 clt700044814.f1



Method BLASTX
NCBI GI g3355476
BLAST score 314
E value 3.0e-29
Match length 87
% identity 64

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 287501

Contig ID 216831_1.R1011 5'-most EST clt700043205.f1

Seq. No. 287502

Contig ID 216837_1.R1011 5'-most EST ceu700429605.h1

Method BLASTX
NCBI GI g1001311
BLAST score 200
E value 1.0e-15
Match length 114
% identity 40

NCBI Description (D64006) hypothetical protein [Synechocystis sp.]

Seq. No. 287503

Contig ID 216861_1.R1011 5'-most EST xsy700210305.h1

Seq. No. 287504

Contig ID 216884_1.R1011 5'-most EST clt700043292.f1

Method BLASTX
NCBI GI g2499613
BLAST score 272
E value 2.0e-24
Match length 61
% identity 85

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG MMK2

>gi_1204129_emb_CAA57719_ (X82268) protein kinase [Medicago

sativa]

Seq. No. 287505

Contig ID 216918_1.R1011 5'-most EST ceu700428444.h1

Seq. No. 287506

Contig ID 216934 1.R1011 5'-most EST clt700043371.f1

Seq. No. 287507

Contig ID 216963_1.R1011 5'-most EST clt700043415.f1

Seq. No. 287508

Contig ID 217027_1.R1011 5'-most EST clt700043525.f1

Seq. No. 287509



Contig ID 217060_1.R1011
5'-most EST clt700043627.f1
Method BLASTX
NCBI GI g4580398

BLAST score 192 E value 1.0e-14 Match length 75 % identity 55

NCBI Description (AC007171) putative protein kinase APK1A [Arabidopsis

thaliana]

Seq. No. 287510

Contig ID 217122_1.R1011 5'-most EST wyr700238378.h1

Seq. No. 287511

Contig ID 217132_1.R1011 5'-most EST ceu700425481.h1

Seq. No. 287512

Contig ID 217132 2.R1011 5'-most EST ceu700427079.h1

Seq. No. 287513

Contig ID 217296 1.R1011 5'-most EST clt700044129.r1

Method BLASTX
NCBI GI g2289010
BLAST score 293
E value 2.0e-26
Match length 79
% identity 75

NCBI Description (AC002335) FKBP type peptidyl-prolyl cis-trans isomerase

isolog [Arabidopsis thaliana]

Seq. No. 287514

Contig ID 217301_1.R1011 5'-most EST ceu700425350.h1

Method BLASTX
NCBI GI g4220515
BLAST score 223
E value 3.0e-18
Match length 123
% identity 44

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 287515

Contig ID 217368_1.R1011 5'-most EST nwy700446494.h1

Seq. No. 287516

Contig ID 217404 1.R1011 5'-most EST uwc700152571.h1

Seq. No. 287517

Contig ID 217449_1.R1011 5'-most EST clt700044371.f1



```
Method
                   BLASTX
NCBI GI
                   q4583546
BLAST score
                   239
                   4.0e-20
E value
                   82
Match length
                   61
% identity
                   (AJ010819) GrpE protein [Arabidopsis thaliana]
NCBI Description
                   287518
Seq. No.
                   217454 1.R1011
Contig ID
5'-most EST
                   clt700044376.f1
                   BLASTX
Method
NCBI GI
                   g2341033
BLAST score
                   160
                   6.0e-11
E value
Match length
                   39
                   72
% identity
NCBI Description
                   (AC000104) Similar to Babesia aldo-keto reductase
                   (gb M93122). [Arabidopsis thaliana]
                   287519
Seq. No.
                   217465_1.R1011
Contig ID
5'-most EST
                   ceu700\overline{4}23818.h1
Method
                   BLASTX
                   g2352492
NCBI GI
BLAST score
                   458
                   7.0e-46
E value
Match length
                   118
% identity
                   71
                   (AF005047) transport inhibitor response 1 [Arabidopsis
NCBI Description
                   thaliana] >gi 2352494 (AF005048) transport inhibitor
                   response 1 [Arabidopsis thaliana]
Seq. No.
                   287520
                   217482 1.R1011
Contig ID
5'-most EST
                   ceu700423857.hl
Seq. No.
                   287521
Contig ID
                   217509 1.R1011
5'-most EST
                   clt700044520.f1
                   287522
Seq. No.
                   217558 1.R1011
Contig ID
5'-most EST
                   fwa700\overline{0}99139.h1
                   287523
Seq. No.
Contig ID
                   217594 1.R1011
5'-most EST
                   pmx700091971.h1
Seq. No.
                   287524
```

217607 1.R1011 Contig ID $xsy700\overline{2}17196.h1$ 5'-most EST

BLASTX Method g2252840 NCBI GI BLAST score 200 E value 7.0e-20 Match length 135



% identity 41
NCBI Description (AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No. 287525

Contig ID 217622_1.R1011 5'-most EST clt700044708.f1

Method BLASTX
NCBI GI g1673344
BLAST score 151
E value 8.0e-10
Match length 49
% identity 59

NCBI Description (D64002) hypothetical protein [Synechocystis sp.]

Seq. No. 287526

Contig ID 217771_1.R1011 5'-most EST yyf700351286.h1

Method BLASTX
NCBI GI g4508077
BLAST score 296
E value 3.0e-27
Match length 66
% identity 83

NCBI Description (AC005882) 62114 [Arabidopsis thaliana]

Seq. No. 287527

Contig ID 217790_1.R1011 5'-most EST clt700044927.f1

Seq. No. 287528

Contig ID 217840_1.R1011 5'-most EST 1tv700479663.h1

Seq. No. 287529

Contig ID 217899_1.R1011 5'-most EST ceu700422477.h1

Seq. No. 287530

Contig ID 217946_1.R1011 5'-most EST clt700045166.f1

Seq. No. 287531

Contig ID 217965_1.R1011 5'-most EST clt700045194.f1

Method BLASTX
NCBI GI g3650378
BLAST score 256
E value 9.0e-22
Match length 240
% identity 12

NCBI Description (AL031740) putative rRNA biogenesis protein; rrp5 homolog;

multiple S1 rna binding domain protein [Schizosaccharomyces

pombe]

Seq. No. 287532

Contig ID 217969_1.R1011



```
5'-most EST
                   clt700045203.f1
Method
                   BLASTX
NCBI GI
                   a1773014
BLAST score
                   426
                   3.0e-42
E value
                   111
Match length
% identity
                   77
                   (Y10338) chloride channel Stclc1 [Solanum tuberosum]
NCBI Description
                   287533
Seq. No.
Contig ID
                   218017_1.R1011
5'-most EST
                   fdz701163715.h1
                   287534
Seq. No.
                   218029_1.R1011
Contig ID
                   xmt700\overline{2}64547.h1
5'-most EST
Method
                   BLASTX
                   g3786009
NCBI GI
                   484
BLAST score
                   5.0e-49
E value
                   102
Match length
% identity
                   90
NCBI Description
                   (AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.
                   287535
                   218084 2.R1011
Contig ID
5'-most EST
                   clt700045374.f1
Method
                   BLASTX
NCBI GI
                   q2934902
BLAST score
                   175
E value
                   9.0e-13
Match length
                   34
% identity
                   100
NCBI Description
                   (AF039304) cpSecY [Zea mays]
Seq. No.
                   287536
Contig ID
                   218178 1.R1011
5'-most EST
                   clt700045521.f1
                   287537
Seq. No.
                   218195 1.R1011
Contig ID
5'-most EST
                   uer700579686.h1
Method
                   BLASTX
NCBI GI
                   g4098238
BLAST score
                   168
                   2.0e-23
E value
Match length
                   114
% identity
                   51
                   (U76384) o-methyltransferase [Triticum aestivum]
NCBI Description
                   287538
Seq. No.
```

218199 1.R1011 Contig ID 5'-most EST fwa700100247.hl

287539 Seq. No.

218236 1.R1011 Contig ID 5'-most EST clt700045619.f1



Seq. No. 287540

Contig ID 218239_1.R1011 5'-most EST clt700045622.f1

Method BLASTX
NCBI GI g4544409
BLAST score 421
E value 2.0e-41
Match length 124
% identity 66

NCBI Description (AC006955) putative transcription factor [Arabidopsis thaliana] >gi_4585920 gb_AAD25580.1_AC007211_2 (AC007211)

putative scarecrow homolog [Arabidopsis thaliana]

Seq. No. 287541

Contig ID 218291_1.R1011 5'-most EST clt700045702.f1

Seq. No. 287542

Contig ID 218349_1.R1011 5'-most EST clt700045789.f1

Seq. No. 287543

Contig ID 218359_1.R1011 5'-most EST clt700045811.f1

Method BLASTN
NCBI GI g3451055
BLAST score 35
E value 6.0e-10
Match length 71
% identity 87

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20

(ESSAII project)

Seq. No. 287544

Contig ID 218371_1.R1011 5'-most EST wyr700242570.h1

Method BLASTX
NCBI GI g4646218
BLAST score 525
E value 2.0e-53
Match length 128
% identity 76

NCBI Description (AC007290) putative GTP-binding protein [Arabidopsis

thaliana]

Seq. No. 287545

Contig ID 218396_1.R1011 5'-most EST clt700045863.f1

Seq. No. 287546

Contig ID 218419 1.R1011 5'-most EST wty700165628.h1

Seq. No. 287547

Contig ID 218456_1.R1011 5'-most EST nwy700448104.h1



```
      Seq. No.
      287548

      Contig ID
      218462_1.R1011

      5'-most EST
      ceu700424932.h1

      Seq. No.
      287549

      Contig ID
      218468 1.R1011
```

5'-most EST clt700045979.f1

Method BLASTX

NCBI GI g1001814

BLAST score 150

E value 1.0e-09

Match length 135

% identity 30

NCBI Description (D64005) hypothetical protein [Synechocystis sp.]

 Seq. No.
 287550

 Contig ID
 218498_1.R1011

 5'-most EST
 gwl700612633.h1

 Method
 BLASTX

 NCBI GI
 g3176714

NCBI GI g31/6/1 BLAST score 365 E value 9.0e-35 Match length 91 % identity 76

NCBI Description (AC002392) putative tRNA-splicing endonuclease positive

effector [Arabidopsis thaliana]

Seq. No. 287551

Contig ID 218505_1.R1011 5'-most EST clt700046044.f1

Seq. No. 287552

Contig ID 218546_1.R1011 5'-most EST ceu700431122.h1

Method BLASTX
NCBI GI g3850573
BLAST score 291
E value 2.0e-26
Match length 94
% identity 62

NCBI Description (AC005278) Similar to gi_1652733 glycogen operon protein

GlgX from Synechocystis sp. genome gb D90908. ESTs

gb_H36690, gb_AA712462, gb_AA651230 and gb_N95932 come from

this gene. [Arabidopsis thaliana]

Seq. No. 287553

Contig ID 218641_1.R1011 5'-most EST clt700046442.f1

Seq. No. 287554

Contig ID 218663 1.R1011 5'-most EST xyt700343542.h1

MethodBLASTXNCBI GIg3025205BLAST score258E value2.0e-22



Match length % identity 48

HYPOTHETICAL 65.1 KD PROTEIN SLR1919 NCBI Description

>gi 1652223_dbj_BAA17147_ (D90903) ABC1-like [Synechocystis

sp.]

Seq. No.

287555

Contig ID 5'-most EST 218731 1.R1011 rv1700454603.h1

Method NCBI GI BLASTX q1723953

BLAST score

297

E value Match length 9.0e-39

% identity

108 81

NCBI Description

MINICHROMOSOME MAINTENANCE PROTEIN 6

>gi_2131619_pir__S64219 hypothetical protein YGL201c yeast (Saccharomyces cerevisiae) >gi_1322832_emb_CAA96913_

(Z72723) ORF YGL201c [Saccharomyces cerevisiae]

Seq. No.

287556 .

Contig ID 5'-most EST

218735 1.R1011 ntr700072620.h1

Seq. No.

287557

Contig ID 5'-most EST 218882 1.R1011 wty700163265.hl

Method

BLASTX

NCBI GI BLAST score

g1709921 455

E value

1.0e-75

Match length

176 82

% identity NCBI Description

PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (GARS) (GLYCINAMIDE

RIBONUCLEOTIDE SYNTHETASE) (PHOSPHORIBOSYLGLYCINAMIDE

SYNTHETASE) >gi_945062 (U30896) glycinamide ribonucleotide

(GAR) synthetase [Vigna unguiculata]

Seq. No.

287558

Contig ID 5'-most EST 218907 1.R1011

ntr700071926.h1

Seq. No.

287559

Contig ID

218941 1.R1011

5'-most EST

ntr700071965.hl

Method NCBI GI BLASTX g3367519

BLAST score

390

E value

8.0e-38

Match length

129

% identity NCBI Description

(AC004392) Contains similarity to gb_U51898

Ca2+-independent phospholipase A2 from Rattus norvegicus.

[Arabidopsis thaliana]

Seq. No.

287560

Contig ID

218945 1.R1011

```
ntr700071969.hl
5'-most EST
Method
                  BLASTX
                  g4455232
NCBI GI
                   260
BLAST score
                   9.0e-23
E value
Match length
                   72
                   65
% identity
                  (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
                   287561
Seq. No.
                   218954 1.R1011
Contig ID
5'-most EST
                  ntr700071979.hl
Seq. No.
                   287562
                   218962 1.R1011
Contig ID
                  ntr700075710.hl
5'-most EST
                   BLASTX
Method
                   q4263791
NCBI GI
BLAST score
                   142
                   6.0e-09
E value
                   104
Match length
                   37
% identity
```

NCBI Description (AC006068) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 287563

Contig ID 218987_1.R1011 5'-most EST tfd700573026.h1

Seq. No. 287564

Contig ID 219021_1.R1011 5'-most EST xsy700210933.h1

Method BLASTX
NCBI GI g1730744
BLAST score 221
E value 6.0e-18
Match length 108
% identity 44

NCBI Description HYPOTHETICAL 33.5 KD PROTEIN IN MKS1-MSK1 INTERGENIC REGION

>gi_1077202_pir__S53904 hypothetical protein YNL075w yeast (Saccharomyces cerevisiae) >gi_791110_emb_CAA60184_

(X86470) unknown [Saccharomyces cerevisiae] >gi_1301963_emb_CAA95949_ (Z71351) ORF_YNL075w

[Saccharomyces cerevisiae]

Seq. No. 287565

Contig ID 219036_1.R1011 5'-most EST yyf700349954.h1

Method BLASTX
NCBI GI g2642450
BLAST score 215
E value 2.0e-17
Match length 70
% identity 60

NCBI Description

(AC002391) putative metal ion transporter (Nramp) [Arabidopsis thaliana] >gi_3169188 (AC004401) putative metal ion transporter (Nramp) [Arabidopsis thaliana]



```
Seq. No.
                   287566
Contig ID
                   219085 1.R1011
5'-most EST
                   ntr700072185.h1
                   287567
Seq. No.
Contig ID
                   219086 1.R1011
                   wty700171383.hl
5'-most EST
                   BLASTX
Method
                   g2160175
NCBI GI
BLAST score
                   286
E value
                   5.0e-26
Match length
                   82
% identity
                   71
NCBI Description
                   (AC000132) Strong similarity to Dianthus cysteine
                   proteinase (gb U17135). [Arabidopsis thaliana]
Seq. No.
                   287568
                   219126 1.R1011
Contig ID
5'-most EST
                   ntr700072248.h1
                   287569
Seq. No.
Contig ID
                   219276_1.R1011
5'-most EST
                   wyr700\overline{2}39138.h1
Seq. No.
                   287570
Contig ID
                   219278 1.R1011
                   xjt700\overline{0}95147.h1
5'-most EST
Method
                   BLASTX
                   q1362112
NCBI GI
BLAST score
                   438
                   2.0e-43
E value
Match length
                   124
% identity
                  protein kinase NPK2 (EC 2.7.1.-) - common tobacco
NCBI Description
                   >gi_862342_dbj_BAA06731_ (D31964) NPK2 [Nicotiana tabacum]
                   287571
Seq. No.
                   219300 1.R1011
Contig ID
5'-most EST
                   uwc700151756.h1
Seq. No.
                   287572
                   219363 1.R1011
Contig ID
5'-most EST
                   ntr700075829.h1
Method
                   BLASTX
                   g3551960
NCBI GI
BLAST score
                   405
E value
                   1.0e-39
Match length
                   137
```

% identity 61

(AF082033) senescence-associated protein 15 [Hemerocallis NCBI Description

hybrid cultivar]

287573 Seq. No.

219409 1.R1011 Contig ID ntr700072609.h1 5'-most EST



Seq. No. Contig ID 5'-most EST	287574 219422_1.R1011 ntr700075316.h1
O N-	207575

Seq. No. 287575 Contig ID 219451_1.R1011 5'-most EST zuv700354721.h1

 Seq. No.
 287576

 Contig ID
 219452_1.R1011

 5'-most EST
 xsy700212739.h1

 Seq. No.
 287577

 Contig ID
 219457_1.R1011

 5'-most EST
 gct701167370.h1

 Method
 BLASTX

Method BLASTX
NCBI GI g2829918
BLAST score 449
E value 4.0e-48
Match length 127
% identity 76

NCBI Description (AC002291) similar to "tub" protein gp_U82468_2072162

[Arabidopsis thaliana]

Method BLASTX
NCBI GI g3785989
BLAST score 254
E value 6.0e-22
Match length 113
% identity 42

NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]

 Seq. No.
 287581

 Contig ID
 219503_1.R1011

 5'-most EST
 ntr700072726.h1

Seq. No. 287582 Contig ID 219513_1.R1011 5'-most EST ntr700072739.h1

Seq. No. 287584 Contig ID 219548_1.R1011



5'-most EST xjt700094929.h1

Seq. No. 287585

Contig ID 219548 3.R1011 5'-most EST wty700162793.h1

Method BLASTN
NCBI GI g408384
BLAST score 33
E value 3.0e-09
Match length 37
% identity 97

NCBI Description Rattus norvegicus clone ndf20 neu differentiation factor

mRNA, complete cds

Seq. No. 287586

Contig ID 219561_1.R1011 5'-most EST ntr700072788.h1

Method BLASTX
NCBI GI g2618691
BLAST score 527
E value 7.0e-54
Match length 144
% identity 74

NCBI Description (AC002510) putative chloroplast envelope Ca2+-ATPase

[Arabidopsis thaliana]

Seq. No. 287587

Contig ID 219610_1.R1011 5'-most EST ntr700072852.h1

Seq. No. 287588

Contig ID 219624_1.R1011 5'-most EST ntr700073595.h1

Seq. No. 287589

Contig ID 219654_1.R1011 5'-most EST ntr700072918.h1

Method BLASTX
NCBI GI g4544386
BLAST score 1092
E value 1.0e-119
Match length 302
% identity 67

NCBI Description (AC007047) putative cell division control protein

[Arabidopsis thaliana]

Seq. No. 287590

Contig ID 219664 1.R1011 5'-most EST ntr700072934.h1

Seq. No. 287591

Contig ID 219665 1.R1011 5'-most EST yd1700405402.h1

Method BLASTX
NCBI GI g1495259
BLAST score 227
E value 6.0e-19

```
Match length
% identity
                  (X97826) orf04 [Arabidopsis thaliana]
NCBI Description
                  287592
Seq. No.
                  219742 1.R1011
Contig ID
5'-most EST
                  ntr700073040.h1
Method
                  BLASTX
NCBI GI
                  g478740
                  185
BLAST score
                  5.0e-14
E value
                  77
Match length
% identity
                  60
                  phenylalanine ammonia-lyase (EC 4.1.3.5) - rice
NCBI Description
                  287593
Seq. No.
                  219764 1.R1011
Contig ID
                  ntr700073073.h1
5'-most EST
Method
                  BLASTX
                  g4049518
NCBI GI
BLAST score
                   294
                  1.0e-26
E value
                                Ç,
                  90
Match length
                   57
% identity
                  (AL031852) conserved hypothetical protein
NCBI Description
                   [Schizosaccharomyces pombe]
                   287594
Seq. No.
                   219806 1.R1011
Contig ID
                  ntr700073135.hl
5'-most EST
                   287595
Seq. No.
                   219813 1.R1011
Contig ID
5'-most EST
                  ntr700073146.h1
                   287596
Seq. No.
Contig ID
                   219824 1.R1011
5'-most EST
                   ntr700073159.h1
Seq. No.
                   287597
                   219827 1.R1011
Contig ID
```

Contig ID 219827_1.R1011 5'-most EST ntr700073162.h1

Method BLASTX
NCBI GI g2511533
BLAST score 366
E value 4.0e-35
Match length 71
% identity 96

NCBI Description (AF008121) alpha-tubulin 2 [Eleusine indica]

Seq. No. 287598

Contig ID 219845 1.R1011 5'-most EST ntr700073180.h1

Method BLASTX
NCBI GI g3522946
BLAST score 157
E value 1.0e-10



Match length 116 % identity 32 NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana] Seq. No. 287599

Contig ID 219856_1.R1011
5'-most EST ntr700073194.h1
Method BLASTX
NCBI GI g2735841
BLAST score 201

BLAST score 201 E value 8.0e-16 Match length 90 % identity 41

NCBI Description (AF010283) No definition line found [Sorghum bicolor]

Seq. No. 287600

Contig ID 219866_1.R1011 5'-most EST dyk700104526.h1 Method BLASTX

Method BLASTX
NCBI_GI g2642661
BLAST score 333
E value 3.0e-31
Match length 85
% identity 66

NCBI Description (AF034545) copalyl pyrophosphate synthase [Stevia

rebaudiana]

Seq. No. 287601

Contig ID 219895_1.R1011 5'-most EST pmx700083568.h1

Method BLASTN
NCBI GI g516553
BLAST score 44
E value 2.0e-15
Match length 56
% identity 95

NCBI Description Zea mays B73 cyclin IaZm mRNA, partial cds

Seq. No. 287602

Contig ID 219895_2.R1011 5'-most EST xjt700092663.h1

Seq. No. 287603

Contig ID 219914 1.R1011 5'-most EST wyr700238978.h1

Method BLASTX
NCBI GI g1293688
BLAST score 145
E value 2.0e-09
Match length 83
% identity 39

NCBI Description (U53827) STA1-2 [Silene latifolia ssp. alba] >gi_1293692

(U53829) STA1-18 [Silene latifolia ssp. alba]

Seq. No. 287604

Contig ID 219929 1.R1011 5'-most EST pmx700086243.h1



```
287605
Seq. No.
                   219950 1.R1011
Contig ID
                   ntr700073323.h1
5'-most EST
                   287606
Seq. No.
                   219975 1.R1011
Contig ID
                   rvt700550716.h1
5'-most EST
                   BLASTX
Method
                   g4454467
NCBI GI
BLAST score
                   587
                   9.0e-61
E value
Match length
                   171
% identity
                   63
                   (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                   287607
Seq. No.
                   220019 1.R1011
Contig ID
5'-most EST
                   hbs701185769.hl
Method
                   BLASTX
                   g461928
NCBI GI
                   182
BLAST score
                   1.0e-13
E value
Match length
                   107
% identity
                   37
                   SORBITOL DEHYDROGENASE (L-IDITOL 2-DEHYDROGENASE)
NCBI Description
                   >gi 322198 pir A45052 L-iditol 2-dehydrogenase (EC
                   1.1.1.14) - Bacillus subtilis >gi_304153 (M96947) sorbitol dehydrogenase [Bacillus subtilis] >gi_2632928_emb_CAB12434_
                    (Z99107) sorbitol dehydrogenase [Bacillus subtilis]
                   287608
Seq. No.
                   220020 1.R1011
Contig ID
5'-most EST
                   ntr700073406.h1
Method
                   BLASTX
                   g4454464
NCBI GI
BLAST score
                   169
                   6.0e-12
E value
Match length
                   38
% identity
                   74
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
                   287609
Seq. No.
Contig ID
                   220025 1.R1011
5'-most EST
                   ntr700073415.h1
                   287610
Seq. No.
Contig ID
                   220028 1.R1011
5'-most EST
```

xsy700210473.hl

Seq. No. 287611

220031 1.R1011 Contig ID wty700163735.h1 5'-most EST

Method BLASTN NCBI GI g3821780 BLAST score 36 7.0e-11 E value



Match length 36 % identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 287612

Contig ID 220052_1.R1011 5'-most EST ntr700073456.h1

Seq. No. 287613

Contig ID 220082 1.R1011 5'-most EST ntr700073506.h1

Seq. No. 287614

Contig ID 220126_1.R1011 5'-most EST ntr700073563.h1

Method BLASTX
NCBI GI g461812
BLAST score 316
E value 5.0e-29
Match length 158
% identity 41

NCBI Description CYTOCHROME P450 72 (CYPLXXII) (PROBABLE

GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081)

Cytochrome P-450 protein [Catharanthus roseus]

>gi_445604_prf__1909351A cytochrome P450 [Catharanthus

roseus]

Seq. No. 287615

Contig ID 220169_1.R1011 5'-most EST xyt700343146.h1

Method BLASTX
NCBI GI g3914006
BLAST score 572
E value 1.0e-69
Match length 140
% identity 97

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi_1816588

(U85495) LON2 [Zea mays]

Seq. No. 287616

Contig ID 220170_1.R1011 5'-most EST uwc700152464.h1

Method BLASTX
NCBI GI g1706551
BLAST score 388
E value 2.0e-37
Match length 125
% identity 65

NCBI Description GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR

((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)

(BETA-1,3-ENDOGLUCANASE) >gi 924953 (U30323) beta

1,3-glucanase [Triticum aestīvum]

Seq. No. 287617

Contig ID 220196_1.R1011 5'-most EST pmx700085677.h1 Method BLASTX



NCBI GI g3005590 BLAST score 478 E value 5.0e-48 Match length 153 % identity 59

NCBI Description (AF051326) rRNA methylase [Arabidopsis thaliana]

Seq. No. 287618

Contig ID 220242_1.R1011 5'-most EST nwy700445047.h1

Seq. No. 287619

Contig ID 220276_1.R1011 5'-most EST ntr700073813.h1

Method BLASTX
NCBI GI g4468798
BLAST score 290
E value 3.0e-26
Match length 73
% identity 75

NCBI Description (AJ010440) GST7 protein [Zea mays]

Seq. No. 287620

Contig ID 220292 1.R1011 5'-most EST ntr700073831.h1

Seq. No. 287621

Contig ID 220304 1.R1011 5'-most EST uwc700155707.h1

Seq. No. 287622

Contig ID 220347_1.R1011 5'-most EST gct701175952.h1

Seq. No. 287623

Contig ID 220355_1.R1011 5'-most EST xyt700343553.h1

Method BLASTX
NCBI GI 92459421
BLAST score 179
E value 6.0e-13
Match length 111
% identity 35

NCBI Description (AC002332) putative calcium-binding EF-hand protein

[Arabidopsis thaliana]

Seq. No. 287624

Contig ID 220400_1.R1011 5'-most EST pwr700451895.h1

Seq. No. 287625

Contig ID 220414 1.R1011 5'-most EST fdz701162952.h1

Seq. No. 287626

Contig ID 220416_1.R1011 5'-most EST fwa700101206.h1



Seq. No. 287628

Contig ID 220459_1.R1011 5'-most EST ntr700074031.h1

Method BLASTX
NCBI GI g3775989
BLAST score 654
E value 1.0e-68
Match length 155
% identity 78

NCBI Description (AJ010458) RNA helicase [Arabidopsis thaliana]

Seq. No. 287629

Contig ID 220463_1.R1011 5'-most EST ntr700074035.h1

Method BLASTX
NCBI GI g4586244
BLAST score 239
E value 4.0e-20
Match length 148
% identity 34

NCBI Description (AL049640) putative protein [Arabidopsis thaliana]

Seq. No. 287630

Contig ID 220465_1.R1011 5'-most EST rvl700454464.h1

Method BLASTX
NCBI GI g3786011
BLAST score 173
E value 4.0e-12
Match length 82
% identity 51

NCBI Description (AC005499) putative elongation factor [Arabidopsis

thaliana]

Seq. No. 287631

Contig ID 220467_1.R1011 5'-most EST ntr700074048.h1

Seq. No. 287632

Contig ID 220482_1.R1011 5'-most EST xmt700262243.h1

Seq. No. 287633

Contig ID 220496_1.R1011 5'-most EST ceu700424594.h1

Seq. No. 287634

Contig ID 220545_1.R1011 5'-most EST hbs701186121.h1 Method BLASTX

NCBI GI g4586068 BLAST score 257



E value 3.0e-22 Match length 114 % identity 48

NCBI Description (AC006194) putative glycerol-3-phosphate permease

[Arabidopsis thaliana]

Seq. No. 287635

Contig ID 220668_1.R1011 5'-most EST xmt700267585.h1

Seq. No. 287636

Contig ID 220670_1.R1011 5'-most EST ntr700074407.h1

Seq. No. 287637

Contig ID 220671_1.R1011 5'-most EST nbm700476309.h1

Seq. No. 287638

Contig ID 220679 1.R1011 5'-most EST ntr700074425.h1

Seq. No. 287639

Contig ID 220757_1.R1011 5'-most EST wyr700242779.h1

Method BLASTX
NCBI GI g3445397
BLAST score 414
E value 8.0e-41
Match length 106
% identity 79

NCBI Description (AJ010166) S-domain receptor-like protein kinase [Zea mays]

Seq. No. 287640

Contig ID 220797_1.R1011 5'-most EST xjt700094469.h1

Seq. No. 287641

Contig ID 220843 1.R1011 5'-most EST ntr700074708.h1

Seq. No. 287642

Contig ID 220846_1.R1011 5'-most EST ymt700220734.h1

Seq. No. 287643

Contig ID 220906_1.R1011 5'-most EST pwr700452058.h1

Seq. No. 287644

Contig ID 220926_1.R1011 5'-most EST ntr700074838.h1

Seq. No. 287645

Contig ID 221043 1.R1011 5'-most EST ntr700074986.h1



287646 Seq. No. Contig ID

221064 1.R1011 ntr700075032.h1 5'-most EST

BLASTX Method g3024501 NCBI GI BLAST score 214 2.0e-17 E value Match length 43 95 % identity

RAS-RELATED PROTEIN RABIIC >gi 1370146_emb_CAA98179_ NCBI Description

(Z73951) RAB11C [Lotus japonicus]

287647 Seq. No.

Contig ID 221068 1.R1011 5'-most EST nbm700468601.h1

287648 Seq. No.

Contig ID 221149 1.R1011 ntr700075153.h1 5'-most EST

287649 Seq. No.

221152 1.R1011 Contig ID 5'-most EST ntr700075157.h1

Seq. No. 287650

Contig ID 221155 1.R1011 5'-most EST ntr700075160.h1

BLASTX Method NCBI GI q1706102 BLAST score 144 5.0e-09 E value Match length 78 40 % identity

CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 160 KD NCBI Description SUBUNIT (CPSF 160 KD SUBUNIT) >gi_1045574 (U37012) cleavage

and polyadenylation specificity factor [Homo sapiens]

287651 Seq. No.

221216 1.R1011 Contig ID 5'-most EST ntr700075248.h1

287652 Seq. No.

221234 1.R1011 Contig ID uwc700152430 5'-most EST

Method BLASTX NCBI GI g416922 BLAST score 223 E value 2.0e-18 Match length 67 70 % identity

DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (DUTPASE) NCBI Description

(DUTP PYROPHOSPHATASE) (P18) >gi 282947 pir JQ1599 dUTP

pyrophosphatase (EC 3.6.1.23) - tomato

>gi 251897 bbs 109276 (S40549) deoxyuridine triphosphatase,

dUTPase, P18 (EC 3.6.1.23) [tomatoes, Tint Tim cultivar

LA154, Peptide, 169 aa] [Lycopersicon esculentum]



Seq. No. 287653

Contig ID 221239_1.R1011 5'-most EST ntr700075277.h1

Seq. No. 287654

Contig ID 221263_1.R1011 5'-most EST nbm700471649.h1

Seq. No. 287655

Contig ID 221286_1.R1011 5'-most EST ntr700075339.h1

Seq. No. 287656

Contig ID 221305 1.R1011 5'-most EST xjt700095736.h1

Method BLASTX
NCBI GI g1621463
BLAST score 158
E value 8.0e-11
Match length 39
% identity 74

NCBI Description (U73104) laccase [Liriodendron tulipifera]

Seq. No. 287657

Contig ID 221476_1.R1011 5'-most EST ntr700075604.h1

Seq. No. 287658

Contig ID 221549_1.R1011 5'-most EST ntr700075704.h1

Method BLASTX
NCBI GI g4584547
BLAST score 148
E value 3.0e-21
Match length 146
% identity 41

NCBI Description (AL049608) potassium transporter-like protein [Arabidopsis

thaliana]

Seq. No. 287659

Contig ID 221608_1.R1011 5'-most EST ymt700220627.h1

Method BLASTX
NCBI GI g3882211
BLAST score 194
E value 5.0e-15
Match length 99
% identity 42

NCBI Description (AB018288) KIAA0745 protein [Homo sapiens]

Seq. No. 287660

Contig ID 221619 1.R1011 5'-most EST ntr700075814.h1

Method BLASTX
NCBI GI g3702332
BLAST score 310
E value 3.0e-28



Match length 151 % identity 42

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.

Contig ID 221645_1.R1011 5'-most EST ntr700075848.h1

Seq. No. Contig ID 287662 221690_1.R1011 hbs701184261.h1

5'-most EST

287663

287661

Contig ID 5'-most EST

221703_1.R1011 ntr700075920.h1

Seq. No.

Seq. No.

287664

Contig ID 5'-most EST

221714_1.R1011 ntr700075934.h1

Method BLASTX
NCBI GI g4567265
BLAST score 527
E value 8.0e-54
Match length 133
% identity 76

NCBI Description

(AC006841) putative kinesin protein [Arabidopsis thaliana]

Seq. No.

Seq. No.

Contig ID 5'-most EST

221733 1.R1011 ntr700075956.h1

5 MOSC EST

287666

287665

Contig ID 5'-most EST

221824_1.R1011 xyt700342890.h1

Seq. No.

287667

Contig ID 5'-most EST

221944_1.R1011 ntr700076321.h1

Seq. No.

287668

Contig ID 5'-most EST

221986_1.R1011 tfd700570805.h1

Method. BLASTX
NCBI GI g3522943
BLAST score 352
E value 3.0e-33
Match length 148
% identity 24

NCBI Description

(AC004411) putative p-glycoprotein [Arabidopsis thaliana]

Seq. No.

287669

Contig ID 5'-most EST 222061_1.R1011 ypc700798722.h1

Method BLASTX
NCBI GI g2739371
BLAST score 143
E value 5.0e-09



Match length 113 % identity 35

NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No. 287670

Contig ID 222084_1.R1011 5'-most EST yyf700350993.h1

Seq. No. 287671

Contig ID 222098 1.R1011 5'-most EST hbs701184342.h1

Method BLASTX
NCBI GI g2291143
BLAST score 213
E value 8.0e-17
Match length 131
% identity 39

NCBI Description (AF016417) Similar to BZIP transcription factor

[Caenorhabditis elegans]

Seq. No. 287672

Contig ID 222110_1.R1011 5'-most EST ceu700429693.h1

Method BLASTX
NCBI GI 94574141
BLAST score 633
E value 4.0e-66
Match length 176
% identity 68

NCBI Description (AF073698) cysteine synthase [Oryza sativa]

Seq. No. 287673

Contig ID 222110 2.R1011 5'-most EST ntr700076554.h1

Method BLASTX
NCBI GI g4574141
BLAST score 322
E value 5.0e-30
Match length 105
% identity 61

NCBI Description (AF073698) cysteine synthase [Oryza sativa]

Seq. No. 287674

Contig ID 222122_1.R1011 5'-most EST ntr700076570.h1

Seq. No. 287675

Contig ID 222127_1.R1011 5'-most EST ntr700076578.h1

Seq. No. 287676

Contig ID 222299_1.R1011 5'-most EST ymt700223874.h1

Seq. No. 287677

Contig ID 222310 1.R1011 5'-most EST ntr700076838.h1



```
Method
                  BLASTX
                  q3688172
NCBI GI
BLAST score
                  199
                  5.0e-23
E value
Match length
                  82
% identity
                  51
NCBI Description (AL031804) putative protein [Arabidopsis thaliana]
Seq. No.
                  287678
                  222323 1.R1011
Contig ID
```

Seq. No. 287679

5'-most EST

Contig ID 222362_1.R1011 5'-most EST xyt700344896.h1

Seq. No. 287680

Contig ID 222377_1.R1011 5'-most EST yyf700351922.h1

Method BLASTN
NCBI GI 94234845
BLAST score 302
E value 1.0e-169
Match length 306
% identity 100

NCBI Description Zea mays copia-like retrotransposon Sto-17, partial

sequence

ntr700076857.h1

Seq. No. 287681

Contig ID 222378_1.R1011 5'-most EST xjt700093436.h1

Seq. No. 287682

Contig ID 222381_1.R1011 5'-most EST uwc700155416.h1

Seq. No. 287683

Contig ID 222400_1.R1011 5'-most EST ntr700077002.h1

Method BLASTX
NCBI GI g3281868
BLAST score 475
E value 5.0e-48
Match length 96
% identity 90

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 287684

Contig ID 222402_1.R1011 5'-most EST wyr700239581.h1

Method BLASTN
NCBI GI g218190
BLAST score 42
E value 2.0e-14
Match length 73
% identity 91

NCBI Description Rice genomic DNA encoding peroxidase component RP-2 and/or





4 >gi_244767_gb_S80193_S80193 peroxidase isoform RP-2 or RP-4 [Oryza sativa L.=rice, Genomic, 89 nt]

 Seq. No.
 287685

 Contig ID
 222414_1.R1011

 5'-most EST
 wen700333915.h1

 Seq. No.
 287686

Contig ID 222437_1.R1011 5'-most EST ntr700077043.h1

Seq. No. 287687

Contig ID 222455_1.R1011 5'-most EST ntr700077437.h1

Seq. No. 287688
Contig ID 222474 1

Contig ID 222474_1.R1011 5'-most EST ntr700077087.h1

Seq. No. 287689

Contig ID 222490_1.R1011 5'-most EST ntr700077116.h1 Method BLASTN

NCBI GI g1518673 BLAST score 46 E value 9.0e-17 Match length 62 % identity 94

NCBI Description Zea mays beta-D-glucosidase (glu1) gene, intron 4

transposon 1, complete sequence

Seq. No. 287690

Contig ID 222501_1.R1011 5'-most EST ntr700077129.h1

Seq. No. 287691

Contig ID 222559 1.R1011 5'-most EST ntr700077217.h1

Seq. No. 287692

Contig ID 222714_1.R1011 5'-most EST ntr700077423.h1

Method BLASTX
NCBI GI 94097549
BLAST score 148
E value 1.0e-09
Match length 81
% identity 41

NCBI Description (U64907) ATFP4 [Arabidopsis thaliana]

Seq. No. 287693

Contig ID 222743_1.R1011 5'-most EST ntr700077459.h1

Seq. No. 287694

Contig ID 222757_1.R1011 5'-most EST dyk700102132.h1



Seq. No. 287695

Contig ID 222761_1.R1011 5'-most EST ceu700428373.h1

Method BLASTN
NCBI GI g1255218
BLAST score 45
E value 3.0e-16
Match length 88
% identity 90

NCBI Description Zea mays blue-light photoreceptor-like mRNA

Seq. No. 287696

Contig ID 222840_1.R1011 5'-most EST xjt700096175.h1

Seq. No. 287697

Contig ID 222855_1.R1011 5'-most EST uwc700149731.h1

Method BLASTX
NCBI GI g2959767
BLAST score 221
E value 4.0e-18
Match length 55
% identity 73

NCBI Description (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292

(AC005309) glutathione-conjugate transporter AtMRP4

[Arabidopsis thaliana]

Seq. No. 287698

Contig ID 222952_1.R1011 5'-most EST uwc700149948.h1

Seq. No. 287699

Contig ID 223023_1.R1011 5'-most EST uwc700150051.h1

Seq. No. 287700

Contig ID 223038_1.R1011 5'-most EST pmx700089090.h1

Method BLASTX
NCBI GI g2924781
BLAST score 178
E value 7.0e-13
Match length 155
% identity 30

NCBI Description (AC002334) putative cellulose synthase [Arabidopsis

thaliana]

Seq. No. 287701

Contig ID 223061_1.R1011 5'-most EST uwc700150113.h1

Seq. No. 287702

Contig ID 223078_1.R1011 5'-most EST dyk700104731.h1



Seq. No. 287703 Contig ID 223142 1.R1011

Seq. No. 287704

Contig ID 223168_1.R1011 5'-most EST xmt700266529.h1

Seq. No. 287705

Contig ID 223190_1.R1011 5'-most EST uwc700150313.h1

Method BLASTX
NCBI GI g1363492
BLAST score 160
E value 5.0e-13
Match length 82
% identity 48

NCBI Description outer envelope membrane protein OEP75 precursor - garden

pea >gi_576507 (L36858) outer membrane protein [Pisum sativum] >gi_633607_emb_CAA58720_ (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]

Seq. No. 287706

Contig ID 223194_1.R1011 5'-most EST uwc700150330.h1

Method BLASTX
NCBI GI g1785744
BLAST score 189
E value 1.0e-14
Match length 50
% identity 68

NCBI Description (Y08502) orf158 [Arabidopsis thaliana]

Seq. No. 287707

Contig ID 223200_1.R1011 5'-most EST uwc700150338.h1

Seq. No. 287708

Contig ID 223216_1.R1011 5'-most EST pmx700085232.h1

Seq. No. 287709

Contig ID 223246_1.R1011 5'-most EST pmx700085177.h1

Seq. No. 287710

Contig ID 223267_1.R1011 5'-most EST cjh700196989.h1

Method BLASTX
NCBI GI g2589164
BLAST score 559
E value 1.0e-57
Match length 126
% identity 88

NCBI Description (D88452) aldehyde oxidase-2 [Zea mays]

Seq. No. 287711



Contig ID	223270 1.R1011
5'-most EST	$xyt700\overline{3}44233.h1$

Seq.	No.	287712

Contig ID 223276_1.R1011 5'-most EST uwc700150443.h1

Seq. No. 287713

Contig ID 223289_1.R1011 5'-most EST xsy700212957.h1

Seq. No. 287714

Contig ID 223307_1.R1011 5'-most EST uwc700150477.h1

Seq. No. 287715

Contig ID 223343_1.R1011 5'-most EST uwc700150522.h1 Method BLASTX

NCBI GI g480009
BLAST score 212
E value 6.0e-17
Match length 140
% identity 34

NCBI Description LIS-1 protein - human

Seq. No. 287716

Contig ID 223436_1.R1011 5'-most EST wyr700240186.h1

Seq. No. 287717

Contig ID 223447 1.R1011 5'-most EST uwc700150655.h1

Seq. No. 287718

Contig ID 223490 1.R1011 5'-most EST uwc700150710.h1

Seq. No. 287719

Contig ID 223510 1.R1011 5'-most EST kem700612116.h1

Method BLASTX
NCBI GI g1722856
BLAST score 320
E value 1.0e-29
Match length 127
% identity 50

NCBI Description CHROMOSOME ASSEMBLY PROTEIN XCAP-E >gi_1079282_pir__B55094 chromosomal protein XCAP-E - African clawed frog >gi_563814

(U13674) XCAP-E [Xenopus laevis]

Seq. No. 287720

Contig ID 223513_1.R1011 5'-most EST pmx700088517.h1

Seq. No. 287721

Contig ID 223556_1.R1011



5'-most EST uwc700150808.h1

 Seq. No.
 287722

 Contig ID
 223605_1.R1011

 5'-most EST
 zuv700352749.h1

Seq. No. 287723

Contig ID 223619_1.R1011 5'-most EST uwc700150883.h1

Seq. No. 287724

Contig ID 223637_1.R1011 5'-most EST xsy700217065.h1

Method BLASTX
NCBI GI 94585975
BLAST score 153
E value 4.0e-10
Match length 34
% identity 82

NCBI Description (AC005287) Hypothetical protein [Arabidopsis thaliana]

∜ √

Seq. No. 287725

Contig ID 223646 1.R1011 5'-most EST uwc700150921.h1

Seq. No. 287726

Contig ID 223744_1.R1011 5'-most EST uwc700151048.h1

Seq. No. 287727

Contig ID 223757_1.R1011 5'-most EST uwc700151066.h1

Seq. No. 287728

Contig ID 223821_1.R1011 5'-most EST wty700166791.h1

Method BLASTX
NCBI GI g4584981
BLAST score 213
E value 6.0e-23
Match length 126
% identity 51

NCBI Description (AF088279) NADPH oxidase; RBOH1; gp91; phox homolog

[Potamogeton crispus]

Seq. No. 287729

Contig ID 223834_1.R1011 5'-most EST hbs701182887.h1

Seq. No. 287730

Contig ID 223839_1.R1011 5'-most EST fdz701163136.h1

Seq. No. 287731

Contig ID 223854_1.R1011 5'-most EST uwc700151183.h1



Seq. No. 287732

Contig ID 223884_1.R1011 5'-most EST dyk700105080.h1

Seq. No. 287733

Contig ID 223893_1.R1011 5'-most EST xyt700344392.h1

Seq. No. 287734

Contig ID 223907_1.R1011 5'-most EST nbm700465247.h1

Seq. No. 287735

Contig ID 223921_1.R1011 5'-most EST rvt700550122.h1

Method BLASTX
NCBI GI g4309734
BLAST score 534
E value 1.0e-54
Match length 151
% identity 66

NCBI Description (AC006439) putative 26S proteosome regulatory subunit 8

[Arabidopsis thaliana]

Seq. No. 287736

Contig ID 223966_2.R1011 5'-most EST uwc700151341.h1

Method BLASTX
NCBI GI g3152559
BLAST score 409
E value 3.0e-40
Match length 97
% identity 74

NCBI Description (AC002986) Similarity to A. thaliana gene product

F21M12.20, gb_AC000132. EST gb_Z25651 comes from this gene.

[Arabidopsis Thaliana]

Seq. No. 287737

Contig ID 223994_1.R1011 5'-most EST uwc700151385.h1

Method BLASTX
NCBI GI g2244785
BLAST score 187
E value 5.0e-14
Match length 48
% identity 73

NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 287738

Contig ID 224001_1.R1011 5'-most EST wyr700242068.h1

Seq. No. 287739

Contig ID 224008_1.R1011 5'-most EST uwc700151413.h1

Seq. No. 287740



```
Contig ID
                  224029 1.R1011
5'-most EST
                  uwc700153478.h1
                  BLASTX
Method
NCBI GI
                  q3360289
BLAST score
                  244
                  8.0e-21
E value
Match length
                  122
% identity
                  44
NCBI Description
                  (AF023164) leucine-rich repeat transmembrane protein kinase
                  1 [Zea mays]
                  287741
Seq. No.
Contig ID
                  224031 1.R1011
5'-most EST
                  nbm700473307.h1
Method
                  BLASTX
                  q4455188
NCBI GI
BLAST score
                  235
E value
                  1.0e-19
Match length
                  98
                  52
% identity
NCBI Description (AL035521) putative protein [Arabidopsis thaliana]
                  287742
Seq. No.
Contig ID
                  224048 1.R1011
5'-most EST
                  uwc700151464.h1
Seq. No.
                  287743
                  224049 1.R1011
Contig ID
5'-most EST
                  pwr700448804.h1
                  BLASTX
Method
                  g3256770
NCBI GI
BLAST score
                  306
                  2.0e-27
E value
Match length
                   314
% identity
                  32
NCBI Description
                  (AP000002) 318aa long hypothetical UDP-glucose 4-epimerase
                   [Pyrococcus horikoshii]
Seq. No.
                  287744
Contig ID
                  224073 1.R1011
5'-most EST
                  ymt700222779.h1
Seq. No.
                  287745
Contig ID
                  224079 1.R1011
5'-most EST
                  hbs701180966.h1
Method
                  BLASTX
NCBI GI
                  q1890577
BLAST score
                   451
E value
                   6.0e-45
Match length
                  111
% identity
```

(X93175) xyloglucan endotransglycosylase (XET) [Hordeum NCBI Description

vulgare]

Seq. No. 287746

224095 1.R1011 Contig ID 5'-most EST wyr700243403.h1



```
BLASTX
Method
NCBI GI
                  q2696229
BLAST score
                  220
E value
                  4.0e-18
Match length
                  73
                  58
% identity
NCBI Description (D55712) chitinase [Oryza sativa]
                  287747
Seq. No.
                  224100 1.R1011
Contig ID
5'-most EST
                  xmt700\overline{2}63068.h1
Seq. No.
                  287748
Contig ID
                  224122 1.R1011
5'-most EST
                  uwc700151612.h1
                  BLASTX
Method
                  g1617270
NCBI GI
                  373
BLAST score
E value
                  6.0e-36
                  92
Match length
                  70
% identity
NCBI Description (X94624) acyl-CoA synthetase [Brassica napus]
                  287749
Seq. No.
Contig ID
                  224135_1.R1011
5'-most EST
                  hbs701181490.h1
                  BLASTX
Method
NCBI GI
                  q4455245
BLAST score
                  261
E value
                  1.0e-22
Match length
                  145
                  41
% identity
NCBI Description (AL035523) hypothetical protein [Arabidopsis thaliana]
                  287750
Seq. No.
Contig ID
                  224187 1.R1011
5'-most EST
                  uwc700151708.h1
                  BLASTX
Method
NCBI GI
                  q2275219
BLAST score
                  583
                  2.0e-60
E value
                  150
Match length
% identity
                  79
NCBI Description (AC002337) unknown protein [Arabidopsis thaliana]
                   287751
Seq. No.
Contig ID
                  224202 1.R1011
5'-most EST
                  uwc700151728.h1
```

224221 1.R1011 Contig ID uwc700151753.h1 5'-most EST

287753 Seq. No.

224241 1.R1011 Contig ID uwc700151779.h1 5'-most EST



Contig ID 224258_1.R1011 5'-most EST uwc700151796.h1

Method BLASTX
NCBI GI g2244934
BLAST score 153
E value 3.0e-10
Match length 41
% identity 71

NCBI Description (Z97339) similarity to SYNAPTOBREVIN-RELATED PROTEIN

[Arabidopsis thaliana]

Seq. No. 287755

Contig ID 224317_1.R1011 5'-most EST uwc700151884.h1

Method BLASTX
NCBI GI g3121829
BLAST score 154
E value 3.0e-10
Match length 77
% identity 47

NCBI Description CHROMATIN ASSEMBLY FACTOR I P60 SUBUNIT (CAF-I 60 KD

SUBUNIT) >gi_2134915_pir__B56731 chromatin assembly factor I p60 chain - human >gi_882260 (U20980) chromatin assembly

factor-I p60 subunit [Homo sapiens]

Seq. No. 287756

Contig ID 224335_1.R1011 5'-most EST xsy700210402.h1

Method BLASTX
NCBI GI g2137762
BLAST score 331
E value 5.0e-31
Match length 104
% identity 58

NCBI Description serine C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain -

mouse

Seq. No. 287757

Contig ID 224364_1.R1011 5'-most EST xjt700094027.h1

Seq. No. 287758

Contig ID 224381_1.R1011 5'-most EST uwc700151986.h1

Method BLASTX
NCBI GI g2558654
BLAST score 178
E value 6.0e-13
Match length 110
% identity 38

NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]

Seq. No. 287759

Contig ID 224417_1.R1011 5'-most EST wen700332219.h1

Method BLASTX



```
g4539677
NCBI GI
                  169
BLAST score
                  1.0e-21
E value
Match length
                  68
% identity
                  71
                  (AF061282) patatin-like protein [Sorghum bicolor]
NCBI Description
                  287760
Seq. No.
                  224427 1.R1011
Contig ID
                  uwc700152054.h1
5'-most EST
                  BLASTX
Method
                  g282964
NCBI GI
BLAST score
                  310
                  1.0e-28
E value
Match length
                  67
                  79
% identity
                  transforming protein (myb) homolog (clone myb.Ph3) - garden
NCBI Description
                  petunia >gi_20563_emb_CAA78386_ (Z13996) protein 1 [Petunia
                  x hybrida]
Seq. No.
                  287761
                  224446 1.R1011
Contig ID
                  vux700160268.hl
5'-most EST
                  287762
Seq. No.
                  224476 1.R1011
Contig ID
5'-most EST
                  dhd700197974.h1
                  287763
Seq. No.
                  224484 1.R1011
Contig ID
                  xmt700266920.h1
5'-most EST
                  287764
Seq. No.
                  224577 1.R1011
Contig ID
5'-most EST
                  uwc700152262.h1
                  287765
Seq. No.
Contig ID
                  224638_1.R1011
5'-most EST
                  gct701179126.h1
Seq. No.
                   287766
                   224680 1.R1011
Contig ID
                  uwc700152392.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                   g4062933
                   48
BLAST score
                   4.0e-18
E value
                   68
Match length
% identity
                  Hordeum vulgare mRNA for formate dehydrogenase, complete
NCBI Description
                   cds
                   287767
```

224703 1.R1011 Contig ID 5'-most EST wyr700242096.hl

Method BLASTX g1546700 NCBI GI



```
BLAST score
E value
                  2.0e-47
                  125
Match length .
                  74
% identity
                 (X98804) peroxidase ATP18a [Arabidopsis thaliana]
NCBI Description
                  287768
Seq. No.
                  224720 1.R1011
Contig ID
                  rv1700455674.hl
5'-most EST
                  287769
Seq. No.
                  224725 1.R1011
```

Contig ID 5'-most EST wyr700240985.h1

287770 Seq. No.

224770 1.R1011 Contig ID uwc700156380.h1 5'-most EST

Seq. No. 287771

224798_1.R1011 Contig ID 5'-most EST uwc700152577.h1

Method BLASTX g2708744 NCBI GI BLAST score 273 E value 3.0e-24Match length 93 % identity 51

(AC003952) putative Bop-like zinc finger protein NCBI Description

[Arabidopsis thaliana]

287772 Seq. No.

224825 1.R1011 Contig ID pmx700091017.h1 5'-most EST

Method BLASTX q4538911 NCBI GI BLAST score 170 ිE value 2.0e-15 Match length 95 45 % identity

(AL049482) hypothetical protein [Arabidopsis thaliana] NCBI Description

287773 Seq. No.

224825 2.R1011 Contig ID 5'-most EST uwc700152612.h1

Method BLASTX g4538911 NCBI GI BLAST score 175 E value 1.0e-12 Match length 139 % identity 32

NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]

287774 Seq. No.

224853 1.R1011 Contig ID uwc700152730.h1 5'-most EST

287775 Seq. No.



224890 1.R1011 Contig ID 5'-most EST uwc700152735.h1 BLASTX Method

q1657619 NCBI GI 259 BLAST score 8.0e-23 E value Match length 76 % identity 62

(U72504) G5p [Arabidopsis thaliana] >gi 3068710 (AF049236) NCBI Description putative transmembrane protein G5p [Arabidopsis thaliana]

287776 Seq. No.

Contig ID 224891_1.R1011 $dyk700\overline{1}05714.h1$ 5'-most EST

287777 Seq. No.

224911 1.R1011 Contig ID hbs701185742.h1 5'-most EST BLASTN

Method g2589163 NCBI GI BLAST score 74 1.0e-33 E value 98 Match length 94

NCBI Description Zea mays mRNA for aldehyde oxidase-2, complete cds

287778 Seq. No.

% identity

Contig ID 224933_1.R1011 5'-most EST nbm700476919.h1

BLASTX Method g2262114 NCBI GI BLAST score 225 2.0e-18 E value Match length 136 % identity 41

(AC002343) cellulose synthase isolog [Arabidopsis thaliana] NCBI Description

287779 Seq. No.

224941 1.R1011 Contig ID 5'-most EST uwc700152816.h1

287780 Seq. No.

224950 1.R1011 Contig ID 5'-most EST $xsy700\overline{2}13221.h1$

287781 Seq. No.

Contig ID 224983 1.R1011 5'-most EST xjt700096528.h1

Seq. No. 287782

225020 1.R1011 Contig ID uwc700152941.h1 5'-most EST

BLASTX Method NCBI GI g2507426 BLAST score 423 6.0e-42 E value Match length 100



% identity 77

NCBI Description ALANYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR

(ALANINE--TRNA LIGASE) (ALARS) >gi_1673365_emb_CAA80380_(Z22673) mitochondrial tRNA-Ala synthetase [Arabidopsis

thaliana]

287784

Seq. No. Contig ID 287783 225039_1.R1011

5'-most EST

ymt700221708.h1

Seq. No. Contig ID

225040 1.R1011

5'-most EST

tfd700570807.hl

Method BLASTX
NCBI GI g3193330
BLAST score 163
E value 3.0e-11

Match length 67 % identity 48

NCBI Description (AF069299) contains similarity to Medicago sativa corC

(GB:L22305) [Arabidopsis thaliana]

Seq. No. 287785

Contig ID 225115_1.R1011 5'-most EST uwc700153110.h1

Seq. No. 287786

Contig ID 225122_1.R1011 5'-most EST uwc700153122.h1

Seq. No. 287787

Contig ID 225189_1.R1011 5'-most EST uwc700153215.h1

Seq. No. 287788

Contig ID 225230_1.R1011 5'-most EST vux700159732.h1

Method BLASTX
NCBI GI g3953609
BLAST score 188
E value 5.0e-14
Match length 149
% identity 30

NCBI Description (AB010108) MCM6 [Drosophila melanogaster]

Seq. No. 287789

Contig ID 225323_1.R1011 5'-most EST uwc700153452.h1

Method BLASTX
NCBI GI 94584538
BLAST score 294
E value 1.0e-26
Match length 127
% identity 46

NCBI Description (AL049608) hypothetical protein [Arabidopsis thaliana]

Seq. No.

287790



Contig ID 225349_1.R1011 5'-most EST nbm700473881.h1

Method BLASTX
NCBI GI g2911042
BLAST score 372
E value 4.0e-36
Match length 85
% identity 85

NCBI Description (AL021961) Phosphoglycerate dehydrogenase - like protein

[Arabidopsis thaliana]

Seq. No. 287791

Contig ID 225382_1.R1011 5'-most EST uwc700153536.h1

Seq. No. 287792

Contig ID 225388 1.R1011 5'-most EST vux700160356.h1

Seq. No. 287793

Contig ID 225404 1.R1011 5'-most EST uwc700153565.h1

Seq. No. 287794

Contig ID 225518 1.R1011 5'-most EST pmx700091208.h1

Method BLASTX
NCBI GI g3063446
BLAST score 410
E value 2.0e-40
Match length 102
% identity 78

NCBI Description (AC003981) F22013.8 [Arabidopsis thaliana]

Seq. No. 287795

Contig ID 225539_1.R1011 5'-most EST uwc700153777.h1

Seq. No. 287796

Contig ID 225625_1.R1011 5'-most EST uwc700153890.h1

Seq. No. 287797

Contig ID 225652_1.R1011 5'-most EST xsy700209651.h1

Seq. No. 287798

Contig ID 225666 1.R1011 5'-most EST wev700405013.h1

Seq. No. 287799

Contig ID 225722 1.R1011 5'-most EST uwc700154026.h1

Seq. No. 287800

Contig ID 225762_1.R1011 5'-most EST xjt700093709.h1



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287801
Seq. No.
                  225783 1.R1011
Contig ID
                  wyr700237240.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2130145
BLAST score
                  227
                  5.0e-19
E value
                  87
Match length
                  55
% identity
                  seed storage protein opaque-2 - maize >gi_1144536 (U35063)
NCBI Description
                  opaque-2 heterodimerizing protein 1b [Zea mays]
Seq. No.
                  287802
                  225791 1.R1011
Contig ID
5'-most EST
                  uwc700154121.h1
                  287803
Seq. No.
Contig ID
                  225793 1.R1011
5'-most EST
                  uwc700154123.hl
                  BLASTX
Method
NCBI GI
                  g4455213
BLAST score
                   485
E value
                   5.0e-49
Match length
                  126
% identity
                   74
                   (AL035440) glutamine amidotransferase/cyclase [Arabidopsis
NCBI Description
                   thaliana]
                   287804
Seq. No.
                   225806 1.R1011
Contig ID
5'-most EST
                  nbm700474519.h1
Seq. No.
                   287805
                   225822 1.R1011
Contig ID
5'-most EST
                   xjt700094013.h1
Method
                   BLASTN
                   q3983662
NCBI GI
BLAST score
                   34
E value
                   1.0e-09
Match length
                   94
                   84
% identity
NCBI Description Oryza sativa mRNA for importin-betal, complete cds
```

Seq. No. 287806 225841 1.R1011 Contig ID 5'-most EST yyf700350345.hl

287807 Seq. No. 225846 1.R1011 Contig ID

5'-most EST uwc700154202.h1

287808 Seq. No. 225888 1.R1011 Contig ID gct701175279.hl 5'-most EST

Seq. No. 287809



Contig ID 225903 1.R1011 5'-most EST uwc700154320.h1 Method BLASTX

NCBI GI g3176686
BLAST score 445
E value 2.0e-44
Match length 116
% identity 72

[Arabidopsis thaliana]

Seq. No. 287810

Contig ID 225904_1.R1011 5'-most EST yyf700348995.h1

Seq. No. 287811

Contig ID 225923_1.R1011 __5'-most EST uwc700154355.h1

Seq. No. 287812

Contig ID 226027_1.R1011 5'-most EST nwy700445843.h1

Seq. No. 287813

Contig ID 226057_1.R1011 5'-most EST gwl700613111.h1

Method BLASTX
NCBI GI g3600061
BLAST score 204
E value 7.0e-16
Match length 74
% identity 51

NCBI Description (AF080120) contains similarity to DNA binding proteins

[Arabidopsis thaliana]

Seq. No. 287814

Contig ID 226087_1.R1011 5'-most EST tbg700930323.h1

Seq. No. 287815

Contig ID 226233_1.R1011 5'-most EST vux700162423.h1

Seq. No. 287816

Contig ID 226267_1.R1011 5'-most EST wyr700242771.h1

Method BLASTX
NCBI GI g2618691
BLAST score 140
E value 7.0e-09
Match length 39
% identity 67

NCBI Description (AC002510) putative chloroplast envelope Ca2+-ATPase

[Arabidopsis thaliana]

Seq. No. 287817



Contig ID 226278_1.R1011 5'-most EST tfd700570722.h1

Seq. No. 287818

Contig ID 226323_1.R1011 5'-most EST uwc700155004.h1

Seq. No. 287819

Contig ID 226326_1.R1011 5'-most EST uwc700155246.h1

Method BLASTX
NCBI GI g3212854
BLAST score 278
E value 1.0e-24
Match length 140
% identity 49

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 287820

Contig ID 226355_1.R1011 5'-most EST uwc700155049.h1

Seq. No. 287821

Contig ID 226402_1.R1011 5'-most EST nbm700471655.h1

Method BLASTX
NCBI GI g2462749
BLAST score 256
E value 2.0e-22
Match length 92
% identity 54

NCBI Description (AC002292) Putative Serine/Threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 287822

Contig ID 226419_1.R1011 5'-most EST wen700331921.h1

Seq. No. 287823

Contig ID 226480 1.R1011 5'-most EST wyr700242540.h1

Method BLASTX
NCBI GI g2094888
BLAST score 144
E value 4.0e-09
Match length 34
% identity 71

NCBI Description Cucumber Basic Protein, A Blue Copper Protein

Seq. No. 287824

Contig ID 226486 1.R1011 5'-most EST fwa700097992.h1

Seq. No. 287825

Contig ID 226489_1.R1011 5'-most EST uwc700155251.h1



```
Seq. No.
                   287826
                   226548 1.R1011
Contig ID
5'-most EST
                  uwc700155325.h1
                   287827
Seq. No.
                  226559 1.R1011
Contig ID
5'-most EST
                  uwc700155341.h1
                  BLASTX
Method
                  g2465923
NCBI GI
BLAST score
                  171
                   2.0e-12
E value
Match length
                   74
                   47
% identity
NCBI Description
                  (AF024648) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana]
                   287828
Seq. No.
                   226629 1.R1011
Contig ID
5'-most EST
                  uwc700155461.hl
                   287829
Seq. No.
                   226630 1.R1011
Contig ID
                   xmt700\overline{2}64463.h1
5'-most EST
                                                         . .
Seq. No.
                   287830
                   226636 1.R1011
Contig ID
                   uwc700155475.h1
5'-most EST
                   287831
Seq. No.
Contig ID
                   226677 1.R1011
5'-most EST
                   xsy700211695.hl
Method
                   BLASTX
                   g3980377
NCBI GI
BLAST score
                   151
                   6.0e-10
E value
Match length
                   53
% identity
                   55
NCBI Description (AC004561) unknown protein [Arabidopsis thaliana]
Seq. No.
                   287832
                   226699 1.R1011
Contig ID
5'-most EST
                   wyr700238589.h1
                   BLASTX
Method
NCBI GI
                   g4490706
BLAST score
                   150
E value
                   5.0e-10
Match length
                   43
                   65
% identity
NCBI Description
                  (AL035680) putative protein [Arabidopsis thaliana]
```

Seq. No. Contig ID 5'-most EST

226723 1.R1011 uwc700155612.h1

287833

Seq. No. Contig ID 5'-most EST

287834 226759 1.R1011 uwc700155658.h1



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287835
Seq. No.
                  226829 1.R1011
Contig ID
                  uwc700155758.h1
5'-most EST
                  BLASTX
Method
                  g2853076
NCBI GI
BLAST score
                  280
                   3.0e-25
E value
                  70
Match length
                  76
% identity
                  (AL021768) putative protein [Arabidopsis thaliana]
NCBI Description
                   287836
Seq. No.
Contig ID
                   226851 1.R1011
                  uwc700155783.h1
5'-most EST
                   287837
Seq. No.
                   226902 1.R1011
Contig ID
5'-most EST
                  tfd700573637.h1
                   287838
Seq. No.
                   226911 1.R1011
Contig ID
                   wty700167815.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3834316
BLAST score
                   298
                   1.0e-27
E value
                   93
Match length
                   59
% identity
                   (AC005679) Similar to gb X16648 pathogenesis related
NCBI Description
                   protein from Hordeum vulgare. EST gb Z18206 comes from
                   this gene. [Arabidopsis thaliana]
                   287839
Seq. No.
                   226946_1.R1011
Contig ID
                   uwc700155914.h1
5'-most EST
Method
                   BLASTX
                   q4127346
NCBI GI
                   222
BLAST score
E value
                   3.0e-18
                   60
Match length
                   70
% identity
                   (AJ010448) glutathione transferase [Alopecurus myosuroides]
NCBI Description
                   287840
Seq. No.
                   226955 1.R1011
Contig ID
5'-most EST
                   nbm700\overline{4}71183.h1
Seq. No.
                   287841
                   227010 1.R1011
Contig ID
```

5'-most EST uwc700156031.h1

287842 Seq. No.

227035 1.R1011 Contig ID 5'-most EST tfd700570659.h1

BLASTX Method NCBI GI g1304599



```
BLAST score
                   4.0e-29
E value
Match length
                   127
                   45
% identity
NCBI Description (U41315) ZNF127-Xp [Homo sapiens]
                   287843
Seq. No.
                  227128 1.R1011
Contig ID
5'-most EST
                  pmx700091378.h1
                   BLASTX
Method
NCBI GI
                   g3540194
BLAST score
                   539
                   3.0e-55
E value
                   134
Match length
% identity
                  (AC004260) AtVPS45p [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   287844
                   227131 1.R1011
Contig ID
                   zuv700354678.h1
5'-most EST
Seq. No.
                   287845
                   227151 1.R1011
Contig ID
                   pmx700089128.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4415937
BLAST score
                   505
                   2.0e-51
E value
                   124
Match length
% identity
                   73
                  (AC006418) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   287846
                   227213 1.R1011
Contig ID
                   uwc700156317.h1
5'-most EST
Seq. No.
                   287847
                   227255 1.R1011
Contig ID
                   uwc700156372.h1
5'-most EST
                   BLASTX
Method
                   q4204281
NCBI GI
                   199
BLAST score
                   1.0e-15
E value
                   103
Match length
                   42
% identity
                   (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   287848
Seq. No.
                   227271 1.R1011
```

Contig ID

5'-most EST

287849

Seq. No. 227290 1.R1011 Contig ID 5'-most EST wyr700243910.h1

Seq. No. Contig ID 287850

227297_1.R1011

xjt700095221.hl



5'-most EST vqh700053175.r1

Seq. No. 287851

Contig ID 227308_1.R1011 5'-most EST vqh700053188.r1

Seq. No. 287852

Contig ID 227422_1.R1011 5'-most EST xjt700092042.h1

Seq. No. 287853

Contig ID 227493_1.R1011 5'-most EST xjt700093015.h1

Seq. No. 287854

Contig ID 227568_1.R1011 5'-most EST xjt700092363.h1

Seq. No. 287855

Contig ID 227617_1.R1011 5'-most EST xjt700092433.h1

Seq. No. 287856

Contig ID 227726_1.R1011 5'-most EST xjt700092584.h1

Seq. No. 287857

Contig ID 227756_1.R1011 5'-most EST fdz701160707.h1

Method BLASTX
NCBI GI g4063743
BLAST score 250
E value 3.0e-21
Match length 126
% identity 45

NCBI Description (AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No. 287858

Contig ID 227779_1.R1011 5'-most EST xjt700092655.h1

BLASTN

NCBI GI g4519191
BLAST score 37
E value 3.0e-11
Match length 141
% identity 82

Method

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K9P8, complete sequence

Seq. No. 287859

Contig ID 227819_1.R1011 5'-most EST pmx700088835.h1

Seq. No. 287860

Contig ID 227853_1.R1011 5'-most EST xjt700092747.h1



```
      Seq. No.
      287861

      Contig ID
      227856_1.R1011

      5!-most EST
      xjt700092751.h1
```

 Seq. No.
 287862

 Contig ID
 227877_1.R1011

 5'-most EST
 xmt700261558.h1

Method BLASTX
NCBI GI g629846
BLAST score 229
E value 4.0e-19
Match length 46
% identity 100

NCBI Description initiator-binding protein - maize >gi_483444_emb_CAA55693_

(X79086) initiator-binding protein [Zea mays]

Seq. No. 287863

Contig ID 227880_1.R1011 5'-most EST xjt700095860.h1

Seq. No. 287864

Contig ID 227901_1.R1011 5'-most EST vux700157668.h1

Method BLASTX
NCBI GI g3075398
BLAST score 460
E value 6.0e-46
Match length 122
% identity 70

NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]

Seq. No. 287865

Contig ID 227926_1.R1011 5'-most EST pmx700091613.h1

Method BLASTX
NCBI GI g1708191
BLAST score 277
E value 1.0e-24
Match length 77
% identity 61

NCBI Description HEXOSE CARRIER PROTEIN HEX6 >gi_467319 (L08188) hexose

carrier protein [Ricinus communīs]

Seq. No. 287866

Contig ID 227930_1.R1011 5'-most EST hvj700623365.h1

Seq. No. 287867

Contig ID 227964_1.R1011 5'-most EST xjt700092901.h1

Seq. No. 287868

Contig ID 227982_1.R1011 5'-most EST ymt700221931.h1

Seq. No. 287869

Contig ID 227985_1.R1011



```
xjt700092933.h1
5'-most EST
                   287870
Seq. No.
                   228059 1.R1011
Contig ID
                   nbm700\overline{4}68835.h1
5'-most EST
                   287871
Seq. No.
                   228066 1.R1011
Contig ID
5'-most EST
                   xjt700093044.hl
                   287872
Seq. No.
                   228070 1.R1011
Contig ID
                   nbm700\overline{4}71644.h1
5'-most EST
Seq. No.
                   287873
                   228091 1.R1011
Contig ID
5'-most EST
                   xjt700093078.h1
                   BLASTX
Method
                   q4512122
NCBI GI
BLAST score
                   145
                   1.0e-12
E value
                   88
Match length
                   43
% identity
                   (AF131219) chorismate mutase 3 [Arabidopsis thaliana]
NCBI Description
                   287874
Seq. No.
                   228093 1.R1011
Contig ID
                   bdu700\overline{3}82219.h1
5'-most EST
                   287875
Seq. No.
                   228116 1.R1011
Contig ID
                   gwl700613784.h1
5'-most EST
                   BLASTX
Method
                   g2780192
NCBI GI
BLAST score
                    265
                    2.0e-23
E value
                   103
Match length
% identity
                    48
                   (AJ222713) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                    287876
Seq. No.
                    228130 1.R1011
Contig ID
5'-most EST
                    xsy700\overline{2}17466.h1
                    BLASTX
Method
                    g486827
NCBI GI
                    177
```

BLAST score 2.0e-23 E value Match length 72 82

% identity

translation elongation factor Tu.B precursor, chloroplast -NCBI Description

wood tobacco

Seq. No. Contig ID 287877

228142 1.R1011 $xmt700\overline{2}65955.h1$ 5'-most EST

Seq. No.

287878



Contig ID 228150_1.R1011 5'-most EST xjt700093162.h1 Method BLASTX

NCBI GI g3874563
BLAST score 206
E value 2.0e-16
Match length 98
% identity 45

NCBI Description (Z81042) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5

comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ... >gi_3924825 emb_CAB05549_ (Z83113) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5

comes from this gene; cDNA

Seq. No. 287879

Contig ID 228189 1.R1011 5'-most EST xjt700093220.h1

Seq. No. 287880

Contig ID 228198_1.R1011 5'-most EST xjt700093241.h1

Method BLASTX
NCBI GI g529707
BLAST score 178
E value 4.0e-13
Match length 98
% identity 37

NCBI Description (U13070) No definition line found [Caenorhabditis elegans]

Seq. No. 287881

Contig ID 228238_1.R1011 5'-most EST xjt700093358.h1

Seq. No. 287882

Contig ID 228281_1.R1011 5'-most EST xjt700093414.h1

Method BLASTX
NCBI GI g2708741
BLAST score 378
E value 1.0e-36
Match length 101
% identity 70

NCBI Description (AC003952) hypothetical protein [Arabidopsis thaliana]

Seq. No. 287883

Contig ID 228290_1.R1011 5'-most EST xjt700095090.h1

Method BLASTX
NCBI GI g3522942
BLAST score 368
E value 8.0e-47
Match length 148
% identity 60





```
NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]
```

 Seq. No.
 287884

 Contig ID
 228322 1.R1011

 5'-most EST
 wty700164568.h1

Method BLASTX
NCBI GI g2244831
BLAST score 352
E value 1.0e-33
Match length 101
% identity 68

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 287885

Contig ID 228335_1.R1011 5'-most EST xyt700345255.h1

Method BLASTX
NCBI GI g2739371
BLAST score 473
E value 2.0e-47
Match length 160
% identity 58

NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No. 287886

Contig ID 228360_1.R1011 5'-most EST xjt700093518.h1

Seq. No. 287887

Contig ID 228390_1.R1011 5'-most EST pmx700090215.h1

Method BLASTN
NCBI GI g22229
BLAST score 250
E value 1.0e-138
Match length 313
% identity 95

% identity 95 NCBI Description Z.mays cab-m7 gene for light harvesting chlorophyll a/b

binding protein

Seq. No. 287888

Contig ID 228391_1.R1011 5'-most EST hvj700622904.h1

Method BLASTX
NCBI GI g4585991
BLAST score 384
E value 1.0e-60
Match length 171
% identity 66

NCBI Description (AC005287) very similar to mouse Dhm1 and Dhm2 [Arabidopsis

thaliana]

Seq. No. 287889

Contig ID 228460_1.R1011 5'-most EST xsy700209652.h1

Seq. No. 287890



	Action in the second se
Contig ID	228578_1.R1011
5'-most EST	xjt700093850.h1
Seq. No. Contig ID 5'-most EST	287891 228590_1.R1011 xjt700095514.h1
Seq. No.	287892
Contig ID	228598_1.R1011

5'-most EST

Contig ID 228602_1.R1011 5'-most EST xjt700093880.h1

Method BLASTX
NCBI GI g2392895
BLAST score 235
E value 6.0e-20
Match length 89
% identity 56

NCBI Description (AF017056) brassinosteroid insensitive 1 [Arabidopsis

thaliana]

xjt700093874.hl

Seq. No. 287894

Contig ID 228608_1.R1011 5'-most EST xjt700093886.h1

Seq. No. 287895

Contig ID 228611_1.R1011 5'-most EST xjt700093891.h1

Seq. No. 287896

Contig ID 228616_1.R1011 5'-most EST xmt700267184.h1

Method BLASTX
NCBI GI g3334141
BLAST score 169
E value 3.0e-12
Match length 42
% identity 69

NCBI Description CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5

(CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5) >gi_2737890 (U59149) nucleolar protein CaCbf5p [Candida

albicans]

Seq. No. 287897

Contig ID 228623_1.R1011 5'-most EST xsy700209496.h1

Seq. No. 287898

Contig ID 228662_1.R1011 5'-most EST xsy700210863.h1

Method BLASTX
NCBI GI g218179
BLAST score 245
E value 1.0e-34
Match length 98

% identity

98

NCBI Description AUXIN-BINDING PROTEIN 4 PRECURSOR (ABP)



```
% identity
                  (D10207) H-ATPase [Oryza sativa] >gi_444339_prf__1906387A H
NCBI Description
                  ATPase [Oryza sativa]
                  287899
Seq. No.
                  228690 1.R1011
Contig ID
                  xyt700346957.h1
5'-most EST
                  BLASTX
Method
                  g3645898
NCBI GI
                  233
BLAST score
                  1.0e-19
E value
                  86
Match length
                  52
% identity
                  (U68408) in-frame stop codon; possibly a post-transposition
NCBI Description
                  mutation [Zea mays]
                   287900
Seq. No.
                   228707 1.R1011
Contig ID
                  xjt700094029.h1
5'-most EST
                   BLASTX
Method
                   g2130136
NCBI GI
                   373
BLAST score
                   5.0e-38
E value
                   95
Match length
                   75
% identity
NCBI Description homeotic protein Hox2b - maize
                   287901
Seq. No.
                   228719 1.R1011
Contig ID
5'-most EST
                   xsy700\overline{2}11518.h1
                   287902
Seq. No.
                   228728 1.R1011
Contig ID
                   xjt700094053.hl
5'-most EST
                   BLASTX
Method
                   g1001708
NCBI GI
                   325
BLAST score
                   2.0e-30
E value
                   108
Match length
                   56
% identity
NCBI Description (D64004) NifS [Synechocystis sp.]
                   287903
Seq. No.
                   228779 1.R1011
Contig ID
5'-most EST
                   xjt700094130.h1
                   287904
Seq. No.
                   228810 1.R1011
Contig ID
5'-most EST
                   zuv700354902.h1
                   BLASTX
Method
NCBI GI
                   q461451
                   300
BLAST score
                   2.0e-27
E value
                   57
Match length
```

40065

>gi 418698 pir B43033 auxin-binding protein 4 precursor -

E**17 *. *.



maize >gi_168399 (L08426) auxin-binding protein [Zea mays]
>gi_442526_bbs_139535 (S66813) ZmERabp4=auxin-binding
protein [Zea mays=corn, seedling, Peptide, 204 aa] [Zea
mays]

287905 Seq. No. 228842 1.R1011 Contig ID wyr700242461.hl 5'-most EST BLASTX Method g1764100 NCBI GI 323 BLAST score 4.0e-30 E value 100 Match length 67 % identity (U81805) GDP-D-mannose-4,6-dehydratase [Arabidopsis NCBI Description thaliana] 287906 Seq. No.

Seq. No. 287906 Contig ID 228936_1.R1011 5'-most EST fwa700100938.h1

Seq. No. 287907

Contig ID 228975_1.R1011 5'-most EST uer700579617.h1

Seq. No. 287908

Contig ID 229023_1.R1011 5'-most EST xjt700094511.h1

Seq. No. 287909

Contig ID 229034 1.R1011 5'-most EST xjt700094524.h1

Method BLASTX
NCBI GI g3025189
BLAST score 386
E value 2.0e-37
Match length 133
% identity 55

NCBI Description HYPOTHETICAL 67.1 KD PROTEIN SLL1770

>gi_1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis

sp.]

Seq. No. 287910

Contig ID 229041_1.R1011 5'-most EST xjt700094532.h1

Seq. No. 287911

Contig ID 229052_1.R1011 5'-most EST xjt700094544.h1

Seq. No. 287912

Contig ID 229071 1.R1011 5'-most EST xjt700094570.h1

Seq. No. 287913

Contig ID 229104_1.R1011 5'-most EST xjt700094615.h1



```
Method BLASTN
NCBI GI g3769431
BLAST score 293
E value 1.0e-164
Match length 329
% identity 97
```

NCBI Description Zea mays RNA polymerase sigma factor 2 (sig2) mRNA, nuclear mRNA encoding chloroplast protein, partial cds

Seq. No. 287914

Contig ID 229106_1.R1011 5'-most EST hbs701182911.h1

Seq. No. 287915

Contig ID 229165_1.R1011 5'-most EST pmx700084922.h1

Method BLASTX
NCBI GI g1495366
BLAST score 271
E value 6.0e-24
Match length 122
% identity 48

NCBI Description (Z69370) nitrite transporter [Cucumis sativus]

 Seq. No.
 287917

 Contig ID
 229202 1.R1011

 5'-most EST
 xjt700094782.h1

 Method
 BLASTY

Method BLASTX
NCBI GI g3176686
BLAST score 196
E value 4.0e-28
Match length 108
% identity 54

NCBI Description (AC003671) Similar to high affinity potassium transporter, HAK1 protein gb U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

Seq. No.287918Contig ID229209_1.R10115'-most ESTxjt700094793.h1

Seq. No. 287919

Contig ID 229259_1.R1011 5'-most EST nbm700475890.h1 Method BLASTX

Method BLASTX
NCBI GI g1710807
BLAST score 417
E value 7.0e-41
Match length 164
% identity 50

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_1185390

(U21105) alphacpn60 [Pisum sativum]

Method

NCBI GI BLAST score

E value



```
287920
Seq. No.
                  229261 1.R1011
Contig ID
                  nbm700\overline{4}71053.h1
5'-most EST
Method
                  BLASTX
                  g2340108
NCBI GI
                   558
BLAST score
                   3.0e-92
E value
                   168
Match length
                   95
% identity
NCBI Description (U65948) starch branching enzyme IIa [Zea mays]
                   287921
Seq. No.
                   229270 1.R1011
Contig ID
5'-most EST
                   rvt700550167.h1
                   287922
Seq. No.
                   229275 1.R1011
Contig ID
                   wen700\overline{3}36253.h1
5'-most EST
Seq. No.
                   287923
                   229458 1.R1011
Contig ID
                   nbm700473878.h1
5'-most EST
                   BLASTX
Method
                   g1167982
NCBI GI
BLAST score
                   252
                   8.0e-22
E value
Match length
                   107
% identity
                   51
                   (U43892) ABC transporter-7 [Mus musculus]
NCBI Description
                   287924
Seq. No.
                   229464 1.R1011
Contig ID
                   xjt700095133.h1
5'-most EST
                   BLASTX
Method
                   g3075397
NCBI GI
                   401
BLAST score
                   6.0e-39
E value
                   163
Match length
                   51
% identity
                   (AC004484) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    287925
Seq. No.
                    229520 1.R1011
Contig ID
5'-most EST
                   xsy700212808.h1
                    287926
Seq. No.
                    229539 1.R1011
Contig ID
5'-most EST
                    ceu700423673.h1
Seq. No.
                    287927
 Contig ID
                    229542 1.R1011
                    wty700172593.hl
 5'-most EST
                    BLASTX
```

40068

g1353193

309 3.0e-28



Match length % identity 52

NCBI Description

O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268 O-methyltransferase (EC 2.1.1.-) - maize >gi_404070

(L14063) O-methyltransferase [Zea mays]

287928 Seq. No.

229600 1.R1011 Contig ID xjt700095331.hl 5'-most EST

Seq. No. 287929

229650 1.R1011 Contig ID xjt700095394.hl 5'-most EST

BLASTX Method g2244790 NCBI GI BLAST score 360 E value 2.0e-34 Match length 108 71 % identity

NCBI Description (Z97336) kinesin homolog [Arabidopsis thaliana]

Seq. No. 287930

229667 1.R1011 Contig ID xjt700095429.h1 5'-most EST

BLASTX Method g3047108 NCBI GI BLAST score 179 6.0e-13 E value 53 Match length 72 % identity

(AF058919) No definition line found [Arabidopsis thaliana] NCBI Description

287931 Seq. No.

229707 1.R1011 Contig ID fwa700101143.hl 5'-most EST

287932 Seq. No.

229716 2.R1011 Contig ID ymt700221350.hl 5'-most EST

287933 Seq. No.

229836 1.R1011 Contig ID xjt700096163.hl 5'-most EST

287934 Seq. No.

229870 1.R1011 Contig ID vmj700053736.rl 5'-most EST

BLASTX Method g4587595 NCBI GI 234 BLAST score 1.0e-19 E value Match length 67 % identity

(AC006951) putative proline-rich protein APG [Arabidopsis NCBI Description

thaliana]

287935 Seq. No.



Contig ID	229881_1.R1011
5'-most EST	xjt700095717.h1
Sea. No.	287936

Contig ID 229883_1.R1011 5'-most EST xjt700095719.h1

Seq. No. 287937

Contig ID 229884_1.R1011 5'-most EST xjt700095722.h1

Seq. No. 287938

Contig ID 229897_1.R1011 5'-most EST rv1700455833.h1

Seq. No. 287939

Contig ID 229904_1.R1011 5'-most EST xjt700095746.h1

Seq. No. 287940

Contig ID 229905_1.R1011 5'-most EST xjt700095747.h1

Seq. No. 287941

Contig ID 229971_1.R1011 5'-most EST xmt700256786.h1

Seq. No. 287942

Contig ID 230036_1.R1011 5'-most EST ymt700223540.h1

Method BLASTX
NCBI GI g4314378
BLAST score 148
E value 2.0e-09
Match length 55
% identity 45

NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 287943

Contig ID 230045_1.R1011 5'-most EST xjt700095932.h1

Method BLASTX
NCBI GI g4115384
BLAST score 228
E value 5.0e-19
Match length 51
% identity 82

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 287944

Contig ID 230070_1.R1011 5'-most EST ceu700429242.h1

Method BLASTX
NCBI GI g1888357
BLAST score 429
E value 1.0e-42
Match length 106



% identity
NCBI Description

(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi 1890154 emb CAA72432 (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

Seq. No. 287945

Contig ID 230125_1.R1011 5'-most EST vux700161055.h1

Method BLASTX
NCBI GI g538502
BLAST score 370
E value 8.0e-49
Match length 136
% identity 73

NCBI Description (L36231) peroxidase [Stylosanthes humilis]

Seq. No. 287946

Contig ID 230143_1.R1011 5'-most EST xjt700096061.h1

Method BLASTX
NCBI GI g1617206
BLAST score 197
E value 2.0e-15
Match length 88
% identity 51

NCBI Description (Z72489) CP12 [Pisum sativum]

Seq. No. 287947

Contig ID 230183_1.R1011 5'-most EST xjt700096111.h1

Seq. No. 287948

Contig ID 230213_1.R1011 5'-most EST ymt700223294.h1

Seq. No. 287949

Contig ID 230226_1.R1011 5'-most EST nbm700472344.h1

Method BLASTX
NCBI GI g2134102
BLAST score 171
E value 1.0e-12
Match length 47
% identity 74

NCBI Description kinesin-like protein 1 - African clawed frog

>gi 562793_emb_CAA57539_ (X82012) kinesin-like protein 1

[Xenopus laevis]

Seq. No. 287950

Contig ID 230234 1.R1011 5'-most EST xjt700096182.h1

Seq. No. 287951

Contig ID 230244_1.R1011 5'-most EST vux700160988.h1

Seq. No. 287952

E value

Match length

9.0e-59 123



230347 1.R1011 Contig ID $xmt700\overline{2}58963.h1$ 5'-most EST 287953 Seq. No. Contig ID 230417 1.R1011 xjt700096446.h1 5'-most EST BLASTX Method q4529972 NCBI GI BLAST score 149 E value 1.0e-09 110 Match length 38 % identity (AC002330) putative chloroplast outer envelope 86-like NCBI Description protein [Arabidopsis thaliana] Seq. No. 287954 230421 1.R1011 Contig ID xjt700096505.h1 5'-most EST 4, 287955 Seq. No. 230433 1.R1011 Contig ID wyr700238243.h1 5'-most EST 287956 Seq. No. 230450 1.R1011 Contig ID 5'-most EST xjt700096541.hl 287957 Seq. No. Contig ID 230457 1.R1011 gct701175394.h1 5'-most EST BLASTX Method q2642158 NCBI GI 155 BLAST score 3.0e-18 E value 165 Match length 39 % identity (AC003000) hypothetical protein [Arabidopsis thaliana] NCBI Description 287958 Seq. No. 230476 1.R1011 Contig ID $xjt700\overline{0}96586.h1$ 5'-most EST Method BLASTX g4544451 NCBI GI BLAST score 193 6.0e-15 E value 62 Match length % identity 58 (AC006592) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 287959 230527 1.R1011 Contig ID $xjt700\overline{0}96653.h1$ 5'-most EST BLASTX Method g3617837 NCBI GI BLAST score 568



% identity (AF035820) gibberellin action negative regulator SPY NCBI Description [Hordeum vulgare] 287960 Seq. No. 230593 1.R1011 Contig ID xjt700096733.hl 5'-most EST BLASTX Method g3005983 NCBI GI BLAST score 326 2.0e-30 E value Match length 88 % identity 69 (Y14387) lycopene epsilon-cyclase [Lycopersicon esculentum] NCBI Description Seq. No. 287961 230596 1.R1011 Contig ID xjt700096737.h1 5'-most EST BLASTX Method q2674203 NCBI GI BLAST score 352 1.0e-33 E value 94 Match length 70 % identity (AF036328) CLP protease regulatory subunit CLPX NCBI Description [Arabidopsis thaliana] Seq. No. 287962 230606 1.R1011 Contig ID pmx700090054.h1 5'-most EST BLASTX Method q4263510 NCBI GI 146 BLAST score 3.0e-09 E value 81 Match length 40 % identity (AC004044) hypothetical protein [Arabidopsis thaliana] NCBI Description 287963 Seq. No. 230608 1.R1011 Contig ID 5'-most EST xjt700096759.h1 287964 Seq. No. 230634 1.R1011 Contig ID hbs701182515.h1 5'-most EST BLASTX Method q2842490 NCBI GI 308 BLAST score 3.0e-28 E value

Match length 66 % identity 86

(AL021749) heat-shock protein [Arabidopsis thaliana] NCBI Description

287965 Seq. No.

230650 1.R1011 Contig ID 5'-most EST xjt700096796.h1



```
Seq. No. 287966
Contig ID 230669_
```

Contig ID 230669 1.R1011 5'-most EST xjt700096835.h1

Seq. No. 287967

Contig ID 230722 1.R1011 5'-most EST pmx700081940.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 287968

Contig ID 230784_1.R1011 5'-most EST fdz701163326.h1

Method BLASTX
NCBI GI g3402713
BLAST score 224
E value 4.0e-18
Match length 58
% identity 72

NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No. 287969

Contig ID 230789_1.R1011 5'-most EST fwa700097007.h1

Seq. No. 287970

Contig ID 230822 1.R1011 5'-most EST fwa700097046.h1

Seq. No. 287971

Contig ID 230824_1.R1011 5'-most EST fwa700097050.h1

Seq. No. 287972

Contig ID 230833 1.R1011 5'-most EST fwa700097063.h1

Seq. No. 287973

Contig ID 230846 1.R1011 5'-most EST fwa700101131.h1

Method BLASTX
NCBI GI g3025189
BLAST score 368
E value 4.0e-35
Match length 125
% identity 54

NCBI Description HYPOTHETICAL 67.1 KD PROTEIN SLL1770

>gi 1652753 dbj BAA17672 (D90908) ABC1-like [Synechocystis

sp.]

Seq. No. 287974

Contig ID 230858_1.R1011



5'-most EST xsy700210768.hl

Seq. No. 287975

Contig ID 230868_1.R1011 5'-most EST fwa700097119.h1

Seq. No. 287976

Contig ID 230872_1.R1011 5'-most EST nwy700444451.h1

Seq. No. 287977

Contig ID 230886_1.R1011 5'-most EST uer700577758.h1

Method BLASTX
NCBI GI g4559369
BLAST score 278
E value 3.0e-25
Match length 76
% identity 70

NCBI Description (AC006585) putative Rieske iron-sulfur protein [Arabidopsis

thaliana]

Seq. No. 287978

Contig ID 230951_1.R1011 5'-most EST fwa700097239.h1

Seq. No. 287979

Contig ID 230969_1.R1011 5'-most EST fwa700097265.h1

Method BLASTX
NCBI GI g4559380
BLAST score 321
E value 6.0e-30
Match length 101
% identity 58

NCBI Description (AC006526) putative auxin-responsive GH3 protein

[Arabidopsis thaliana]

Seq. No. 287980

Contig ID 231016_1.R1011 5'-most EST fwa700097324.h1

Seq. No. 287981

Contig ID 231083_1.R1011 5'-most EST fwa700097406.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 8.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 287982

Contig ID 231084 1.R1011 5'-most EST yyf700348137.h1

Method BLASTX



```
q4127346
NCBI GI
BLAST score
                  419
                  3.0e-41
E value
                  111
Match length
% identity
                  (AJ010448) glutathione transferase [Alopecurus myosuroides]
NCBI Description
                  287983
Seq. No.
                  231087 1.R1011
Contig ID
                  fwa700097411.h1
5'-most EST
                  287984
Seq. No.
```

Contig ID 231103_1.R1011 5'-most EST fwa700097435.h1

 Seq. No.
 287985

 Contig ID
 231105_1.R1011

 5'-most EST
 fwa700101415.h1

 Method
 BLASTX

 NCBI GI
 g1345838

 BLAST score
 1021

BLAST score 1021 E value 1.0e-121 Match length 216 % identity 100

NCBI Description PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATURASE)

>gi_2130143_pir__ S65060 phytoene desaturase precursor
maize >gi 1051180 (U37285) phytoene desaturase [Zea mays]

 Seq. No.
 287986

 Contig ID
 231185_1.R1011

 5'-most EST
 fwa700097555.h1

 Method
 BLASTX

 NCBI GI
 g3258570

NCBI GI g3258570
BLAST score 189
E value 2.0e-17
Match length 121
% identity 53

NCBI Description (U89959) Unknown protein [Arabidopsis thaliana]

 Seq. No.
 287987

 Contig ID
 231248_1.R1011

 5'-most EST
 xsy700212862.h1

Seq. No. 287988 Contig ID 231264 1.R1011 5'-most EST fwa700097671.h1

 Seq. No.
 287989

 Contig ID
 231325_1.R1011

 5'-most EST
 fwa700097756.h1

 Seq. No.
 287990

 Contig ID
 231330_1.R1011

 5'-most EST
 pmx700087925.h1

Method BLASTX NCBI GI g4468992 BLAST score 443



E value 6.0e-44
Match length 151
% identity 60

NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 287991

Contig ID 231346_1.R1011 5'-most EST fwa700097784.h1

Seq. No. 287992

Contig ID 231379_1.R1011 5'-most EST nwy700443982.h1

Method BLASTX
NCBI GI g4490748
BLAST score 159
E value 2.0e-11
Match length 36
% identity 83

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 287993

Contig ID 231392_1.R1011 5'-most EST fwa700097860.h1

Method BLASTX
NCBI GI g2492514
BLAST score 410
E value 4.0e-40
Match length 146
% identity 61

NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR

>qi 1483215 emb CAA68141 (X99808) chloroplast FtsH

protease [Arabidopsis thaliana]

Seq. No. 287994

Contig ID 231485_1.R1011 5'-most EST wty700163202.h1

Method BLASTX
NCBI GI g3004555
BLAST score 215
E value 2.0e-17
Match length 114
% identity 13

NCBI Description (AC003673) similar to salt inducible protein [Arabidopsis

thaliana]

Seq. No. 287995

Contig ID 231499 1.R1011 5'-most EST ymt700221550.h2

Method BLASTX
NCBI GI g1805654
BLAST score 315
E value 9.0e-33
Match length 102
% identity 63

NCBI Description (X99972) calmodulin-stimulated calcium-ATPase [Brassica

oleracea]



287996 Seq. No. 231507 1.R1011 Contig ID pmx700087112.h1 5'-most EST

287997 Seq. No.

231516 1.R1011 Contig ID fwa700098746.hl 5'-most EST

287998 Seq. No.

231546 1.R1011 Contig ID fwa700098060.hl 5'-most EST

287999 Seq. No.

231573 1.R1011 Contig ID fwa700098106.h1 5'-most EST

288000 Seq. No.

231591 1.R1011 Contig ID fwa700098130.hl 5'-most EST

BLASTX Method g2827039 NCBI GI 374 BLAST score 6.0e-36 E value 134 Match length 57 % identity

(AF008444) chloroplast processing enzyme [Arabidopsis NCBI Description

thaliana]

288001 Seq. No.

231634 1.R1011 Contig ID fwa700098196.hl 5'-most EST

BLASTX Method g4507079 NCBI GI 146 BLAST score 5.0e-09 E value 116 Match length 33 % identity

SWI/SNF related, matrix associated, actin dependent NCBI Description

regulator of chromatin, subfamily c, member 1 >gi 1549239 (U66615) SWI/SNF complex 155 KDa subunit [Homo sapiens]

Seq. No.

288002 231670 1.R1011 Contig ID fwa700101276.hl 5'-most EST

288003 Seq. No.

231737 1.R1011 Contig ID zuv700352747.h1 5'-most EST

288004 Seq. No.

Contig ID 231804 1.R1011 5'-most EST fwa700098541.hl

288005 Seq. No.

Contig ID 231856 1.R1011 $ceu700\overline{4}29746.h1$ 5'-most EST



```
Seq. No.
Contig ID
                  231873 1.R1011
                  fwa700098715.h1
5'-most EST
                  BLASTX
Method
                  g2384956
NCBI GI
                  240
BLAST score
                  6.0e-20
E value
Match length
                  160
% identity
                  (AF022985) No definition line found [Caenorhabditis
NCBI Description
                  elegans]
                  288007
Seq. No.
Contig ID
                  231978 1.R1011
                  fwa700098847.hl
5'-most EST
                  288008
Seq. No.
                  232014 1.R1011
Contig ID
5'-most EST
                  fwa700099058.hl
                  288009
Seq. No.
                  232020 2.R1011
Contig ID
                  uer700583867.hl
5'-most EST
                  288010
Seq. No.
                  232025 1.R1011
Contig ID
                  tfd700573296.h1
5'-most EST
                  BLASTX
Method
                  g2760837
NCBI GI
BLAST score
                   151
                   9.0e-10
E value
                   115
Match length
% identity
                   31
                  (AC003105) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                   288011
Seq. No.
Contig ID
                   232054 1.R1011
                   fwa700098953.h1
5'-most EST
Seq. No.
                   288012
                   232058 1.R1011
Contig ID
                   ymt700219521.h1
5'-most EST
                   BLASTX
Method
                   q2500139
NCBI GI
BLAST score
                   404
                   2.0e-39
E value
```

127 Match length % identity

PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1) NCBI Description

>gi 1653916 dbj BAA18826 (D90917) peptide chain release

factor [Synechocystis sp.]

288013 Seq. No.

232078 1.R1011 Contig ID $fdz701\overline{1}66822.h1$ 5'-most EST

BLASTX Method g4572671 NCBI GI



```
BLAST score
                   2.0e-67
E value
Match length
                  144
                   86
% identity
                   (AC006954) putative cyclic nucleotide regulated ion channel
NCBI Description
                   [Arabidopsis thaliana]
                   288014
Seq. No.
                   232110 1.R1011
Contig ID
                   tfd700569295.h2
5'-most EST
                   288015
Seq. No.
Contig ID
                   232114 1.R1011
5'-most EST
                   fwa700099032.h1
                   BLASTX
Method
                   g2864602
NCBI GI
BLAST score
                   443
                   4.0e-44
E value
Match length
                   115
                   71
% identity
                  (Y12071) thylakoid lumen rotamase [Spinacia oleracea]
NCBI Description
                   288016
Seq. No.
                   232191_1.R1011
Contig ID
5'-most EST
                   xsy700\overline{2}13856.h1
                   BLASTX
Method
                   q4204297
NCBI GI
                   206
BLAST score
                   2.0e-17
E value
                   69
Match length
                   64
% identity
                   (AC003027) ADK1 [Arabidopsis thaliana]
NCBI Description
                   288017
Seq. No.
                   232272 1.R1011
Contig ID
5'-most EST
                   fwa700099326.hl
Method
                   BLASTX
                   q3789954
NCBI GI
                   372
BLAST score
E value
                   1.0e-47
                   99
Match length
                   94
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
                   288018
Seq. No.
                   232329 1.R1011
Contig ID
                   fwa700099392.h1
5'-most EST
Method
                   BLASTX
```

NCBI GI g2760327 BLAST score 522 E value 2.0e-53 120 Match length 57 % identity

(AC002130) F1N21.12 [Arabidopsis thaliana] NCBI Description

288019 Seq. No.



```
Contig ID
                   232394 1.R1011
5'-most EST
                   fwa700099496.h1
Method
                   BLASTX
NCBI GI
                   q2583127
BLAST score
                   482
E value
                   1.0e-48
Match length
                   114
                   80
% identity
                  (AC002387) putative sialoglycoprotease [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   288020
Contig ID
                   232396 1.R1011
5'-most EST
                   fwa700099503.h1
Seq. No.
                   288021
Contig ID
                   232426 1.R1011
5'-most EST
                   fwa700099545.h1
Seq. No.
                   288022
Contig ID
                   232429 1.R1011
5'-most EST
                   xsy700208077.h1
Method
                   BLASTX
NCBI GI
                   g4336608
BLAST score
                   751
E value
                   4.0e-80
Match length
                   145
% identity
                   100
NCBI Description (AF099111) sigma factor; Sig2 [Zea mays]
                   288023
Seq. No.
Contig ID
                   232433 1.R1011
5'-most EST
                   fwa700099560.h1
Seq. No.
                   288024
Contig ID
                   232454 1.R1011
5'-most EST
                   fwa700099595.h1
Seq. No.
                   288025
Contig ID
                   232495 1.R1011
5'-most EST
                  pmx700090123.h1
                   288026
Seq. No.
                   232507 1.R1011
Contig ID
5'-most EST
                  mwy700440496.h1
Seq. No.
                   288027
Contig ID
                   232528 1.R1011
5'-most EST
                   pwr700452529.h1
Method
                   BLASTX
```

NCBI GI g3860266 BLAST score 145 E value 4.0e-09 Match length 102

% identity

39

NCBI Description (AC005824) hypothetical protein [Arabidopsis thaliana]



```
Seq. No.
                  288028
Contig ID
                  232593 1.R1011
                  pmx700083336.h1
5'-most EST
                  288029
Seq. No.
Contig ID
                  232601 1.R1011
5'-most EST
                  fwa700099824.h1
                  288030
Seq. No.
                  232604_1.R1011
Contig ID
5'-most EST
                  fwa700099828.hl
                  288031
Seq. No.
Contig ID
                  232631 1.R1011
5'-most EST
                  wty700171728.hl
                  BLASTX
Method
                  g4455180
NCBI GI
                  770
BLAST score
E value
                  4.0e-82
Match length
                  198
                  74
% identity
                  (AL035521) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  288032
Contig ID
                  232637 1.R1011
                  rvt700553094.h1
5'-most EST
                  BLASTX
Method
                  g4416301
NCBI GI
BLAST score
                  386
E value
                  8.0e-39
Match length
                  143
                  66
% identity
NCBI Description (AF105716) gag protein [Zea mays]
                  288033
Seq. No.
                  232638 1.R1011
Contig ID
5'-most EST
                  fwa700099876.h1
                  BLASTN
Method
                  q2463510
NCBI GI
BLAST score
                   342
                   0.0e + 00
E value
                   425
Match length
                   39
% identity
                  Z.mays small nuclear RNA genes snoR1.1, snoR2.2, snoR3.2,
NCBI Description
                  U14.1a, U14.1b, U14.1c and U14.1d
Seq. No.
                   288034
Contig ID
                   232649 1.R1011
                   fwa700099892.h1
5'-most EST
```

Seq. No. 288035

232663 1.R1011 Contig ID 5'-most EST ymt700223605.h1

Seq. No. 288036

232678 1.R1011 Contig ID wty700166073.h1 5'-most EST



```
288037
Seq. No.
                  232708 1.R1011
Contig ID
                  fwa700099970.h1
5'-most EST
                  BLASTX
Method
                  g3004565
NCBI GI
BLAST score
                  328
E value
                  4.0e-40
Match length
                  121
                  69
% identity
                  (AC003673) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  288038
Seq. No.
Contig ID
                  232834 1.R1011
                  fwa700100274.h1
5'-most EST
                  288039
Seq. No.
```

232849 1.R1011 Contig ID 5'-most EST $xsy700\overline{2}10331.h1$ Method BLASTX g2245004 NCBI GI 183 BLAST score

9.0e-14E value Match length 94 40 % identity

(Z97341) similarity to membrane transport protein NCBI Description

[Arabidopsis thaliana]

288040 Seq. No.

Contig ID 232949 1.R1011 5'-most EST fwa700100443.h1

288041 Seq. No.

233002 1.R1011 Contig ID 5'-most EST fwa700100523.h1

BLASTX Method NCBI GI g3152568 BLAST score 224 E value 2.0e-18 Match length 108 % identity 53

(AC002986) Similar to hypothetical protein product NCBI Description

gb_Z97337 from A. thaliana. EST gb_H76597 comes from this

- 70

gene. [Arabidopsis thaliana]

288042 Seq. No.

233003 1.R1011 Contig ID fwa700100524.h1 5'-most EST

Method BLASTX NCBI GI q3176874 BLAST score 314 E value 4.0e-29 Match length 91 66 % identity

NCBI Description (AF065639) cucumisin-like serine protease [Arabidopsis

thaliana]



```
Seq. No.
                  288043
Contig ID
                  233054 1.R1011
                  nbm700\overline{4}64908.h1
5'-most EST
                  288044
Seq. No.
                  233120 1.R1011
Contig ID
5'-most EST
                  fwa700100705.h1
                  288045
Seq. No.
                  233151 1.R1011
Contig ID
                  fwa700100759.hl
5'-most EST
                  BLASTX
Method
                  g2598569
NCBI GI
BLAST score
                  184
E value
                  6.0e-14
Match length
                  94
% identity
                  44
                  (Y15290) putative start codon [Medicago truncatula]
NCBI Description
Seq. No.
                  288046
                  233236 1.R1011
Contig ID
                  nbm700470276.hl
5'-most EST
                  BLASTX
Method
                  q3482978
NCBI GI
BLAST score
                  216
                  2.0e-17
E value
Match length
                  100
% identity
                  53
                  (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
                   288047
Seq. No.
                   233288 1.R1011
Contig ID
5'-most EST
                   fwa700100959.h1
                  BLASTX
Method
NCBI GI
                   g2275199
BLAST score
                  172
E value
                   2.0e-12
Match length
                  108
% identity
                   43
NCBI Description
                  (AC002337) hypothetical protein [Arabidopsis thaliana]
                   288048
Seq. No.
                   233318 1.R1011
Contig ID
5'-most EST
                   wen700335116.h1
                   288049
Seq. No.
Contig ID
                   233340 1.R1011
5'-most EST
                   fwa700101043.h1
```

288050 Seq. No.

Contig ID 233369 1.R1011 5'-most EST fwa700101094.h1

Method BLASTX g3176667 NCBI GI BLAST score 259 E value 2.0e-22 Match length 144



% identity 42

NCBI Description (AC004393) Similar to hypothetical 41.9KD protein

gb_1001369 from sequence of Synechocystis sp. gb_D64006.

[Arabidopsis thaliana]

Seq. No.

Contig ID

233455_1.R1011

5'-most EST Method

uer700577560.hl BLASTX

NCBI GI BLAST score E value g4586253 269 8.0e-24

288051

Match length 67 % identity 69

NCBI Description (AL049640) auxilin-like protein [Arabidopsis thaliana]

Seq. No.

Contig ID 5'-most EST 288052

233618_1.R1011 zuv700352657.h1

Seq. No.

288053

Contig ID 5'-most EST

233701_1.R1011 dyk700102684.h1

Seq. No.

288054

Contig ID 5'-most EST

233725_1.R1011 pwr700452101.h1

Seq. No.

288055

Contig ID 5'-most EST

233726 1.R1011 fwa700101595.h1

Seq. No.

288056

Contig ID 5'-most EST

233749_1.R1011 xmt700265178.h1

Seq. No.

288057

Contig ID 5'-most EST 233891_1.R1011 fwa700101841.h1

Seq. No.

288058

Contig ID 5'-most EST

233949_1.R1011 xsy700208380.h1

Seg. No.

288059

Contig ID 5'-most EST

233990_1.R1011 ymt700222806.h1

Method NCBI GI BLAST score E value BLASTX g1255425 146

E value 5.0e-09 Match length 177 % identity 23

NCBI Description (U53154) No definition line found [Caenorhabditis elegans]

Seq. No.

288060

Contig ID

234097 1.R1011



```
lhp700053443.rl
5'-most EST
                  288061
Seq. No.
Contig ID
                  234120 1.R1011
                  xmt700263004.h1
5'-most EST
                   288062
Seq. No.
                  234166 1.R1011
Contig ID
5'-most EST
                  dyk700102034.h1
Method
                  BLASTX
                   g2618699
NCBI GI
                   176
BLAST score
                   9.0e-13
E value
                   96
Match length
% identity
                   36
                  (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
                   288063
Seq. No.
                   234195 1.R1011
Contig ID
                   dyk700105164.h1
5'-most EST
                   288064
Seq. No.
                   234227 1.R1011
Contig ID
                   hvj700620119.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g283004
BLAST score
                   251
E value
                   2.0e-23
Match length
                   91
                   39
% identity
                  DNA-binding protein Gt-2 - rice >gi_20249_emb_CAA48328_
NCBI Description
                   (X68261) gt-2 [Oryza sativa]
                   288065
Seq. No.
                   234263 1.R1011
Contig ID
5'-most EST
                   nbm700\overline{4}68318.h1
                   288066
Seq. No.
                   234271_1.R1011
Contig ID
5'-most EST
                   wyr700241978.hl
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
                   9.0e-11
E value
Match length
                   48
% identity
                   67
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   288067
Seq. No.
                   234275 1.R1011
Contig ID
5'-most EST
                   dyk700103736.h1
```

Method BLASTX NCBI GI q4204912 BLAST score 466 E value 8.0e-47

Match length 106 % identity





NCBI Description (U58918) MEK kinase [Arabidopsis thaliana]

Seq. No. 288068

Contig ID 234285_1.R1011 5'-most EST dyk700102190.h1

Method BLASTX
NCBI GI g2129581
BLAST score 549
E value 2.0e-56
Match length 151
% identity 73

NCBI Description envelope Ca2+-ATPase precursor - Arabidopsis thaliana

>gi_471089_dbj_BAA03091_ (D13984) chloroplast envelope

Ca2+-ATPase precursor [Arabidopsis thaliana]

>gi_4165448_emb_CAA49558_ (X69940) envelope Ca2+-ATPase

[Arabidopsis thaliana]

Seq. No. 288069

Contig ID 234302_1.R1011 5'-most EST dyk700102464.h1

Method BLASTX
NCBI GI g2655098
BLAST score 174
E value 6.0e-13
Match length 102
% identity 48

NCBI Description (AF023472) peptide transporter [Hordeum vulgare]

Seq. No. 288070

Contig ID 234364_1.R1011 5'-most EST dyk700102311.h1

Seq. No. 288071

Contig ID 234372_1.R1011 5'-most EST wyr700238918.h1

Method BLASTX
NCBI GI g4220608
BLAST score 303
E value 9.0e-28
Match length 75
% identity 81

NCBI Description (AB019525) nicotianamine synthase 7 [Hordeum vulgare]

Seq. No. 288072

Contig ID 234372_2.R1011 5'-most EST dyk700102320.h1

Method BLASTX
NCBI GI g4220608
BLAST score 262
E value 5.0e-23
Match length 69
% identity 77

NCBI Description (AB019525) nicotianamine synthase 7 [Hordeum vulgare]

Seq. No. 288073

Contig ID 234372 3.R1011 5'-most EST wyr700242550.h1

Match length

NCBI Description

% identity

95 77



```
BLASTX
Method
NCBI GI
                   g4586378
BLAST score
                   157
E value
                   2.0e-22
Match length
                  79
                   69
% identity
                  (AB021746) nicotianamine synthase 1 [Oryza sativa]
NCBI Description
                   288074
Seq. No.
                   234395 1.R1011
Contig ID
                   tfd700569126.h1
5'-most EST
                   288075
Seq. No.
                   234399 1.R1011
Contig ID
5'-most EST
                   wyr700237418.h1
Method
                   BLASTN
                   q984040
NCBI GI
BLAST score
                   33
                   4.0e-09
E value
                   57
Match length
% identity
                   89
                  Rice mRNA for EL3 gene, complete cds
NCBI Description
                   288076
Seq. No.
                   234431 1.R1011
Contig ID
                   ymt700221890.h1
5'-most EST
Seq. No.
                   288077
                   234505 1.R1011
Contig ID
                   dyk700102505.h1
5'-most EST
                   BLASTX
Method
                   g3063710
NCBI GI
                   149
BLAST score
                   1.0e-09
E value
Match length
                   55
                   53
% identity
                  (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
                   288078
Seq. No.
Contig ID
                   234545 1.R1011
5'-most EST
                   dyk700102555.h1
                   288079
Seq. No.
Contig ID
                   234771 1.R1011
5'-most EST
                   gct701178974.hl
                   288080
Seq. No.
                   234776 1.R1011
Contig ID
5'-most EST
                   wyr700\overline{2}39429.h1
                   BLASTX
Method
NCBI GI
                   q2130080
BLAST score
                   377
E value
                   2.0e-36
```

40088

Nramp1 protein - rice >gi 1470320 bbs 177441 (S81897)

OsNramp1=Nramp1 homolog/Bcg product homolog [Oryza sativa,



indica, cv. IR 36, etiolated shoots, Peptide, 517 aa] [Oryza sativa] >gi_2231132 (L41217) integral membrane protein [Oryza sativa]

 Seq. No.
 288081

 Contig ID
 234814_1.R1011

 5'-most EST
 dyk700102914.h1

Seq. No. 288082

Contig ID 234837_1.R1011 5'-most EST dyk700102941.h1

Seq. No. 288083

Contig ID 234859_1.R1011 5'-most EST wyr700240324.h1

Seq. No. 288084

Contig ID 234902_1.R1011 5'-most EST dyk700103038.h1

Method BLASTX
NCBI GI 94468798
BLAST score 169
E value 3.0e-26
Match length 119
% identity 57

NCBI Description (AJ010440) GST7 protein [Zea mays]

Seq. No. 288085

Contig ID 234981_1.R1011 5'-most EST dyk700103147.h1

Seq. No. 288086

Contig ID 234987_1.R1011 5'-most EST dyk700103157.h1

Method BLASTX
NCBI GI g4127781
BLAST score 489
E value 3.0e-49
Match length 165
% identity 32

NCBI Description (AJ012588) Notchless protein [Drosophila melanogaster]

Seq. No. 288087

Contig ID 234999 1.R1011 5'-most EST dyk700103172.h1

Seq. No. 288088

Contig ID 235009_1.R1011 5'-most EST dyk700103185.h1 Method BLASTX

NCBI GI g3941480
BLAST score 192
E value 8.0e-15
Match length 48
% identity 77

NCBI Description (AF062894) putative transcription factor [Arabidopsis

thaliana]



```
288089
Seq. No.
Contig ID
                   235046 1.R1011
                   pwr700449460.hl
5'-most EST
                   BLASTX
Method
                   g2673911
NCBI GI
BLAST score
                   155
E value
                   2.0e-10
Match length
                   63
% identity
                   52
                   (AC002561) putative squamosa-promoter binding protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   288090
                   235060 1.R1011
Contig ID
                   dyk700103252.h1
5'-most EST
                   BLASTX
Method
                   g2244785
NCBI GI
BLAST score
                   337
                   9.0e-32
E value
                   91
Match length
% identity
                   67
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   288091
Seq. No.
Contig ID
                   235113 1.R1011
5'-most EST
                   dyk700\overline{1}06936.h1
                   288092
Seq. No.
Contig ID
                   235169 1.R1011
                   ceu700\overline{4}34042.h1
5'-most EST
                   BLASTX
Method
                   g4006908
NCBI GI
BLAST score
                   146
                   5.0e-09
E value
Match length
                   164
                   25
% identity
                   (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
                   288093
Seq. No.
                   235205 1.R1011
Contig ID
                   dyk700103444.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3540195
BLAST score
                   327
                   2.0e-30
E value
                   137
Match length
                   23
% identity
                  (AC004260) Unknown protein [Arabidopsis thaliana]
NCBI Description
```

288094

Seq. No.

235223 1.R1011 Contig ID 5'-most EST dyk700103465.h1

Seq. No. 288095

235239 1.R1011 Contig ID 5'-most EST dyk700103485.h1



```
Seq. No.
                   288096
                   235310 1.R1011
Contig ID
                   dyk700103583.hl
5'-most EST
                   288097
Seq. No.
                   235317 1.R1011
Contig ID
5'-most EST
                   dyk700\overline{1}03590.h1
Method
                   BLASTX
                   g3894158
NCBI GI
BLAST score
                   147
                   2.0e-09
E value
                   121
Match length
% identity
                   36
                   (AC005312) similar to phloem-specific lectin [Arabidopsis
NCBI Description
                   thaliana]
                   288098
Seq. No.
                   235379 1.R1011
Contig ID
                   wyr700237701.h1
5'-most EST
                   288099
Seq. No.
                   235441 1.R1011
Contig ID
5'-most EST
                   dyk700103821.hl
                   288100
Seq. No.
                   235445 1.R1011
Contig ID
                   dyk700104527.h1
5'-most EST
Seq. No.
                   288101
                   235519 1.R1011
Contig ID
5'-most EST
                   dyk700103933.h1
                   288102
Seq. No.
Contig ID
                   235533 1.R1011
                   dyk700103951.hl
5'-most EST
                   288103
Seq. No.
                   235553 1.R1011
Contig ID
5'-most EST
                   uer700577723.h1
                   BLASTX
Method
                   q2262105
NCBI GI
BLAST score
                   280
                   4.0e-25
E value
Match length
                   88
                   59
% identity
                  (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   288104
Contig ID
                   235610 1.R1011
5'-most EST
                   dyk700104058.h1
```

Method BLASTX

g1871192 NCBI GI BLAST score 445 E value 2.0e-44Match length 86 % identity 91



(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No. 288105

NCBI Description

Contig ID 235626_1.R1011 5'-most EST gct701175423.h1

Method BLASTX
NCBI GI g4115388
BLAST score 375
E value 4.0e-36
Match length 120
% identity 57

NCBI Description (AC005967) putative prolylcarboxypeptidase [Arabidopsis

thaliana]

Seq. No. 288106

Contig ID 235661_1.R1011 5'-most EST dyk700104137.h1

Method BLASTX
NCBI GI g4455356
BLAST score 406
E value 1.0e-39
Match length 130
% identity 60

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 288107

Contig ID 235687_1.R1011 5'-most EST dyk700104177.h1

Method BLASTX
NCBI GI g3258575
BLAST score 340
E value 4.0e-32
Match length 93
% identity 68

NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 288108

Contig ID 235699_1.R1011 5'-most EST tfd700576395.h1

Method BLASTX
NCBI GI g2708532
BLAST score 387
E value 5.0e-37
Match length 135
% identity 55

NCBI Description (AF029351) putative RNA binding protein [Nicotiana tabacum]

Seq. No. 288109

Contig ID 235736 1.R1011 5'-most EST dyk700106376.h1

Method BLASTX
NCBI GI g2088651
BLAST score 320
E value 2.0e-29
Match length 169
% identity 43



NCBI Description (AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No. 288110

Contig ID 235793_1.R1011 5'-most EST uer700578911.h1

Seq. No. 288111

Contig ID 235879_1.R1011 5'-most EST dyk700104486.h1

Method BLASTX
NCBI GI g4558669
BLAST score 303
E value 7.0e-28
Match length 92
% identity 64

NCBI Description (AC007063) putative vanadate resistance protein

[Arabidopsis thaliana]

Seq. No. 288112

Contig ID 235955_1.R1011 5'-most EST zuv700355843.h1

Seq. No. 288113

Contig ID 235999 1.R1011 5'-most EST dyk700104664.h1

Seq. No. 288114

Contig ID 236007_1.R1011 5'-most EST dyk700104673.h1

Method BLASTX
NCBI GI g2459412
BLAST score 240
E value 2.0e-20
Match length 108
% identity 45

NCBI Description (AC002332) putative G9a protein [Arabidopsis thaliana]

Seq. No. 288115

Contig ID 236017_1.R1011 5'-most EST wyr700237614.h1

Seq. No. 288116

Contig ID 236046_1.R1011 5'-most EST dyk700104725.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 7.0e-11
Match length 48
% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 288117

Contig ID 236074_1.R1011 5'-most EST dyk700104757.h1



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Seq. No. 288118
Contig ID 236081_1.R1011
5'-most EST dyk700105664.h1

Seq. No. 288119
Contig ID 236102_1.R1011
5'-most EST yyf700351932.h1
```

 Seq. No.
 288120

 Contig ID
 236139_1.R1011

 5'-most EST
 ymt700220711.h1

 Method
 BLASTX

 NCBI GI
 g3152572

 BLAST score
 261

 F. walks
 7.00-31

E value 7.0e-31
Match length 165
% identity 49

NCBI Description (AC002986) Contains homology to DNAJ heatshock protein qb U32803 from Haemophilus influenzae. [Arabidopsis

thaliana]

Seq. No. 288121

Contig ID 236173_1.R1011 5'-most EST vux700156936.h1

Seq. No. 288122

Contig ID 236240_1.R1011 5'-most EST wyr700235569.h1

Method BLASTX
NCBI GI g4262237
BLAST score 190
E value 3.0e-14
Match length 71
% identity 54

NCBI Description (AC006200) hypothetical protein [Arabidopsis thaliana]

Seq. No. 288123

Contig ID 236261_1.R1011 5'-most EST zuv700352627.h1

Method BLASTX
NCBI GI g2673914
BLAST score 476
E value 7.0e-48
Match length 132
% identity 64

NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No. 288124

Contig ID 236275 1.R1011 5'-most EST dyk700105078.h1

Method BLASTX
NCBI GI g3860263
BLAST score 275
E value 2.0e-24
Match length 93
% identity 56

NCBI Description (AC005824) putative cytochrome p450 protein [Arabidopsis



thaliana]

 Seq. No.
 288125

 Contig ID
 236377_1.R1011

 5'-most EST
 dyk700105230.h1

 Method
 BLASTX

 NCBI GI
 g1706130

 BLAST score
 735

 E value
 4.0e-78

Match length 157 % identity 87

NCBI Description CDPK-RELATED PROTEIN KINASE (PK421) >gi_2129917_pir__S60052

calcium-dependent protein kinase homolog - carrot

>gi_1103386_emb_CAA58750_ (X83869) CDPK-related protein

kinase [Daucus carota]

Seq. No. 288126

Contig ID 236379_1.R1011 5'-most EST dyk700105233.h1

Seq. No. 288127

Contig ID 236459_1.R1011 5'-most EST gct701174568.h1

Method BLASTX
NCBI GI g2829887
BLAST score 227
E value 1.0e-18
Match length 73
% identity 53

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 288128

Contig ID 236509_1.R1011 5'-most EST dyk700105416.h1

Method BLASTX
NCBI GI g2642446
BLAST score 379
E value 2.0e-46
Match length 124
% identity 80

NCBI Description (AC002391) similar to auxin-responsive GH3 protein

[Arabidopsis thaliana]

Seq. No. 288129

Contig ID 236686_1.R1011 5'-most EST gct701180485.h1

Method BLASTX
NCBI GI g4314355
BLAST score 223
E value 4.0e-18
Match length 95
% identity 43

NCBI Description (AC006340) unknown protein [Arabidopsis thaliana]

Seq. No. 288130

Contig ID 236715 1.R1011 5'-most EST wyr700241324.h1



```
BLASTX
Method
                  g678547
NCBI GI
BLAST score
                  266
                  2.0e-23
E value
                  107
Match length
                  50
% identity
                  (L13654) peroxidase [Lycopersicon esculentum]
NCBI Description
                  288131
Seq. No.
                  236781 1.R1011
Contig ID
                  rv1700454627.h1
5'-most EST
```

288132 Seq. No.

Contig ID 236782 1.R1011 5'-most EST nbm700466485.hl

288133 Seq. No.

236817 1.R1011 Contig ID pwf700321706.h1 5'-most EST

288134 Seq. No.

236817 2.R1011 Contig ID zuv700353241.h1 5'-most EST

Seq. No. 288135

236831 1.R1011 Contig ID 5'-most EST wty700163102.h1

288136 Seq. No.

236837 1.R1011 Contig ID 5'-most EST $dyk700\overline{1}05883.h1$

288137 Seq. No.

236853_1.R1011 Contig ID wyr700239075.h1 5'-most EST

BLASTX Method NCBI GI q2246641 270 BLAST score 6.0e-24 E value Match length 106 % identity 53

(AF006635) P-type ATPase [Caenorhabditis elegans] NCBI Description

288138 Seq. No.

Contig ID 236860 1.R1011 5'-most EST nbm700465910.h1

288139 Seq. No.

Contig ID 236900 1.R1011 hvj700622955.h1 5'-most EST

Method BLASTX NCBI GI q4468984 BLAST score 375 E value 3.0e-36 Match length 108 % identity 72

NCBI Description (AL035605) putative protein [Arabidopsis thaliana]



```
288140
Seq. No.
                   236925 1.R1011
Contig ID
                   dyk700\overline{1}06012.h1
5'-most EST
                   288141
Seq. No.
                   236962 1.R1011
Contig ID
5'-most EST
                   pmx700\overline{0}85020.h1
Method
                   BLASTX
                   g4249404
NCBI GI
                   642
BLAST score
                   4.0e-67
E value
                   203
Match length
% identity
                   60
                   (AC006072) putative nuclear protein SA-1 [Arabidopsis
NCBI Description
                   thaliana]
                   288142
Seq. No.
                   237001 1.R1011
Contig ID
5'-most EST
                   qw1700615204.h1
                   288143
Seq. No.
                   237023 1.R1011
Contig ID
                   pmx700\overline{0}91528.h1
5'-most EST
Seq. No.
                   288144
                   237079_1.R1011
Contig ID
                   dyk700106223.h1
5'-most EST
                   BLASTX
Method
                   g3355308
NCBI GI
BLAST score
                   177
                   8.0e-14
E value
                   94
Match length
                   50
% identity
                   (AJ009695) wall-associated kinase 4 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   288145
Contig ID
                   237087 1.R1011
5'-most EST
                   gct701170711.h1
Seq. No.
                    288146
                    237147 1.R1011
Contig ID
                   wyr700\overline{2}36652.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3540193
                    213
BLAST score
                    3.0e-17
E value
Match length
                    78
% identity
                    55
                   (AC004122) Unknown protein [Arabidopsis thaliana]
NCBI Description
                    288147
Seq. No.
```

Contig ID 237250_1.R1011 5'-most EST yyf700349430.h1

Seq. No. 288148

Contig ID 237262_1.R1011



5'-most EST dyk700106481.h1

Seq. No. 288149

Contig ID 237292_1.R1011 5'-most EST dyk700106521.h1

Seq. No. 288150

Contig ID 237322_1.R1011 5'-most EST dyk700106561.h1

Seq. No. 288151

Contig ID 237345 1.R1011 5'-most EST dyk700106592.h1

Method BLASTX
NCBI GI g2880043
BLAST score 160
E value 4.0e-11
Match length 62
% identity 55

NCBI Description (AC002340) putative 3-hydroxyisobutyryl-coenzyme A

hydrolase [Arabidopsis thaliana]

Seq. No. 288152

Contig ID 237404_1.R1011 5'-most EST dyk700106665.h1

Method BLASTX
NCBI GI g2245066
BLAST score 274
E value 6.0e-30
Match length 104
% identity 63

NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No. 288153

Contig ID 237440_1.R1011 5'-most EST dyk700106724.h1

Seq. No. 288154

Contig ID 237502 1.R1011 5'-most EST dyk700106808.h1

Seq. No. 288155

Contig ID 237568_1.R1011 5'-most EST dyk700106891.h1

Method BLASTX
NCBI GI g710308
BLAST score 243
E value 8.0e-42
Match length 110
% identity 88

NCBI Description (U11693) victorin binding protein [Avena sativa]

Seq. No. 288156

Contig ID 237647 1.R1011 5'-most EST xmt700265954.h1

Method BLASTX NCBI GI g3142303



BLAST score 273 E value 5.0e-24 Match length 148 % identity 38

NCBI Description (AC002411) Strong similarity to MRP-like ABC transporter gb_U92650 from A. thaliana and canalicular multi-drug resistance protein gb_L49379 from Rattus norvegicus.

[Arabidopsis thaliana]

Seq. No. 288157

Contig ID 237649_1.R1011 5'-most EST wyr700235109.h1

Seq. No. 288158

Contig ID 237698_1.R1011 5'-most EST wyr700235169.h1

Method BLASTX
NCBI GI g799369
BLAST score 416
E value 4.0e-41
Match length 97
% identity 84

NCBI Description (U25111) metalloendopeptidase [Pisum sativum]

Seq. No. 288159

Contig ID 237759_1.R1011 5'-most EST ymt700222670.h1

Seq. No. 288160

Contig ID 237795_1.R1011 5'-most EST wyr700235284.h1

Seq. No. 288161

Contig ID 237825_1.R1011 5'-most EST wyr700235326.h1

Seq. No. 288162

Contig ID 237882_1.R1011 5'-most EST gct701174332.h1

Seq. No. 288163

Contig ID 237895_1.R1011 5'-most EST uer700582072.h1

Method BLASTX
NCBI GI g3335060
BLAST score 732
E value 8.0e-78
Match length 164
% identity 86

NCBI Description (AF025842) plasma membrane-type calcium ATPase [Arabidopsis

thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma

membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]

Seq. No. 288164

Contig ID 237915_1.R1011 5'-most EST wyr700235435.h1



Seq. No. 288165

Contig ID 237921_1.R1011 5'-most EST gct701173817.h1

Seq. No. 288166

Contig ID 237922_1.R1011 5'-most EST wyr700238810.h1

Method BLASTX
NCBI GI g131772
BLAST score 192
E value 1.0e-23
Match length 77
% identity 82

NCBI Description 40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)

>gi_82723_pir__A30097 ribosomal protein S14 (clone MCH1) -

maize

Seq. No. 288167

Contig ID 237946_1.R1011 5'-most EST wyr700235489.h1

Seq. No. 288168

Contig ID 237961_1.R1011 5'-most EST xsy700214066.h1

Seq. No. 288169

Contig ID 237962_1.R1011 5'-most EST xmt700267446.h1

Method BLASTX
NCBI GI g3075393
BLAST score 231
E value 5.0e-19
Match length 120
% identity 43

NCBI Description (AC004484) hypothetical protein [Arabidopsis thaliana]

Seq. No. 288170

Contig ID 237963_1.R1011 5'-most EST wyr700235518.h1

Method BLASTX
NCBI GI g2500570
BLAST score 189
E value 3.0e-14
Match length 109
% identity 40

NCBI Description RIBONUCLEASE PH-LIKE PROTEIN B0564.1

Seq. No. 288171

Contig ID 237967_1.R1011 5'-most EST afb700380980.h1

Seq. No. 288172

Contig ID 237998_1.R1011 5'-most EST xmt700266038.h1

Seq. No. 288173

Contig ID 238098 1.R1011



5'-most EST nbm700466165.h1

Method BLASTX
NCBI GI g598073
BLAST score 207
E value 4.0e-25
Match length 104
% identity 59

NCBI Description (L36806) GT-1 [Arabidopsis thaliana]

Seq. No. 288174

Contig ID 238111_1.R1011 5'-most EST wyr700237639.h1

Seq. No. 288175

Contig ID 238117_1.R1011 5'-most EST wyr700235756.h1

Seq. No. 288176

Contig ID 238138_1.R1011 5'-most EST wyr700235793.h1

Method BLASTX
NCBI GI g1076609
BLAST score 150
E value 7.0e-10
Match length 32
% identity 78

NCBI Description NTL1 protein - curled-leaved tobacco

Seq. No. 288177

Contig ID 238152 1.R1011 5'-most EST wyr700235953.h1

Method BLASTX
NCBI GI g3258575
BLAST score 293
E value 1.0e-26
Match length 112
% identity 52

NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 288178

Contig ID 238155 1.R1011 5'-most EST xmt700263789.h1

Seq. No. 288179

Contig ID 238197_1.R1011 5'-most EST wyr700242992.h1

Seq. No. 288180

Contig ID 238212_1.R1011 5'-most EST vux700161862.h1

Seq. No. 288181

Contig ID 238270_1.R1011 5'-most EST xsy700209757.h1

Method BLASTX
NCBI GI g4115925
BLAST score 307



E value 2.0e-28

Match length 85 % identity 69

NCBI Description (AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]

(Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein

[Arabidopsis thaliana]

Seq. No. 288182

Contig ID 238309_1.R1011 5'-most EST vux700157645.h1

Method BLASTX
NCBI GI g1168841
BLAST score 188
E value 4.0e-14
Match length 104
% identity 39

NCBI Description CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCL PRECURSOR

>gi_1360937_pir__S54747 cycL protein - Bradyrhizobium
japonicum >gi_563333_emb_CAA80245_ (Z22517) CycL
[Bradyrhizobium japonicum] >gi_572604_emb_CAA86576_

(Z46607) cycL [Bradyrhizobium japonicum]

Seq. No. 288183

Contig ID 238421_1.R1011 5'-most EST wyr700236164.h1

Seq. No. 288184

Contig ID 238434_1.R1011 5'-most EST ymt700220380.h1

Seq. No. 288185

Contig ID 238438_1.R1011 5'-most EST tfd700570829.h1

Seq. No. 288186

Contig ID 238439_1.R1011 5'-most EST wyr700236195.h1

Seq. No. 288187

Contig ID 238449_1.R1011 5'-most EST wyr700236213.h1

Method BLASTX
NCBI GI g2134962
BLAST score 264
E value 2.0e-23
Match length 84
% identity 57

NCBI Description cyclophilin-like protein CyP-60 - human >gi_1199598

(U37219) cyclophilin-like protein CyP-60 [Homo sapiens] >gi_1587642_prf__2207180A cyclophilin:ISOTYPE=CyP-60 [Homo

sapiens]

Seq. No. 288188

Contig ID 238488_1.R1011 5'-most EST fdz701164331.h1

Method BLASTX



```
NCBI GI
                  g3548808
BLAST score
                  273
E value
                  2.0e-24
                  91
Match length
                  58
% identity
                  (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
                  288189
Seq. No.
                  238519 1.R1011
Contig ID
5'-most EST
                  wyr700238825.hl
                  288190
Seq. No.
                  238614 1.R1011
Contig ID
5'-most EST
                  xsy700210912.h1
                  BLASTX
Method
                  g3549626
NCBI GI
                  176
BLAST score
                  6.0e-13
E value
                  99
Match length
                  36
% identity
                  (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
NCBI Description
                  288191
Seq. No.
                  238640 1.R1011
Contig ID
5'-most EST
                  wyr700236501.h1
Method
                  BLASTX
                  g1170619
NCBI GI
                  353
BLAST score
                  9.0e-34
E value
Match length
                  96
% identity
                  77
                  KINESIN-LIKE PROTEIN A >gi 479594 pir S34830
NCBI Description
                  kinesin-related protein katA - Arabidopsis thaliana
                  >gi_303502_dbj_BAA01972_ (D11371) kinesin-like motor
                  protein heavy chain [Arabidopsis thaliana]
                  >gi_2911084_emb_CAA17546.1_ (AL021960) kinesin-related
                  protein katA [Arabidopsis thaliana]
Seq. No.
                  288192
                  238697 1.R1011
Contig ID
5'-most EST
                  ymt700222160.h1
Seq. No.
                  288193
                  238699 1.R1011
Contig ID
5'-most EST
                  wyr700236583.h1
Seq. No.
                  288194
```

238726 1.R1011 Contig ID 5'-most EST ceu700431043.hl

Method BLASTX NCBI GI g3250692 BLAST score 480 E value 2.0e-48 Match length 107 % identity

(AL024486) putative protein [Arabidopsis thaliana] NCBI Description



```
288195
Seq. No.
                   238746 1.R1011
Contig ID
5'-most EST
                  xsy700214227.h1
Method
                  BLASTX
                   g4249419
NCBI GI
                   449
BLAST score
                   1.0e-44
E value
                   126
Match length
% identity
                   68
                   (AC006072) hypothetical protein, 3' partial [Arabidopsis
NCBI Description
                   thaliana]
                   288196
Seq. No.
                   238787 1.R1011
Contig ID
5'-most EST
                   wyr700243314.h1
Method
                   BLASTX
                   q4220598
NCBI GI
BLAST score
                   419
                   2.0e-41
E value
                   101
Match length
% identity
                   80
                   (AB011266) nicotianamine Synthase 4 [Hordeum vulgare]
NCBI Description
                   288197
Seq. No.
                   238807 1.R1011
Contig ID
                   wyr700\overline{2}36766.h1
5'-most EST
                   288198
Seq. No.
                   238812 1.R1011
Contig ID
5'-most EST
                   wyr700236775.hl
                   288199
Seq. No.
                   238826 1.R1011
Contig ID
5'-most EST
                   wyr700236802.hl
                   288200
Seq. No.
                   238865 1.R1011
Contig ID
                   kem700\overline{6}10725.h1
5'-most EST
                   288201
Seq. No.
Contig ID
                   238890 1.R1011
5'-most EST
                   wyr700236930.h1
                   BLASTX
Method
                   g2598575
NCBI GI
BLAST score
                   295
                   1.0e-26
E value
Match length
                   89
                   66
% identity
NCBI Description (Y15293) MtN21 [Medicago truncatula]
```

Seq. No.

288202

Contig ID 238965 1.R1011 5'-most EST xsy700213973.h1

Method BLASTX NCBI GI g2735017 BLAST score 397 E value 8.0e-39



Match length 111 % identity 70

NCBI Description (U82481) KI domain interacting kinase 1 [Zea mays]

Seq. No. 288203

Contig ID 239030_1.R1011 5'-most EST wyr700237122.h1

Seq. No. 288204

Contig ID 239103_1.R1011 5'-most EST tfd700571049.h1

Method BLASTX
NCBI GI g3925231
BLAST score 407
E value 6.0e-40
Match length 105
% identity 79

NCBI Description (AF037033) anionic peroxidase H [Zea mays]

Seq. No. 288205

Contig ID 239173_1.R1011 5'-most EST uer700582816.h1

Seq. No. 288206

Contig ID 239192_1.R1011 5'-most EST wyr700237338.h1

Seq. No. 288207

Contig ID 239233_1.R1011 5'-most EST wyr700237994.h1

Seq. No. 288208

Contig ID 239242_1.R1011 5'-most EST xyt700345452.h1

Method BLASTX
NCBI GI g3128195
BLAST score 621
E value 6.0e-65
Match length 132
% identity 89

NCBI Description (AC004521) putative phosphoribosyl pyrophosphate synthetase

[Arabidopsis thaliana] >gi_3341673 (AC003672) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis

thaliana]

Seq. No. 288209

Contig ID 239250_1.R1011 5'-most EST wyr700242903.h1

Method BLASTX
NCBI GI g2244913
BLAST score 381
E value 6.0e-37
Match length 112
% identity 72

NCBI Description (Z97339) similar to SEN1 protein - yeast [Arabidopsis

thaliana]



```
288210
Seq. No.
                    239263 1.R1011
Contig ID
5'-most EST
                    nbm700466420.h1
                    288211
Seq. No.
                    239274 1.R1011
Contig ID
                    wyr700237452.h1
5'-most EST
                    BLASTX
Method
NCBI GI
                    g2761012
                    195
BLAST score
                    4.0e-15
E value
                    102
Match length
                    38
% identity
NCBI Description
                    (AF039721) leishmanolysin [Leishmania major]
                    288212
Seq. No.
                    239317 1.R1011
Contig ID
                    wen700\overline{3}34129.h1
5'-most EST
                    288213
Seq. No.
                    239371 1.R1011
Contig ID
                    wyr700237574.h1
5'-most EST
Method
                    BLASTX
                    g3913437
NCBI GI
BLAST score
                    434
                    3.0e-43
E value
Match length
                    95
% identity
                    92
                    PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                    HELICASE >gi_1402875_emb_CAA66825_ (X98130) RNA helicase [Arabidopsis thaliana] >gi_1495271_emb_CAA66613_ (X97970)
                    RNA helicase [Arabidopsis thaliana]
                    288214
Seq. No.
Contig ID
                    239403_1.R1011
5'-most EST
                    xmt700\overline{2}66070.h1
Seq. No.
                    288215
Contig ID
                    239470_1.R1011
5'-most EST
                    wyr700237709.hl
Method
                    BLASTX
NCBI GI
                    q2291142
BLAST score
                    210
E value
                    1.0e-16
Match length
                    116
% identity
                    39
```

(AF016417) No definition line found [Caenorhabditis NCBI Description

elegans]

288216 Seq. No.

Contig ID 239477 1.R1011 5'-most EST wyr700237717.hl

Seq. No. 288217

Contig ID 239494 1.R1011 wyr700240726.h1 5'-most EST



288218 Seq. No. Contig ID 239504 1.R1011 5'-most EST gct701169236.h1 288219 Seq. No. 239508 1.R1011 Contig ID 5'-most EST wyr700238130.h1 Seq. No. 288220

239552 1.R1011 Contig ID 5'-most EST gct701172388.h1 BLASTX Method g987267 NCBI GI BLAST score 468 E value 3.0e-47

Match length 102 % identity 82

NCBI Description (U32579) DWARF3 [Zea mays]

Seq. No. 288221

239556 1.R1011 Contig ID 5'-most EST $wyr700\overline{2}37811.h1$

Seq. No. 288222

Contig ID 239559 1.R1011 5'-most EST $wyr700\overline{2}37814.h1$

Seq. No. 288223

Contig ID 239593 1.R1011 5'-most EST $xdb700\overline{3}41996.h1$

Seq. No. 288224

239594 1.R1011 Contig ID 5'-most EST $wyr700\overline{2}37854.h1$

Method BLASTX g3953479 NCBI GI BLAST score 216 E value 2.0e-17 Match length 75 % identity 51

NCBI Description (AC002328) F2202.24 [Arabidopsis thaliana]

288225 Seq. No.

Contig ID 239609 1.R1011 $xsy700\overline{2}13732.h1$ 5'-most EST

Method BLASTN q4160401 NCBI GI BLAST score 37 E value 2.0e-11 Match length 61 % identity 90

NCBI Description Zea mays eIF-5 gene, exons 1-2

288226 Seq. No.

Contig ID 239619 1.R1011 $wty700\overline{1}65462.h1$ 5'-most EST

Method BLASTX



```
NCBI GI
                  g3549626
BLAST score
                  247
E value
                  3.0e-21
                  103
Match length
                  52
% identity
                  (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
NCBI Description
                  288227
Seq. No.
Contig ID
                  239620 1.R1011
                  yyf700350791.h1
5'-most EST
Method
                  BLASTX
                  g4586107
NCBI GI
BLAST score
                  320
E value
                  1.0e-29
Match length
                  150
% identity
                  13
                  (AL049638) putative disease resistance protein [Arabidopsis
NCBI Description
                  thaliana]
                  288228
Seq. No.
                  239647 1.R1011
Contig ID
5'-most EST
                  wyr700237924.hl
                  288229
Seq. No.
Contig ID
                  239674 1.R1011
5'-most EST
                  pmx700082624.h1
Seq. No.
                  288230
Contig ID
                  239818 1.R1011
5'-most EST
                  wyr700238152.h1
Seq. No.
                  288231
                  239830 1.R1011
Contig ID
5'-most EST
                  xdb700339866.h1
Method
                  BLASTX
                  g2827514
NCBI GI
BLAST score
                  325
E value
                  2.0e-30
Match length
                  110
% identity
                  60
                  (AL021633) predicted protein [Arabidopsis thaliana]
NCBI Description
                  288232
Seq. No.
                  239855 1.R1011
Contig ID
5'-most EST
                  wyr700238371.h1
Method
                  BLASTX
NCBI GI
                  g2104425
BLAST score
                  185
```

E value 4.0e-14 Match length 91 % identity 44

(Z95395) hypothetical protein [Schizosaccharomyces pombe] NCBI Description

Seq. No.

288233

Contig ID 5'-most EST 239870 1.R1011 wyr700238218.hl



```
Seq. No.
                   288234
                  239916 1.R1011
Contig ID
5'-most EST
                  vux700160306.h1
                  BLASTX
Method
                   g2160185
NCBI GI
BLAST score
                   493
                   6.0e-50
E value
Match length
                   122
% identity
                   68
                  (ACO00132) Similar to S. pombe ISP4 (gb D83992).
NCBI Description
                   [Arabidopsis thaliana]
                   288235
Seq. No.
                   239946_1.R1011
Contig ID
5'-most EST
                  nbm700476295.h1
                   288236
Seq. No.
Contig ID
                   239968 1.R1011
5'-most EST
                  wyr700240551.h1
Method
                  BLASTX
NCBI GI
                   g2245087
                   240
BLAST score
                   4.0e-20
E value
                   165
Match length
% identity
                   39
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   288237
                   240012 1.R1011
Contig ID
5'-most EST
                   wyr700238392.h1
Method
                   BLASTX
NCBI GI
                   g4586378
BLAST score
                   351
E value
                   1.0e-33
Match length
                   77
% identity
                   82
NCBI Description (AB021746) nicotianamine synthase 1 [Oryza sativa]
                   288238
Seq. No.
Contig ID
                   240038 1.R1011
5'-most EST
                   wyr700238440.hl
                   288239
Seq. No.
Contig ID
                   240053 1.R1011
5'-most EST
                   wyr700\overline{2}38462.h1
Seq. No.
                   288240
Contig ID
                   240064 1.R1011
```

25

5'-most EST hbs701185673.h1

Seq. No. 288241

240082 1.R1011 Contig ID 5'-most EST tfd700573438.h2

Seq. No. 288242

240144 1.R1011 Contig ID $nbm700\overline{4}71089.h1$ 5'-most EST



Method BLASTX
NCBI GI g3021270
BLAST score 242
E value 2.0e-20
Match length 74
% identity 69

NCBI Description (AL022347) serine/threonine kinase -like protein

[Arabidopsis thaliana]

Seq. No. 288243

Contig ID 240202 1.R1011 5'-most EST wyr700238712.h1

Seq. No. 288244

Contig ID 240244_1.R1011 5'-most EST wyr700238760.h1

Method BLASTX
NCBI GI g3080433
BLAST score 299
E value 3.0e-27
Match length 110
% identity 52

NCBI Description (AL022605) putative gamma-glutamyltransferase [Arabidopsis

thaliana]

Seq. No. 288245

Contig ID 240314_1.R1011 5'-most EST xmt700264360.h1

Method BLASTX
NCBI GI g1705585
BLAST score 324
E value 3.0e-30
Match length 66
% identity 97

NCBI Description PHOSPHOENOLPYRUVATE CARBOXYLASE 2 (PEPCASE)

>gi_82710_pir__JH0667 phosphoenolpyruvate carboxylase (EC 4.1.1.31) C3-form - maize >gi_429149_emb_CAA43709_ (X61489)

phosphoenolpyruvate carboxylase [Zea mays]

Seq. No. 288246

Contig ID 240356 1.R1011 5'-most EST ceu700423809.h1

Seq. No. 288247

Contig ID 240407_1.R1011 5'-most EST wyr700238977.h1

Method BLASTX
NCBI GI g4200122
BLAST score 309
E value 1.0e-28
Match length 91
% identity 62

NCBI Description (AJ009555) hypothetical protein [Arabidopsis thaliana]

Seq. No. 288248

Contig ID 240426 1.R1011 5'-most EST tfd700572571.h1



Method BLASTX
NCBI GI g3335060
BLAST score 222
E value 3.0e-18
Match length 108
% identity 43

NCBI Description (AF025842) plasma membrane-type calcium ATPase [Arabidopsis

thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma

membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]

Seq. No. 288249

Contig ID 240463_1.R1011 5'-most EST wyr700239072.h1

Method BLASTX
NCBI GI g3582000
BLAST score 243
E value 7.0e-21
Match length 59
% identity 76

NCBI Description (AJ010942) hexose transporter protein [Lycopersicon

esculentum]

Seq. No. 288250

Contig ID 240505_1.R1011 5'-most EST wyr700239136.h1

Seq. No. 288251

Contig ID 240649_1.R1011 5'-most EST wyr700239341.h1

Seq. No. 288252

Contig ID 240656_1.R1011 5'-most EST ceu700430136.h1

Method BLASTX
NCBI GI g2739382
BLAST score 531
E value 9.0e-58
Match length 265
% identity 48

NCBI Description (AC002505) myosin heavy chain-like protein [Arabidopsis

thaliana]

Seq. No. 288253

Contig ID 240664_1.R1011 5'-most EST wyr700239361.h1

Seq. No. 288254

Contig ID 240757_1.R1011 5'-most EST wyr700239487.h1

Method BLASTX
NCBI GI g266567
BLAST score 280
E value 3.0e-25
Match length 86
% identity 62

NCBI Description MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR

(ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II)



>gi_421956_pir__S23558 mitochondrial processing peptidase
(EC 3.4.99.41) alpha chain precursor - potato
>gi_21493_emb_CAA46990_ (X66284) mitochondrial processing
peptidase [Solanum tuberosum]

288255 Seq. No. 240776 1.R1011 Contig ID 5'-most EST wyr700239522.h1 Method BLASTX g2335097 NCBI GI BLAST score 279 E value 7.0e-25 Match length 117

49

NCBI Description (AC002339) putative receptor-like protein kinase

[Arabidopsis thaliana]

Seq. No. 288256

% identity

Contig ID 240797_1.R1011 5'-most EST xmt700263194.h1

Seq. No. 288257

Contig ID 240803_1.R1011 5'-most EST wyr700239556.h1

Seq. No. 288258

Contig ID 240819_1.R1011 5'-most EST wyr700239575.h1

Seq. No. 288259

Contig ID 240825_1.R1011 5'-most EST wyr700239582.h1

Seq. No. 288260

Contig ID 240876_1.R1011 5'-most EST gct701173203.h2 Method BLASTX

Method BLASTX
NCBI GI g3548810
BLAST score 191
E value 5.0e-29
Match length 155
% identity 49

NCBI Description (AC005313) putative chloroplast nucleoid DNA binding

protein [Arabidopsis thaliana]

Seq. No. 288261

Contig ID 240925_1.R1011 5'-most EST wyr700239731.h1

Seq. No. 288262

Contig ID 240926 1.R1011 5'-most EST wyr700239732.h1

Method BLASTX
NCBI GI g629602
BLAST score 163
E value 1.0e-13
Match length 97



% identity 45

NCBI Description probable imbibition protein - wild cabbage

>gi_488787_emb_CAA55893_ (X79330) putative imbibition

protein [Brassica oleracea]

Seq. No. 288263

Contig ID 240934_1.R1011 5'-most EST nbm700466365.h1

Method BLASTX
NCBI GI g3540188
BLAST score 283
E value 1.0e-25
Match length 85

% identity 61

NCBI Description (AC004122) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 288264

Contig ID 240989_1.R1011 5'-most EST wyr700243534.h1

Method BLASTX
NCBI GI g4455356
BLAST score 309
E value 1.0e-31
Match length 105
% identity 66

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 288265

Contig ID 241009 1.R1011 5'-most EST hbs701182275.h1

Seq. No. 288266

Contig ID 241025_1.R1011 5'-most EST ceu700421701.h1

Method BLASTX
NCBI GI g4567197
BLAST score 414
E value 2.0e-40
Match length 159
% identity 53

NCBI Description (AC007168) unknown protein [Arabidopsis thaliana]

Seq. No. 288267

Contig ID 241079_1.R1011 5'-most EST wyr700243637.h1

Seq. No. 288268

Contig ID 241132_1.R1011 5'-most EST wyr700240012.h1

Seq. No. 288269

Contig ID 241153_1.R1011 5'-most EST wty700170052.h1

Seq. No. 288270

Contig ID 241198_1.R1011 5'-most EST wyr700240093.h1

E value

Match length

NCBI Description

% identity

1.0e-30

[Arabidopsis thaliana]

107 59



```
288271
Seq. No.
                   241208 1.R1011
Contig ID
                   wyr700240114.hl
5'-most EST
                   288272
Seq. No.
                   241224 1.R1011
Contig ID
5'-most EST
                   xyt700345332.h1
                   288273
Seq. No.
                   241242 1.R1011
Contig ID
5'-most EST
                   wyr700\overline{2}40162.h1
Seq. No.
                   288274
Contig ID
                   241266 1.R1011
                   uer700\overline{5}81351.h1
5'-most EST
                   BLASTX
Method
                   g2500036
NCBI GI
                   683
BLAST score
E value
                   4.0e-72
                   159
Match length
                   79
% identity
                  DIHYDROOROTASE PRECURSOR (DHOASE) >gi_2121273 (AF000146)
NCBI Description
                   dihydroorotase [Arabidopsis thaliana]
                   >gi 3292818 emb CAA19808 (AL031018) dihydroorotase
                   [Arabidopsis thaliana]
                   288275
Seq. No.
                   241271 1.R1011
Contig ID
5'-most EST
                   ypc700800974.h1
                   288276
Seq. No.
                   241300 1.R1011
Contig ID
                   nbm700467711.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4490706
BLAST score
                   317
                   4.0e-29
E value
Match length
                   84
                   67
% identity
                  (AL035680) putative protein [Arabidopsis thaliana]
NCBI Description
                   288277
Seq. No.
                   241304 1.R1011
Contig ID
5'-most EST
                   wyr700240238.hl
                   288278
Seq. No.
                   241362 1.R1011
Contig ID
5'-most EST
                   pmx700089080.h1
                   BLASTX
Method
NCBI GI
                   q3341672
BLAST score
                   198
```

40114

(ACO03672) putative heme A: farnesyltransferase, 5' partial



Seq. No. 288279

Contig ID 241376_1.R1011 5'-most EST nbm700476085.h1

Method BLASTX
NCBI GI g3377805
BLAST score 221
E value 3.0e-18
Match length 70
% identity 60

NCBI Description (AF075597) contains similarity to several apoptosis or

programmed cell death proteins such as rat apoptosis

protein RP-8 (GB:M80601) [Arabidopsis thaliana]

>gi_3912928_gb_AAC78712.1_ (AF001308) putative zinc finger

protein [Arabidopsis thaliana]

Seq. No. 288280

Contig ID 241409_1.R1011 5'-most EST wty700163114.h1

Seq. No. 288281

Contig ID 241461_1.R1011 5'-most EST xsy700208066.h1

Method BLASTX
NCBI GI g2961378
BLAST score 277
E value 1.0e-24
Match length 66
% identity 36

NCBI Description (AL022141) putative protein [Arabidopsis thaliana]

Seq. No. 288282

Contig ID 241478_1.R1011 5'-most EST wyr700240461.h1

Method BLASTX
NCBI GI g2618691
BLAST score 666
E value 5.0e-79
Match length 195
% identity 81

NCBI Description (AC002510) putative chloroplast envelope Ca2+-ATPase

[Arabidopsis thaliana]

Seq. No. 288283

Contig ID 241519_1.R1011 5'-most EST xyt700343089.h1

Seq. No. 288284

Contig ID 241530_1.R1011 5'-most EST wyr700240534.h1

Seq. No. 288285

Contig ID 241539_1.R1011 5'-most EST ymt700218731.h1

Method BLASTX NCBI GI g464365 BLAST score 286



E value 8.0e-26 Match length 102 % identity 54

NCBI Description PEROXIDASE P7 >gi 66306_pir_OPNB7 peroxidase (EC 1.11.1.7)

- turnip

Seq. No. 288286

Contig ID 241546_1.R1011 5'-most EST wyr700240552.h1

Method BLASTX
NCBI GI g3901012
BLAST score 177
E value 6.0e-13
Match length 91
% identity 40

NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus

sylvatica]

Seq. No. 288287

Contig ID 241623_1.R1011 5'-most EST bdu700383189.h1

Seq. No. 288288

Contig ID 241652_1.R1011 5'-most EST wyr700240687.h1

Method BLASTX
NCBI GI g312179
BLAST score 354
E value 9.0e-34
Match length 71
% identity 96

NCBI Description (X73151) glyceraldehyde 3-phosphate dehydrogenase

(phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]

>gi 1185554 (U45858) glyceraldehyde-3-phosphate

dehydrogenase [Zea mays]

Seq. No. 288289

Contig ID 241657_1.R1011 5'-most EST wyr700240704.h1

Seq. No. 288290

Contig ID 241663_1.R1011 5'-most EST wyr700241467.h1

Seq. No. 288291

Contig ID 241701 1.R1011 5'-most EST xsy700212401.h1

Seq. No. 288292

Contig ID 241742_1.R1011 5'-most EST wyr700240812.h1

Method BLASTX
NCBI GI g2499115
BLAST score 557
E value 2.0e-57
Match length 144

% identity NCBI Description VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi 1835788 (U86662) VPS41 [Lycopersicon esculentum] 288293 Seq. No. 241838_1.R1011 Contig ID 5'-most EST wyr700240927.h1 Method BLASTX g453244 NCBI GI BLAST score 244 7.0e-21 E value Match length 92 % identity 52 NCBI Description (X77467) catechol O-methyltransferase [Hordeum vulgare] 288294 Seq. No. 241908 1.R1011 Contig ID $wyr700\overline{2}41012.h1$ 5'-most EST Method BLASTX NCBI GI q4325368 BLAST score 663 E value 5.0e-72 Match length 152 % identity 81 NCBI Description (AF128396) Arabidopsis thaliana flavin-type blue-light photoreceptor (SW:Q43125) (Pfam: PF00875, Score=765.2, E=2.6e-226, N=1) [Arabidopsis thaliana] 288295 241915 1.R1011 wyr700243122.h1 BLASTX q3075398

Seq. No. Contig ID 5'-most EST Method NCBI GI BLAST score 169

5.0e-12 E value Match length 62 53 % identity

NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]

288296 Seq. No.

Contig ID 241934 1.R1011 $xmt700\overline{2}67056.h1$ 5'-most EST

288297 Seq. No.

241941 1.R1011 Contig ID 5'-most EST wty700164302.hl

Method BLASTX g3688173 NCBI GI BLAST score 267 2.0e-23 E value Match length 93 57 % identity

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

288298 Seq. No.

Contig ID 241976 1.R1011 5'-most EST wyr700241092.hl



```
Seq. No.
                  288299
Contig ID
                  241990 1.R1011
5'-most EST
                  fdz701166704.h1
                   288300
Seq. No.
                   241995 1.R1011
Contig ID
                  wyr700241117.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                   g2459430
BLAST score
                   183
                   2.0e-13
E value
Match length
                   90
% identity
                   44
NCBI Description
                  (AC002332) putative CUC2 protein [Arabidopsis thaliana]
Seq. No.
                   288301
                   242028 1.R1011
Contig ID
5'-most EST
                  wyr700241155.h1
Seq. No.
                   288302
Contig ID
                   242032 2.R1011
5'-most EST
                   gct701177676.h1
Method
                  BLASTX
NCBI GI
                   q3548810
BLAST score
                   204
E value
                   3.0e-16
Match length
                   114
% identity
                   45
                  (AC005313) putative chloroplast nucleoid DNA binding
NCBI Description
                  protein [Arabidopsis thaliana]
Seq. No.
                   288303
Contig ID
                   242075 1.R1011
5'-most EST
                   fdz701161574.h1
Method
                   BLASTX
NCBI GI
                   g2244771
BLAST score
                   150
E value
                   8.0e-10
Match length
                   66
% identity
                   47
                  (Z97335) kinesin homolog [Arabidopsis thaliana]
NCBI Description
                   288304
Seq. No.
                   242092 1.R1011
Contig ID
5'-most EST
                   vux700158369.h1
Method
                   BLASTX
NCBI GI
                   g4558556
BLAST score
                   315
                   3.0e-29
E value
Match length
                   82
% identity
                   66
```

NCBI Description (AC007138) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 288305

Contig ID 242114_1.R1011



71

5'-most EST wyr700241261.h1
Method BLASTX
NCBI GI g2342686
BLAST score 352
E value 3.0e-34
Match length 101

NCBI Description (AC000106) Similar to Saccharomyces hypothetical protein YDR051c (gb_Z49209). ESTs gb_T44436,gb_42252 come from this

gene. [Arabidopsis thaliana]

Seq. No. 288306

% identity

Contig ID 242146_1.R1011 5'-most EST wyr700241301.h1

Method BLASTX
NCBI GI 94454469
BLAST score 519
E value 8.0e-53
Match length 161
% identity 59

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 288307

Contig ID 242244_1.R1011 5'-most EST gct701180317.h1

Method BLASTN
NCBI GI g4585620
BLAST score 37
E value 2.0e-11
Match length 103
% identity 93

NCBI Description Zea mays hmgi/y gene, exons 1-2

Seq. No. 288308

Contig ID 242257_1.R1011 5'-most EST wyr700241432.h1

Seq. No. 288309

Contig ID 242268_1.R1011 5'-most EST pwr700452537.h1

Method BLASTX
NCBI GI g4115913
BLAST score 210
E value 1.0e-16
Match length 95
% identity 44

NCBI Description (AF118222) contains similarity to Iron/Ascorbate family of

oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88, N=1) [Arabidopsis thaliana] >gi_4539409_emb_CAB40042.1_

(AL049524) putative flavanone 3-beta-hydroxylase

[Arabidopsis thaliana]

Seq. No. 288310

Contig ID 242271_1.R1011 5'-most EST wyr700241447.h1

Method BLASTX NCBI GI g2618699



```
BLAST score
                  3.0e-11
E value
Match length
                  77
% identity
                  40
                  (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
                  288311
Seq. No.
                  242276 1.R1011
Contig ID
                  wyr700241453.hl
5'-most EST
Method
                  BLASTX
                  g3482929
NCBI GI
BLAST score
                  302
                  1.0e-27
E value
Match length
                  84
% identity
                   73
                   (AC003970) Putative transcription factor [Arabidopsis
NCBI Description
                   thaliana]
                   288312
Seq. No.
Contig ID
                   242286 1.R1011
5'-most EST
                   wyr700241468.hl
Method
                   BLASTN
                   g3821780
NCBI GI
BLAST score
                   36
                   7.0e-11
E value
Match length
                   48
                   67
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   288313
Seq. No.
                   242341 1.R1011
Contig ID
                   yyf700348514.hl
5'-most EST
                   288314
Seq. No.
                   242380 1.R1011
Contig ID
                   fdz701166667.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3608145
                   177
BLAST score
                   6.0e-13
E value
Match length
                   63
                   54
% identity
                   (AC005314) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   288315
Seq. No.
                   242409 1.R1011
Contig ID
                   wyr700241627.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q294845
BLAST score
                   472
E value
                   2.0e-47
Match length
                   122
% identity
                   72
                   (L13655) membrane protein [Saccharum hybrid cultivar
NCBI Description
```

Seq. No. 288316

H65-7052]



Contig ID 242427_1.R1011 5'-most EST pmx700082580.h1

Seq. No. 288317

Contig ID 242429_1.R1011 5'-most EST wty700171695.h1

Seq. No. 288318

Contig ID 242459_1.R1011 5'-most EST wyr700241691.h1

Seq. No. 288319

Contig ID 242690_1.R1011 5'-most EST pmx700091875.h1

Method BLASTX
NCBI GI g2665890
BLAST score 658
E value 3.0e-69
Match length 135
% identity 90

NCBI Description (AF035944) calcium-dependent protein kinase [Fragaria x

ananassa]

Seq. No. 288320

Contig ID 242742_1.R1011 5'-most EST hbs701186292.h1

Seq. No. 288321

Contig ID 242765_1.R1011 5'-most EST wyr700242124.h1

Seq. No. 288322

Contig ID 242773 1.R1011 5'-most EST xmt700262819.h1

Seq. No. 288323

Contig ID 242775_1.R1011 5'-most EST xmt700266957.h1

Seq. No. 288324

Contig ID 242831_1.R1011 5'-most EST gct701179027.h1

Method BLASTX
NCBI GI g1097875
BLAST score 397
E value 6.0e-39
Match length 87
% identity 87

NCBI Description peroxidase: ISOTYPE=RPA [Oryza sativa]

Seq. No. 288325

Contig ID 242899 1.R1011 5'-most EST ymt700219768.h1

Method BLASTX
NCBI GI g3451321
BLAST score 189
E value 1.0e-14



Match length 90 % identity 42

(AL031323) putative transcription or splicing factor NCBI Description

[Schizosaccharomyces pombe]

Seq. No. Contig ID

288326 242929 2.R1011 wyr700242368.hl

Seq. No.

288327

Contig ID 5'-most EST

5'-most EST

242933 1.R1011 $xmt700\overline{2}66169.h1$

Seq. No.

288328

Contig ID 5'-most EST

242939 1.R1011 wty700162829.h1

Seq. No.

288329

Contig ID 5'-most EST 242952 1.R1011 fdz701161168.h1

Seq. No.

288330

Contig ID 5'-most EST 242973 1.R1011 wyr700242430.h1

Method NCBI GI BLASTX g3549679

BLAST score E value

308 3.0e-28

Match length % identity

98 63

NCBI Description (AL031394) putative protein [Arabidopsis thaliana]

Seq. No.

288331

Contig ID 5'-most EST

242993_1.R1011 $wyr700\overline{2}42456.h1$

Seq. No.

288332

Contig ID 5'-most EST

242994 1.R1011 wyr700242457.h1

Seq. No.

288333

Contig ID 5'-most EST 242997 1.R1011 $vux700\overline{1}60109.h1$

Method NCBI GI

BLASTX g1352469

BLAST score E value

495 2.0e-50

Match length

95 100

% identity NCBI Description

BETA-FRUCTOFURANOSIDASE, CELL WALL ISOZYME PRECURSOR

(SUCROSE-6-PHOSPHATE HYDROLASE) (INVERTASE) >gi_736359 (U17695) invertase [Zea mays] >gi_1582380_prf__2118364A

cell wall invertase [Zea mays]

Seq. No. Contig ID 288334

5'-most EST

243000 1.R1011 $wyr700\overline{2}42465.h1$



```
288335
Seq. No.
                   243036_1.R1011
Contig ID
5'-most EST
                   ypc700803536.h1
Seq. No.
                   288336
Contig ID
                   243096 1.R1011
5'-most EST
                   wyr700\overline{2}42590.h1
Method
                   BLASTX
NCBI GI
                   g2323410
BLAST score
                   152
E value
                   3.0e-10
Match length
                   45
% identity
                   64
NCBI Description
                  (AF015913) Skb1Hs [Homo sapiens]
                   288337
Seq. No.
Contig ID
                   243096 2.R1011
5'-most EST
                   ymt700219552.h1
Method
                   BLASTX
                   g2323410
NCBI GI
BLAST score
                   356
                   6.0e-34
E value
Match length
                   120
% identity
                   60
NCBI Description
                  (AF015913) Skb1Hs [Homo sapiens]
                   288338
Seq. No.
                   243122_1.R1011
Contig ID
5'-most EST
                   wyr700242626.hl
Method
                   BLASTX
NCBI GI
                   g2130141
BLAST score
                   233
E value
                   2.0e-19
Match length
                   114
                   61
% identity
NCBI Description
                   mudrA protein - maize transposon MuDR >gi 540581 (M76978)
                   mudrA [Zea mays] >gi 595816 (U14597) mudrA gene product
                   [Zea mays]
Seq. No.
                   288339
Contig ID
                   243197 1.R1011
                   yyf700\overline{3}50012.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4154359
BLAST score
                   202
E value
                   8.0e-16
Match length
                   89
% identity
                   48
```

NCBI Description (AF113541) putative ethylene response sensor [Phalaenopsis

sp. 'KCbutterfly']

Seq. No. 288340

Contig ID 243216 1.R1011 5'-most EST wyr700242756.h1

Seq. No. 288341



Contig ID 243256_1.R1011 5'-most EST wyr700242802.h1

Method BLASTX
NCBI GI g4539394
BLAST score 348
E value 6.0e-33
Match length 128
% identity 13

NCBI Description (AL035526) putative protein [Arabidopsis thaliana]

Seq. No. 288342

Contig ID 243271_1.R1011 5'-most EST wyr700242822.h1

Method BLASTX
NCBI GI g1888357
BLAST score 509
E value 8.0e-52
Match length 134
% identity 70

NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]

>qi 1890154 emb CAA72432 (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

Seq. No. 288343

Contig ID 243288_1.R1011 5'-most EST wyr700242840.h1

Seq. No. 288344

Contig ID 243352_1.R1011 5'-most EST gct701173742.h1

Method BLASTX
NCBI GI 94586112
BLAST score 423
E value 3.0e-45
Match length 146
% identity 67

NCBI Description (AL049638) putative protein [Arabidopsis thaliana]

Seq. No. 288345

Contig ID 243403_1.R1011 5'-most EST wyr700242989.h1

Seq. No. 288346

Contig ID 243424 1.R1011 5'-most EST wyr700243066.h1

Seq. No. 288347

Contig ID 243502_1.R1011 5'-most EST zuv700356087.h1

Seq. No. 288348

Contig ID 243531_1.R1011 5'-most EST wyr700243150.h1

Method BLASTX
NCBI GI g4263783
BLAST score 240
E value 2.0e-20



Match length 89 % identity 53

NCBI Description (AC006068) putative DNAJ protein [Arabidopsis thaliana]

Seq. No. 288349

Contig ID 243534 1.R1011 5'-most EST wyr700243157.h1

Method BLASTX
NCBI GI g2829864
BLAST score 285
E value 2.0e-25
Match length 85
% identity 65

NCBI Description (AC002396) similar to zinc metalloproteinases [Arabidopsis

thaliana]

Seq. No. 288350

Contig ID 243578_1.R1011 5'-most EST tfd700570605.h1

Seq. No. 288351

Contig ID 243714_1.R1011 5'-most EST wyr700243410.h1

Method BLASTX
NCBI GI g1170619
BLAST score 406
E value 5.0e-40
Match length 89
% identity 90

NCBI Description KINESIN-LIKE PROTEIN A >gi_479594_pir__S34830

kinesin-related protein katA - Arabidopsis thaliana >gi_303502_dbj_BAA01972_ (D11371) kinesin-like motor

protein heavy chain [Arabidopsis thaliana]

>gi_2911084_emb_CAA17546.1_ (AL021960) kinesin-related

protein katA [Arabidopsis thaliana]

Seq. No. 288352

Contig ID 243738_1.R1011 5'-most EST wyr700243443.h1

Seq. No. 288353

Contig ID 243802_1.R1011 5'-most EST wyr700243527.h1

Method BLASTX
NCBI GI g4586056
BLAST score 297
E value 9.0e-44
Match length 128
% identity 72

NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]

Seq. No. 288354

Contig ID 243915_1.R1011 5'-most EST rvt700552128.h1

Method BLASTX NCBI GI g3913525 BLAST score 677



E value 2.0e-71 Match length 147 % identity 88

NCBI Description DNA POLYMERASE DELTA CATALYTIC CHAIN >gi_2895198 (AF020193)

DNA polymerase delta [Glycine max]

Seq. No. 288355

Contig ID 243921_1.R1011 5'-most EST wyr700243684.h1

Seq. No. 288356

Contig ID 243930_1.R1011 5'-most EST gct701778615.h1

Method BLASTX
NCBI GI g2827536
BLAST score 190
E value 1.0e-14
Match length 72
% identity 44

NCBI Description (AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No. 288357

Contig ID 243976_1.R1011 5'-most EST xsy700209356.h1

Method BLASTX
NCBI GI g3445212
BLAST score 261
E value 4.0e-27
Match length 116
% identity 66

NCBI Description (AC004786) putative chloroplast envelope Ca2+-ATPase

[Arabidopsis thaliana]

Seq. No. 288358

Contig ID 244040_1.R1011 5'-most EST rv1700457186.h1

Method BLASTX
NCBI GI g3093294
BLAST score 394
E value 2.0e-38
Match length 109
% identity 62

NCBI Description (Y12782) putative villin [Arabidopsis thaliana]

Seq. No. 288359

Contig ID 244117 1.R1011 5'-most EST tfd700575388.h1

Method BLASTX
NCBI GI g3834323
BLAST score 372
E value 2.0e-35
Match length 170
% identity 40

NCBI Description (AC005679) F9K20.25 [Arabidopsis thaliana]

Seq. No. 288360

Contig ID 244155_1.R1011



```
wyr700243985.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q602605
BLAST score
                   61
E value
                  7.0e-26
Match length
                  117
% identity
NCBI Description
                  Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin
                   288361
Seq. No.
Contig ID
                  244161 1.R1011
5'-most EST
                  ceu700427793.h1
Method
                  BLASTX
NCBI GI
                  q3415009
BLAST score
                  207
E value
                  1.0e-16
Match length
                  91
% identity
                   43
NCBI Description
                  (AF080245) sesquiterpene synthase [Elaeis oleifera]
                   288362
Seq. No.
Contia ID
                  244222 1.R1011
5'-most EST
                  wyr700244079.hl
Seq. No.
                   288363
Contig ID
                  244224 1.R1011
5'-most EST
                  wyr700244081.hl
Method
                  BLASTX
NCBI GI
                   q1885356
BLAST score
                   436
E value
                   3.0e-43
Match length
                  118
% identity
                   69
                  (U59323) type 1 RNA helicase pNORF1 [Homo sapiens]
NCBI Description
                   288364
Seq. No.
Contig ID
                   244290 1.R1011
5'-most EST
                  wyr700244170.hl
Method
                  BLASTX
NCBI GI
                   g4191789
BLAST score
                   223
                   2.0e-18
E value
Match length
                  59
                  78
% identity
                  (AC005917) putative transmembrane transport protein
NCBI Description
                   [Arabidopsis thaliana]
                   288365
Seq. No.
Contig ID
                   244310 1.R1011
5'-most EST
                  xsy700217784.h1
Seq. No.
                   288366
```

Contig ID 244372 1.R1011 5'-most EST rvt700548451,h1 Method BLASTX

NCBI GI g3450842 BLAST score 307



2.0e-28 E value Match length 97 % identity 63 NCBI Description (AF080436) mitogen activated protein kinase kinase [Oryza sativa] Seq. No. 288367 Contig ID 244390 1.R1011 5'-most EST wyr700244309.hl Method BLASTX NCBI GI g4093155 BLAST score 159 E value 5.0e-11 Match length 69 % identity 49 NCBI Description (AF088281) phytochrome-associated protein 1 [Arabidopsis thaliana] Seq. No. 288368 Contig ID 244407 1.R1011 5'-most EST hbs701181365.h1 Method BLASTX NCBI GI g4587562 BLAST score 233 E value 1.0e-19 Match length 46 % identity 91 (AC006550) Belongs to PF_00583 Acetyltransfersase (GNAT) NCBI Description family. [Arabidopsis thaliana] 288369 Seq. No. Contig ID 244424 1.R1011 5'-most EST wyr700244355.h1 Seq. No. 288370 Contig ID 244448 1.R1011 5'-most EST gct701174314.h1 Seq. No. 288371 Contig ID 244510 1.R1011 5'-most EST pmx700088866.hl Seq. No. 288372 244547 1.R1011 5'-most EST pmx700090524.h1 288373 Seq. No. Contig ID 244559_1.R1011

Contig ID

5'-most EST $ceu700\overline{4}31111.h1$ Method

BLASTN NCBI GI g3511235 BLAST score 37 2.0e-11 E value Match length 53 % identity 94

Zea mays starch branching enzyme IIb (ae) gene, complete NCBI Description cds



Seq. No. 288374

Contig ID 244598_1.R1011 5'-most EST gct701169242.h1

Seq. No. 288375

Contig ID 244607_1.R1011 5'-most EST mwy700440691.h1

Method BLASTX
NCBI GI g1750108
BLAST score 268
E value 1.0e-23
Match length 107

Match length 107 % identity 53

NCBI Description (U66480) YnbA [Bacillus subtilis] >gi_2634127_emb_CAB13627_

(Z99113) similar to GTP-binding protein protease modulator

[Bacillus subtilis]

Seq. No. 288376

Contig ID 244634_1.R1011 5'-most EST yne700379307.h1

Seq. No. 288377

Contig ID 244668_1.R1011 5'-most EST xtj700378320.h1

Seq. No. 288378

Contig ID 244721_1.R1011 5'-most EST rvt700553224.h1

Seq. No. 288379

Contig ID 244724_1.R1011 5'-most EST xsy700213369.h1

Seq. No. 288380

Contig ID 244812_1.R1011 5'-most EST afb700380962.h1

Seq. No. 288381

Contig ID 244830 1.R1011 5'-most EST rvt700548309.h1

Method BLASTX
NCBI GI g3935157
BLAST score 356
E value 4.0e-34
Match length 91
% identity 71

NCBI Description (AC005106) T25N20.21 [Arabidopsis thaliana]

Seq. No. 288382

Contig ID 244840_1.R1011 5'-most EST ymt700220755.h1

Seq. No. 288383

Contig ID 244847_1.R1011 5'-most EST tfd700571396.h1

Method BLASTX



```
NCBI GI
                   q4115377
BLAST score
                   165
E value
                   1.0e-11
Match length
                   58
% identity
                   60
                   (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                   288384
Seq. No.
                   244884 1.R1011
Contig ID
5'-most EST
                   ypc700804617.hl
Method
                   BLASTX
NCBI GI
                   g3892057
BLAST score
                   191
E value
                   7.0e-15
Match length
                   81
% identity
                   48
                   (AC002330) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   288385
Contig ID
                   244963 1.R1011
5'-most EST
                   pmx700082115.h1
Method
                   BLASTX
NCBI GI
                   g3892050
BLAST score
                   304
E value
                   2.0e-37
Match length
                   131
% identity
                   (AC002330) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   288386
                   245025 1.R1011
Contig ID
5'-most EST
                   pmx700082188.h1
Method
                   BLASTX
                   g3249064
NCBI GI
BLAST score
                   331
                   4.0e-31
E value
Match length
                   101
% identity
                   62
                   (AC004473) Strong similarity to trehalose-6-phosphate
NCBI Description
                   synthase homolog gb 2245136 from A. thaliana chromosome 4
                   contig gb Z97344. [Arabidopsis thaliana]
                   288387
Seq. No.
                   245028 1.R1011
Contig ID
5'-most EST
                   pmx700\overline{0}82192.h1
Method
                   BLASTX
NCBI GI
                   g799369
BLAST score
                   569
                   8.0e-59
E value
Match length
                   134
```

NCBI Description (U25111) metalloendopeptidase [Pisum sativum]

% identity

Seq. No. 245096 1.R1011 Contig ID pmx700082274.h1 5'-most EST

81

288388

Method BLASTX



```
NCBI GI
                  q3511223
BLAST score
                  214
E value
                  3.0e-17
Match length
                  78
% identity
                  (AF069528) plant adhesion molecule 1 [Arabidopsis thaliana]
NCBI Description
                  288389
Seq. No.
Contig ID
                  245149 1.R1011
5'-most EST
                  ltv700479601.h1
Method
                  BLASTX
NCBI GI
                  g2462744
BLAST score
                  196
E value
                  3.0e-15
Match length
                  86
% identity
                  42
NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]
                  288390
Seq. No.
Contig ID
                  245153 1.R1011
5'-most EST
                  pmx700082348.hl
Method
                  BLASTX
                  q2980806
NCBI GI
BLAST score
                  251
E value
                  1.0e-21
Match length
                  79
% identity
NCBI Description
                  (AL022197) putative protein [Arabidopsis thaliana]
Seq. No.
                  288391
Contig ID
                  245167 1.R1011
5'-most EST
                  xsy700213773.h1
Method
                  BLASTX
NCBI GI
                  q4415929
BLAST score
                  285
                  1.0e-25
E value
Match length
                  96
                  54
% identity
                  (AC006418) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  288392
Seq. No.
Contig ID
                  245184 2.R1011
5'-most EST
                  fdz701163565.h1
                  288393
Seq. No.
Contig ID
                  245213 1.R1011
5'-most EST
                  pmx700082432.h1
Seq. No.
                  288394
Contig ID
                  245281 1.R1011
5'-most EST
                  ymt700223753.hl
```

Seq. No. 288395

Contig ID 245286_1.R1011 5'-most EST pmx700082584.h1

Seq. No. 288396



Contig ID	245331 1.R1011
5'-most EST	pmx700084994.h1

Seq. No. 288397

Contig ID 245333_1.R1011 5'-most EST wen700333777.h1

Seq. No. 288398

Contig ID 245353_1.R1011 5'-most EST ymt700218875.h1

Seq. No. 288399

Contig ID 245392 1.R1011 5'-most EST pmx700082717.h1

Seq. No. 288400

Contig ID 245431_1.R1011 5'-most EST pmx700082765.h1

Seq. No. 288401

Contig ID 245436_1.R1011 5'-most EST pmx700082770.h1

Seq. No. 288402

Contig ID 245447_1.R1011 5'-most EST pmx700082784.h1

Method BLASTX
NCBI GI g3249110
BLAST score 286
E value 1.0e-25
Match length 113
% identity 53

NCBI Description (AC003114) T12M4.6 [Arabidopsis thaliana]

Seq. No. 288403

Contig ID 245478_1.R1011 5'-most EST nbm700475408.h1

Seq. No. 288404

Contig ID 245606_1.R1011 5'-most EST pwr700452070.h1

Method BLASTX
NCBI GI 94490319
BLAST score 237
E value 1.0e-33
Match length 143
% identity 50

NCBI Description (AL035678) metal-transporting P-type ATPase [Arabidopsis

thaliana]

Seq. No. 288405

Contig ID 245622 1.R1011 5'-most EST pmx700083031.h1

Method BLASTX
NCBI GI g3281850
BLAST score 703
E value 2.0e-74



Match length 145 % identity 88

NCBI Description (AL031004) monogalactosyldiacylglycerol synthase - like

protein [Arabidopsis thaliana]

Seq. No. 288406

Contig ID 245630_1.R1011 5'-most EST pmx700083040.h1

Seq. No. 288407

Contig ID 245665_1.R1011 5'-most EST xsy700217975.h1

Method BLASTX
NCBI GI g2584787
BLAST score 570
E value 1.0e-58
Match length 179
% identity 60

NCBI Description (X95762) Aminopeptidase P-like [Homo sapiens]

Seq. No. 288408

Contig ID 245723_1.R1011 5'-most EST pmx700083155.h1

Method BLASTX
NCBI GI g3983663
BLAST score 491
E value 7.0e-50
Match length 102
% identity 92

NCBI Description (AB011270) importin-betal [Oryza sativa]

Seq. No. 288409

Contig ID 245737_1.R1011 5'-most EST pmx700083172.h1

Method BLASTX
NCBI GI 94314359
BLAST score 369
E value 1.0e-35
Match length 100
% identity 63

NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 288410

Contig ID 245741_1.R1011 5'-most EST xsy700208483.h1

Method BLASTX
NCBI GI g4587550
BLAST score 322
E value 8.0e-30
Match length 142
% identity 40

NCBI Description (AC006577) EST gb_R64848 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 288411

Contig ID 245768_1.R1011 5'-most EST pmx700083212.h1



```
BLASTX
Method
NCBI GI
                   g3281867
BLAST score
                   278
E value
                   9.0e-25
Match length
                   88
% identity
                   64
                   (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   288412
Contig ID
                   245837 1.R1011
                   xsy700210403.h1
5'-most EST
Seq. No.
                   288413
Contig ID
                   245892 1.R1011
5'-most EST
                   pmx700083368.h1
Seq. No.
                   288414
Contig ID
                   245919 1.R1011
5'-most EST
                   xmt700265454.h1
Method
                   BLASTX
NCBI GI
                   q2104446
BLAST score
                   327
E value
                   2.0e-30
Match length
                   115
% identity
                   57
NCBI Description
                  (Z95396) WD-repeat protein [Schizosaccharomyces pombe]
Seq. No.
                   288415
Contig ID
                   245926 1.R1011
5'-most EST
                   pmx700083421.h1
Seq. No.
                   288416
Contig ID
                   245930 1.R1011
5'-most EST
                   pmx700083426.h1
Method
                   BLASTX
NCBI GI
                   g4585979
BLAST score
                   194
E value
                   4.0e-15
Match length
                   58
                   64
% identity
NCBI Description
                   (AC005287) Similar to ABC-transporter atp-binding protein
                   [Arabidopsis thaliana]
                   288417
Seq. No.
Contig ID
                   245944 1.R1011
5'-most EST
                   xsy700\overline{2}07449.h1
Method
                   BLASTX
NCBI GI
                   g4262140
BLAST score
                   259
```

2.0e-22 E value Match length 91 60 % identity

NCBI Description (AC005275) putative C-type U1 snRNP [Arabidopsis thaliana]

Seq. No. 288418

Contig ID 245981 1.R1011 5'-most EST ceu700422491.h1



```
BLASTX
Method
                  g3608147
NCBI GI
                  166
BLAST score
E value
                  8.0e-12
Match length
                  96
% identity
                   44
                  (AC005314) putative chloroplast 31 kDa ribonucleoprotein
NCBI Description
                  precursor [Arabidopsis thaliana]
Seq. No.
                  288419
                  245993 1.R1011
Contig ID
                  pmx700090034.h1
5'-most EST
Seq. No.
                   288420
Contig ID
                   246043 1.R1011
5'-most EST
                   hvj700621306.h1
Method
                   BLASTN
NCBI GI
                   q4234845
BLAST score
                   214
E value
                   1.0e-117
                   283
Match length
% identity
                   94
                   Zea mays copia-like retrotransposon Sto-17, partial
NCBI Description
                   sequence
                   288421
Seq. No.
Contig ID
                   246054 1.R1011
5'-most EST
                   ceu700422109.h1
Method
                   BLASTX
                   g3820620
NCBI GI
BLAST score
                   392
E value
                   6.0e-38
                   113
Match length
                   70
% identity
                   (AF099970) putative formamidopyrimidine-DNA glycosylase 1
NCBI Description
                   [Arabidopsis thaliana]
                   288422
Seq. No.
                   246114 1.R1011
Contig ID
                   pmx700083721.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3676248
BLAST score
                   345
                   2.0e-32
E value
                   99
Match length
                   63
% identity
                   (AJ011608) DNA polymerase alpha subunit IV (primase)
NCBI Description
                   [Rattus norvegicus]
                   288423
Seq. No.
                   246135 1.R1011
Contig ID
```

5'-most EST xsy700208132.hl

Method BLASTX q2459445 NCBI GI BLAST score 287 E value 6.0e-26 Match length 107



% identity 29
NCBI Description (AC002332) putative ribonucleoprotein [Arabidopsis

thaliana]

Seq. No. 288424

Contig ID 246145_1.R1011 5'-most EST pmx700083763.h1

Seq. No. 288425

Contig ID 246182 1.R1011 5'-most EST pmx700086933.h1

Method BLASTX
NCBI GI g1369852
BLAST score 421
E value 1.0e-41
Match length 104
% identity 82

NCBI Description (L46702) kinesin heavy chain-like protein [Solanum

tuberosum]

Seq. No. 288426

Contig ID 246194_1.R1011 5'-most EST pmx700083822.h1

Method BLASTX
NCBI GI 94583548
BLAST score 485
E value 5.0e-49
Match length 131
% identity 75

NCBI Description (AJ010820) FtsY homolog [Arabidopsis thaliana]

Seq. No. 288427

Contig ID 246205_1.R1011 5'-most EST pwr700453377.h1

Method BLASTX
NCBI GI g1922964
BLAST score 320
E value 1.0e-40
Match length 120
% identity 73

NCBI Description (AC000106) Similar to Schizosaccharomyces CCAAT-binding

factor (gb U88525). EST gb T04310 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 288428

Contig ID 246245_1.R1011 5'-most EST xyt700344123.h1

Seq. No. 288429

Contig ID 246261_1.R1011 5'-most EST pmx700083902.h1

Method BLASTX
NCBI GI g4587566
BLAST score 173
E value 2.0e-12
Match length 45
% identity 64



NCBI Description (AC006550) Contains 2 PF_00400 WD40, G-beta repeats.

[Arabidopsis thaliana]

Seq. No. 288430

Contig ID 246282 1.R1011 5'-most EST xsy700212925.h1

Method BLASTX
NCBI GI g3513451
BLAST score 183
E value 8.0e-14
Match length 92
% identity 37

NCBI Description (U78090) potassium channel regulator 1 [Rattus norvegicus]

Seq. No. 288431

Contig ID 246391_1.R1011 5'-most EST pmx700084064.h1

Seq. No. 288432

Contig ID 246404_1.R1011 5'-most EST pmx700084083.h1

Seq. No. 288433

Contig ID 246411_1.R1011 5'-most EST yyf700347935.h1

Seq. No. 288434

Contig ID 246670_1.R1011 5'-most EST wen700333893.h1

Method BLASTX
NCBI GI g3928084
BLAST score 187
E value 7.0e-14
Match length 166
% identity 33

NCBI Description (AC005770) retrotransposon-like protein [Arabidopsis

thaliana]

Seq. No. 288435

Contig ID 246694_1.R1011 5'-most EST pmx700091359.h1

Method BLASTX
NCBI GI g1170659
BLAST score 156
E value 1.0e-10
Match length 91
% identity 40

NCBI Description KINESIN-LIKE PROTEIN KIF4 >gi 1083417 pir A54803

microtubule-associated motor KIF4 - mouse

>gi_563773_dbj_BAA02167_ (D12646) KIF4 [Mus musculus]

Seq. No. 288436

Contig ID 246696_1.R1011 5'-most EST nbm700467943.h1

Method BLASTX NCBI GI g2760324 BLAST score 274



```
E value
                  5.0e-24
Match length
                  101
% identity
                  45
NCBI Description
                  (AC002130) F1N21.9 [Arabidopsis thaliana]
                  288437
```

Contig ID 246705 1.R1011 5'-most EST pmx700084466.h1 Method BLASTX NCBI GI g1173284 164

BLAST score 2.0e-11 E value Match length 61 % identity 59

Seq. No.

NCBI Description 30S RIBOSOMAL PROTEIN S9 >qi 1075279 pir F64123 ribosomal protein S9 (rpS9) homolog - Haemophilus influenzae (strain Rd KW20) >gi 1574282 (U32823) ribosomal protein S9 (rpS9)

[Haemophilus influenzae Rd]

288438 Seq. No.

Contig ID 246706 1.R1011 5'-most EST pmx700084467.h1

Method BLASTX NCBI GI q4585979 BLAST score 412 E value 2.0e-40 Match length 122 % identity 70

NCBI Description (AC005287) Similar to ABC-transporter atp-binding protein

[Arabidopsis thaliana]

288439 Seq. No.

Contig ID 246715 1.R1011 5'-most EST pmx700084476.h1

Seq. No. 288440

Contig ID 246720 1.R1011 5'-most EST $xsy700\overline{2}17467.h1$

Method BLASTX NCBI GI q4539452 BLAST score 413 E value 2.0e-40 Match length 115 % identity 70

NCBI Description (AL049500) putative phosphoribosylanthranilate transferase

[Arabidopsis thaliana]

Seq. No. 288441

246742 1.R1011 Contig ID 5'-most EST ymt700223954.hl

Method BLASTX NCBI GI q4099482 BLAST score 478 E value 7.0e-48 Match length 174 % identity 54

NCBI Description (U87791) eRFS [Homo sapiens]



```
288442
Seq. No.
Contig ID
                   246748 1.R1011
5'-most EST
                   pmx700084522.h1
Seq. No.
                   288443
Contig ID
                   246753 1.R1011
5'-most EST
                   pmx700084527.h1
Seq. No.
                   288444
Contig ID
                   246766 1.R1011
5'-most EST
                   pmx700090292.h1
Method
                   BLASTX
NCBI GI
                   q4432839
BLAST score
                   395
E value
                   1.0e-38
Match length
                   102
% identity
                   75
                  (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                   288445
Seq. No.
Contig ID
                   246788 1.R1011
5'-most EST
                   nbm700473883.h1
Method
                   BLASTX
NCBI GI
                   g3033384
BLAST score
                   322
E value
                   5.0e-30
                   102
Match length
                   67
% identity
                   (AC004238) putative CTP synthase [Arabidopsis thaliana]
NCBI Description
                   288446
Seq. No.
Contig ID
                   246829 1.R1011
5'-most EST
                   xsy700207929.hl
Method
                   BLASTX
                   g4455309
NCBI GI
BLAST score
                   354
                   1.0e-33
E value
                   130
Match length
                   59
% identity
                   (AL035528) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   288447
                   246868 1.R1011
Contig ID
                   nbm700\overline{4}67712.h1
5'-most EST
Seq. No.
                   288448
Contig ID
                   246875 1.R1011
5'-most EST
                   xsy700\overline{2}17216.h1
                   288449
Seq. No.
```

Contig ID 246910_1.R1011 5'-most EST rvt700552867.h1

Method BLASTX
NCBI GI g3292849
BLAST score 238
E value 6.0e-20



Match length 66 % identity 67

NCBI, Description (AJ007582) arginine methyltransferase [Arabidopsis

thaliana]

Seq. No. 288450

Contig ID 246944_1.R1011 5'-most EST gwl700616617.h1

Seq. No. 288451

Contig ID 246968_1.R1011 5'-most EST ceu700422539.h1

Seq. No. 288452

Contig ID 246976_1.R1011 5'-most EST gwl700614925.h1

Seq. No. 288453

Contig ID 247021_1.R1011 5'-most EST wen700336611.h1

Seq. No. 288454

Contig ID 247066_1.R1011 5'-most EST pmx700084940.h1

Seq. No. 288455

Contig ID 247082_1.R1011 5'-most EST pmx700084961.h1

Method BLASTX
NCBI GI g2244753
BLAST score 427
E value 3.0e-42
Match length 122
% identity 62

NCBI Description (297335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 288456

Contig ID 247127 1.R1011 5'-most EST vux700157447.h1

Method BLASTX
NCBI GI 9728777
BLAST score 294
E value 1.0e-26
Match length 104
% identity 51

NCBI Description ACTIVATOR 1 36 KD SUBUNIT (REPLICATION FACTOR C 36 KD

SUBUNIT) (A1 36 KD SUBUNIT) (RF-C 36 KD SUBUNIT) (RFC36) >gi_1498257 (L07540) replication factor C, 36-kDa subunit

[Homo sapiens]

Seq. No. 288457

Contig ID 247130 1.R1011 5'-most EST xsy700217221.h1

Method BLASTX
NCBI GI g1946356
BLAST score 165
E value 5.0e-13



Match length 94 % identity 49

NCBI Description (U93215) hypotheti

(U93215) hypothetical protein H1.2flk [Arabidopsis thaliana] >gi 2880041 (AC002340) hypothetical protein

H1.2flk [Arabidopsis thaliana]

Seq. No. 288458

Contig ID 247176 1.R1011 5'-most EST afb700380884.h1

Seq. No. 288459

Contig ID 247183_1.R1011 5'-most EST pmx700085090.h1

Seq. No. 288460

Contig ID 247188_1.R1011 5'-most EST gwl700612792.h1

Method BLASTX
NCBI GI g2462831
BLAST score 159
E value 1.0e-10
Match length 78
% identity 49

NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 288461

Contig ID 247191_1.R1011 5'-most EST pmx700085102.h1

Method BLASTX
NCBI GI g3242709
BLAST score 247
E value 2.0e-21
Match length 66
% identity 68

NCBI Description (AC003040) putative guanine nucleotide-binding protein

[Arabidopsis thaliana]

Seq. No. 288462

Contig ID 247225_1.R1011 5'-most EST pmx700085157.h1

Seq. No. 288463

Contig ID 247232_1.R1011 5'-most EST pmx700085164.h1

Method BLASTX
NCBI GI g2558660
BLAST score 227
E value 5.0e-19
Match length 91
% identity 45

NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]

Seq. No. 288464

Contig ID 247316_1.R1011 5'-most EST gwl700614964.h1

Seq. No. 288465



Contig ID 247330_1.R1011 5'-most EST pmx700085288.h1

Seq. No. 288466

Contig ID 247363_1.R1011 5'-most EST pmx700085327.h1 Method BLASTX

NCBI GI g3738306
BLAST score 195
E value 5.0e-15
Match length 114
% identity 38

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 288467

Contig ID 247368_1.R1011 5'-most EST wty700172568.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 48
% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 288468

Contig ID 247371_1.R1011 5'-most EST vux700157082.h1

Seq. No. 288469

Contig ID 247425_1.R1011 5'-most EST pmx700085401.h1

Seq. No. 288470

Contig ID 247445_1.R1011 5'-most EST pmx700085533.h1

Seq. No. 288471

Contig ID 247448_1.R1011 5'-most EST pmx700085426.h1

Seq. No. 288472

Contig ID 247468_1.R1011 5'-most EST pmx700085448.h1

Seq. No. 288473

Contig ID 247493_1.R1011 5'-most EST wty700163774.h1

Method BLASTX
NCBI GI g3059131
BLAST score 217
E value 2.0e-17
Match length 118
% identity 39

NCBI Description (AJ000478) cytochrome P450 [Helianthus tuberosus]

Seq. No. 288474



Contig ID 247500_2.R1011 5'-most EST pmx700085485.h1

Seq. No. 288475

Contig ID 247536_1.R1011 5'-most EST ceu700430757.h1

Seq. No. 288476

Contig ID 247574_1.R1011 5'-most EST pmx700085581.h1

Method BLASTX
NCBI GI g2832683
BLAST score 330
E value 9.0e-31
Match length 95
% identity 58

NCBI Description (AL021712) putative protein [Arabidopsis thaliana]

Seq. No. 288477

Contig ID 247583 1.R1011 5'-most EST wen700332395.h1

Seq. No. 288478

Contig ID 247594_1.R1011 5'-most EST xmt700263874.h1

Seq. No. 288479

Contig ID 247621_1.R1011 5'-most EST gct701179967.h1

Seq. No. 288480

Contig ID 247663_1.R1011 5'-most EST wty700171172.h1

Method BLASTX
NCBI GI g3892057
BLAST score 968
E value 1.0e-105
Match length 251
% identity 52

NCBI Description (AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No. 288481

Contig ID 247693_1.R1011 5'-most EST pmx700085725.h1

Seq. No. 288482

Contig ID 247720_1.R1011 5'-most EST xsy700210043.h1

Seq. No. 288483

Contig ID 247824 1.R1011 5'-most EST pmx700085888.h1

Method BLASTX
NCBI GI g3075398
BLAST score 435
E value 4.0e-43
Match length 128

% identity

NCBI Description

58

[Arabidopsis thaliana]



```
% identity
                  (AC004484) unknown protein [Arabidopsis thaliana]
NCBI Description
                  288484
Seq. No.
Contig ID
                  247839 1.R1011
5'-most EST
                  pmx700085909.h1
                  BLASTX
Method
                  g2341042
NCBI GI
BLAST score
                  271
                  5.0e-24
E value
Match length
                  68
% identity
                  75
                  (AC000104) F19P19.26 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  288485
Contig ID
                  247840 1.R1011
5'-most EST
                  pmx700085911.h1
Method
                  BLASTX
                  g2961384
NCBI GI
                  170
BLAST score
                   4.0e-12
E value
Match length
                  93
% identity
                   (AL022141) aldehyde dehydrogenase like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   288486
                   247888 1.R1011
Contig ID
5'-most EST
                  pmx700085965.h1
                   288487
Seq. No.
Contig ID
                   247967 1.R1011
5'-most EST
                  pmx700086069.h1
Seq. No.
                   288488
Contig ID
                   247975 1.R1011
5'-most EST
                   zuv700353059.h1
Method
                   BLASTX
NCBI GI
                   g2245131
BLAST score
                   277
E value
                   7.0e-25
Match length
                   107
% identity
                  (Z97344) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   288489
Seq. No.
                   247981 1.R1011
Contig ID
5'-most EST
                   tfd700571096.hl
Method
                   BLASTX
                   g1946372
NCBI GI
BLAST score
                   284
                   2.0e-25
E value
Match length
                   101
```

(U93215) yeast hypothetical protein YDB1_SCHPO isolog

Match length

NCBI Description

% identity

146 36



```
288490
Seq. No.
Contig ID
                  248001 1.R1011
5'-most EST
                  pmx700091554.h1
Method
                  BLASTX
NCBI GI
                  q2854158
BLAST score
                  150
E value
                  8.0e-10
Match length
                  85
% identity
                  (AF045641) No definition line found [Caenorhabditis
NCBI Description
                  elegans]
                  288491
Seq. No.
Contig ID
                  248199 1.R1011
5'-most EST
                  uer700577906.h1
Seq. No.
                  288492
Contig ID
                  248213 1.R1011
5'-most EST
                  pmx700086383.h1
                  BLASTX
Method
                  g3776031
NCBI GI
BLAST score
                  610
                  1.0e-63
E value
                  152
Match length
% identity
NCBI Description
                  (AJ010477) RNA helicase [Arabidopsis thaliana]
Seq. No.
                  248219 1.R1011
Contig ID
5'-most EST
                  xmt700258009.h1
                  288494
Seq. No.
Contig ID
                  248263 1.R1011
5'-most EST
                  pmx700087110.h1
Seq. No.
                   288495
Contig ID
                   248265 1.R1011
                  pmx700086453.hl
5'-most EST
Seq. No.
                   288496
Contig ID
                   248268 1.R1011
5'-most EST
                  xsy700213927.hl
Seq. No.
                   288497
                   248284 1.R1011
Contig ID
5'-most EST
                  pmx700086478.h1
Seq. No.
                   288498
                   248292 1.R1011
Contig ID
                  pmx700088035.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2352492
BLAST score
                   331
                   7.0e-31
E value
```

(AF005047) transport inhibitor response 1 [Arabidopsis



) transport inhibito

thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No. 288499

Contig ID 248391_1.R1011 5'-most EST pmx700086641.h1

Method BLASTX
NCBI GI g2765817
BLAST score 199
E value 1.0e-15
Match length 99
% identity 41

NCBI Description (Z95352) AtMlo-h1 [Arabidopsis thaliana]

>qi 3892049 qb AAC78258.1 AAC78258 (AC002330) AtMlo-h1

[Arabidopsis thaliana]

Seq. No. 288500

Contig ID 248403_1.R1011 5'-most EST ypc700802214.h1

Seq. No. 288501

Contig ID 248455_1.R1011 5'-most EST pmx700086722.h1

Seq. No. 288502

Contig ID 248467_1.R1011 5'-most EST pmx700086735.h1

Method BLASTX
NCBI GI g3892709
BLAST score 256
E value 5.0e-22
Match length 108
% identity 50

NCBI Description (AL033545) putative protein [Arabidopsis thaliana]

Seq. No. 288503

Contig ID 248484_1.R1011 5'-most EST pmx700086765.h1

Method BLASTX
NCBI GI 94107001
BLAST score 433
E value 5.0e-43
Match length 110
% identity 69

NCBI Description (D82035) OSK4 [Oryza sativa]

Seq. No. 288504

Contig ID 248502_1.R1011 5'-most EST pmx700086776.h1

Seq. No. 288505

Contig ID 248512 1.R1011 5'-most EST pmx700086793.h1

Seq. No. 288506

Contig ID 248555_1.R1011 5'-most EST pmx700086846.h1



Seq. No. 288507

Contig ID 248566_1.R1011 5'-most EST pmx700086860.h1

Method BLASTX
NCBI GI g3122765
BLAST score 401
E value 6.0e-39
Match length 169
% identity 54

NCBI Description DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT (RPC155)

>gi_2460208 (AF021351) RNA polymerase III largest subunit

[Homo sapiens]

Seq. No. 288508

Contig ID 248584_1.R1011 5'-most EST pmx700086884.h1

Method BLASTX
NCBI GI g3413712
BLAST score 157
E value 9.0e-11
Match length 71
% identity 48

NCBI Description (AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No. 288509

Contig ID 248630_1.R1011 5'-most EST pmx700086943.h1

Seq. No. 288510

Contig ID 248736_1.R1011 5'-most EST pmx700087084.h1

Method BLASTX
NCBI GI g2326372
BLAST score 667
E value 3.0e-70
Match length 157
% identity 77

NCBI Description (Y14404) putative arabinose kinase [Arabidopsis thaliana]

Seq. No. 288511

Contig ID 248759_1.R1011 5'-most EST ypc700805728.h1

Seq. No. 288512

Contig ID 248771_1.R1011 5'-most EST pmx700087136.h1

Seq. No. 288513

Contig ID 248772_1.R1011 5'-most EST gwl700614927.h1

Seq. No. 288514

Contig ID 248849_1.R1011 5'-most EST pmx700087227.h1

Method BLASTX NCBI GI g2245130



```
BLAST score 211
E value 1.0e-16
Match length 127
% identity 42
```

NCBI Description (Z97344) GLABRA2 homolog [Arabidopsis thaliana]

Seq. No.
Contig ID
5'-most EST

288515 248878_1.R1011 pmx700087259.h1

Method BLASTX
NCBI GI g4468817
BLAST score 426
E value 1.0e-42
Match length 110

% identity 72

NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No.

288516

Contig ID 5'-most EST

248915_1.R1011 xsy700207627.h1

Method BLASTX
NCBI GI g4587597
BLAST score 194
E value 7.0e-15
Match length 49
% identity 78

NCBI Description (AC006951) putative MAP kinase phosphatase [Arabidopsis

thaliana]

288517

Seq. No.

Contig ID
5'-most EST

248982_1.R1011 pmx700087393.h1

Method BLASTX
NCBI GI g2827704
BLAST score 172
E value 2.0e-12

Match length 97 % identity 34

NCBI Description (AL021684) LRR-like protein [Arabidopsis thaliana]

Seq. No.

288518

Contig ID 5'-most EST

248990_1.R1011 pmx700087408.h1

Seq. No.

288519

Contig ID 5'-most EST 249038_1.R1011 nbm700472761.h1

Seq. No. Contig ID

288520

Contig ID
5'-most EST

249043 1.R1011 xmt700265552.h1

Seq. No.

288521

Contig ID 249108_1.R1011 5'-most EST pmx700087563.h1

Seq. No.



```
Contig ID
                  249119 1.R1011
5'-most EST
                  hbs701183609.h1
                  BLASTX
Method
                  g4218120
NCBI GI
BLAST score
                  164
E value
                  3.0e-11
Match length
                  36
% identity
                  (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                  thaliana]
                   288523
Seq. No.
                  249150 1.R1011
Contig ID
                  pmx700087622.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3176691
BLAST score
                  621
                  1.0e-64
E value
Match length
                  182
                   68
% identity
                   (AC003671) Contains homology to serine/threonine protein
NCBI Description
                   kinase gb X99618 from Mycobacterium tuberculosis. ESTs
                   gb F14403, gb F14404, and gb N96730 come from this gene.
                   [Arabidopsis thaliana]
                   288524
Seq. No.
Contig ID
                   249177 1.R1011
                  pmx700087656.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4455294
BLAST score
                   305
E value
                   9.0e-28
Match length
                   154
% identity
                   40
                   (AL035528) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   288525
Contig ID
                   249181 1.R1011
5'-most EST
                   pmx700087661.hl
Method
                   BLASTX
NCBI GI
                   g4262173
BLAST score
                   349
E value
                   6.0e-33
Match length
                   128
% identity
                   59
                   (AC005508) 3975 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   288526
                   249205 1.R1011
Contig ID
5'-most EST
                   pmx700087703.h1
Seq. No.
                   288527
```

Contig ID 249252 1.R1011 5'-most EST yyf700348032.h1

Method BLASTX NCBI GI g3687230 BLAST score 332



```
6.0e-31
E value
                  108
Match length
% identity
                   (AC005169) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  288528
Seq. No.
                  249262 1.R1011
Contig ID
                  pmx700087777.h1
5'-most EST
                  288529
Seq. No.
                  249274 1.R1011
Contig ID
                  pmx700087790.h1
5'-most EST
                   288530
Seq. No.
Contig ID
                   249277 1.R1011
5'-most EST
                  nbm700474616.hl
Method
                  BLASTX
NCBI GI
                   g3004555
BLAST score
                   141
                   8.0e-09
E value
Match length
                   78
% identity
                   33
NCBI Description (AC003673) similar to salt inducible protein [Arabidopsis
                   thaliana]
                   288531
Seq. No.
Contig ID
                   249296 1.R1011
                   yyf700347895.h1
5'-most EST
Seq. No.
                   288532
                   249350 1.R1011
Contig ID
                   pmx700087879.h1
5'-most EST
                   288533
Seq. No.
                   249354 1.R1011
Contig ID
5'-most EST
                   pmx700087883.h1
                   288534
Seq. No.
                   249398 1.R1011
Contig ID
                   pmx700087944.h1
5'-most EST
Seq. No.
                   288535
                   249418 1.R1011
Contig ID
                   pmx700087969.h1
5'-most EST
                   288536
Seq. No.
                   249456_1.R1011
Contig ID
                   nwy700447820.hl
5'-most EST
                   {\tt BLASTX}
Method
                   g3169180
NCBI GI
```

Method BLASTX
NCBI GI g3169180
BLAST score 645
E value 1.0e-67
Match length 159
% identity 77

NCBI Description (AC004401) putative casein kinase II catalytic subunit

[Arabidopsis thaliana]



Seq. No. 28853

Contig ID 249468_1.R1011 5'-most EST pmx700088036.h1

Method BLASTX
NCBI GI g3212880
BLAST score 246
E value 4.0e-21
Match length 106
% identity 48

NCBI Description (AC004005) putative Mlo protein [Arabidopsis thaliana]

Seq. No. 288538

Contig ID 249480_1.R1011 5'-most EST xmt700266016.h1

Seq. No. 288539

Contig ID 249491_1.R1011 5'-most EST hbs701182207.h1

Seq. No. 288540

Contig ID 249518_1.R1011 5'-most EST rvt700550236.h1

Seq. No. 288541

Contig ID 249524_1.R1011 5'-most EST pmx700091018.h1

Method BLASTX
NCBI GI g2498329
BLAST score 400
E value 4.0e-39
Match length 106
% identity 75

NCBI Description PATTERN FORMATION PROTEIN EMB30 >gi_2129665_pir__S65571 pattern-formation protein GNOM - Arabidopsis thaliana

>gi_1209633 (U36433) GNOM gene product [Arabidopsis

thaliana] >gi_1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi_1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession

Number J03918 [Arabidopsis thaliana]

Seq. No. 288542

Contig ID 249526_1.R1011 5'-most EST ceu700429669.h1

Method BLASTX
NCBI GI g4104457
BLAST score 372
E value 8.0e-36
Match length 74
% identity 93

NCBI Description (AF036172) 2-oxoglutarate/malate translocator [Zea mays]

Seq. No. 288543

Contig ID 249537_1.R1011 5'-most EST pmx700091526.h1

Seq. No. 288544

NCBI Description



```
249576 1.R1011
Contig ID
5'-most EST
                   pmx700\overline{0}88175.h1
                   BLASTX
Method
NCBI GI
                   q1653665
BLAST score
                   542
                   1.0e-55
E value
Match length
                   141
                   73
% identity
NCBI Description (D90915) peptide chain release factor [Synechocystis sp.]
Seq. No.
                   288545
                   249591 1.R1011
Contig ID
                   wty700165823.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3785976
BLAST score
                   233
E value
                   1.0e-19
Match length
                   103
                   48
% identity
NCBI Description (AC005560) Sec12p-like protein [Arabidopsis thaliana]
                   288546
Seq. No.
                   249596 1.R1011
Contig ID
                   pmx700088202.h1
5'-most EST
Method
                   BLASTX
                   q3056725
NCBI GI
BLAST score
                   205
                   6.0e-23
E value
Match length
                   112
% identity
                   54
NCBI Description (AF034774) ent-kaurene synthase [Arabidopsis thaliana]
Seq. No.
                   288547
Contia ID
                   249630 1.R1011
5'-most EST
                   xmt700\overline{2}65869.h1
Method
                   BLASTX
NCBI GI
                   q4558659
BLAST score
                   369
E value
                   3.0e-35
Match length
                   114
% identity
NCBI Description
                   (AC007063) unknown protein [Arabidopsis thaliana]
Seq. No.
                   288548
Contig ID
                   249643 1.R1011
5'-most EST
                   pmx700088259.hl
Seq. No.
                   288549
Contig ID
                   249656 1.R1011
5'-most EST
                   xyt700344067.hl
Method
                   BLASTX
                   g2792238
NCBI GI
BLAST score
                   152
E value
                   4.0e-10
Match length
                   61
                   44
% identity
```

40152

(AF032697) NBS-LRR type resistance protein [Oryza sativa]



```
288550
Seq. No.
                   249681 1.R1011
Contig ID
                   pmx700\overline{0}88316.h1
5'-most EST
Seq. No.
                   288551
                   249681 2.R1011
Contig ID
                   wty700168272.hl
5'-most EST
Seq. No.
                   288552
Contig ID
                   249701 1.R1011
                   pmx700088341.hl
5'-most EST
                   288553
Seq. No.
Contig ID
                   249709 1.R1011
5'-most EST
                   xsy700\overline{2}14361.h1
                   288554
Seq. No.
Contig ID
                   249720 1.R1011
                   fdz701161314.h1
5'-most EST
                   288555
Seq. No.
                   249732 1.R1011
Contig ID
5'-most EST
                   nbm700466142.h1
                   BLASTX
Method
NCBI GI
                   g3063699
BLAST score
                   322
E value
                   1.0e-29
                   133
Match length
                   50
% identity
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]
                   288556
Seq. No.
                   249785 1.R1011
Contig ID
5'-most EST
                   ypc700802639.h1
                   288557
Seq. No.
Contig ID
                   249803 1.R1011
5'-most EST
                   nbm700\overline{4}77926.h1
Seq. No.
                   288558
Contig ID
                   249843 1.R1011
5'-most EST
                   pmx700088531.h1
Seq. No.
                   288559
Contig ID
                   249943 1.R1011
5'-most EST
                   rvt700549231.h1
Method
                   BLASTX
NCBI GI
                   g2829894
```

BLAST score 309 E value 3.0e-28 Match length 168

% identity 42

NCBI Description (AC002311) Unknown protein [Arabidopsis thaliana]

Seq. No.

Contig ID 249952 1.R1011

288560



```
5'-most EST
                   nbm700469769.h1
                   288561
Seq. No.
Contig ID
                   249975 1.R1011
5'-most EST
                   xsy700\overline{2}11722.h1
                   288562
Seq. No.
                   249976 1.R1011
Contig ID
5'-most EST
                   pmx700088692.h1
Seq. No.
                   288563
Contig ID
                   249984 1.R1011
5'-most EST
                   pmx700088713.h1
                   BLASTX
Method
                   g2864625
NCBI GI
BLAST score
                   346
E value
                   7.0e-33
Match length
                   99
% identity
                   71
                  (AL021811) putative protein [Arabidopsis thaliana]
NCBI Description
                   288564
Seq. No.
                   250007 1.R1011
Contig ID
                   pmx700088737.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1477480
BLAST score
                   646
E value
                   9.0e-68
Match length
                   155
% identity
                   41
                   (U40341) carbamoyl phosphate synthetase large chain
NCBI Description
                   [Arabidopsis thaliana]
                   288565
Seq. No.
Contig ID
                   250030 1.R1011
5'-most EST
                   xyt700\overline{3}45713.h1
Seq. No.
                   288566
Contig ID
                   250198 1.R1011
5'-most EST
                   xyt700\overline{3}46246.h1
Method
                   BLASTX
NCBI GI
                   g4580990
BLAST score
                   206
E value
                   5.0e-16
Match length
                   184
% identity
NCBI Description
                  (AF120335) putative transposase [Arabidopsis thaliana]
Seq. No.
                   288567
Contig ID
                   250237 1.R1011
5'-most EST
                   pmx700089047.h1
Method
                   BLASTX
```

Method BLASTX
NCBI GI g1762428
BLAST score 341
E value 3.0e-32
Match length 117
% identity 21



NCBI Description (U59467) aromatic rich glycoprotein JP630 [Arabidopsis thaliana]

Seq. No. Contig ID

288568

Contig ID 250254_1.R1011 5'-most EST pmx700089067.h1

Seq. No.

288569

BLASTX

Contig ID 5'-most EST Method 250296_1.R1011 xyt700343001.h1

NCBI GI BLAST score E value

g3913525 557 1.0e-57

Match length % identity

118 92

NCBI Description

DNA POLYMERASE DELTA CATALYTIC CHAIN >gi_2895198 (AF020193)
DNA polymerase delta [Glycine max]

Seq. No.
Contig ID
5'-most EST

288570

250355_1.R1011 wty700166686.h1

Seq. No.
Contig ID
5'-most EST

288571

250386_1.R1011 ymt700221928.h1

Seq. No.

288572

Contig ID 5'-most EST

250395_1.R1011 pmx700089244.h1

Seq. No.
Contig ID
5'-most EST

288573

250419_1.R1011 pmx700089271.h1

Seq. No.

288574

Contig ID 5'-most EST 250526_1.R1011 pmx700089406.h1

Seq. No. Contig ID 288575

Contig ID 250566_1.R1011 5'-most EST gwl700615310.h1

Seq. No. Contig ID

288576

Contig ID 250629_1.R1011 5'-most EST pmx700089527.h1

Seq. No.

288577

Contig ID 5'-most EST

250634_1.R1011 pmx700089532.h1

Seq. No.

288578

Contig ID 5'-most EST

250644_1.R1011 pmx700089543.h1

Seq. No.

288579

Contig ID

250679 1.R1011

NCBI GI BLAST score

E value

296

1.0e-26



```
5'-most EST
                   ypc700805579.h1
                   BLASTX
Method
                   g1495251
NCBI GI
BLAST score
                   418
E value
                   2.0e-41
Match length
                   99
% identity
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                   288580
Seq. No.
Contig ID
                   250684 1.R1011
                   pmx700\overline{0}89595.h1
5'-most EST
Method
                   BLASTX
                   g4099605
NCBI GI
BLAST score
                   301
E value
                   1.0e-27
Match length
                   92
% identity
                   62
NCBI Description (U88836) translational activator GCN1 [Homo sapiens]
Seq. No.
                   288581
Contig ID
                   250691 1.R1011
                   pmx700089608.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3461822
BLAST score
                   155
E value
                   2.0e-10
Match length
                   115
% identity
NCBI Description
                  (AC004138) hypothetical protein [Arabidopsis thaliana]
                   288582
Seq. No.
Contig ID
                   250701 1.R1011
5'-most EST
                   xsy700208534.h1
                   288583
Seq. No.
Contig ID
                   250749 1.R1011
                   ypc700807341.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2352084
BLAST score
                   148
E value
                   3.0e-09
Match length
                   92
% identity
                   41
                   (U96613) serine/threonine kinase [Arabidopsis thaliana]
NCBI Description
                   288584
Seq. No.
Contig ID
                   250752 1.R1011
5'-most EST
                   pmx700089702.h1
                   288585
Seq. No.
Contig ID
                   250759 1.R1011
5'-most EST
                   pmx700089709.h1
                   BLASTX
Method
                   g3152620
```



Match length 162 % identity 40

NCBI Description (AC004482) putative C2H2 zinc finger protein [Arabidopsis

thaliana]

Seq. No. 288586

Contig ID 250815_1.R1011 5'-most EST pmx700089775.h1

Seq. No. 288587

Contig ID 250896_1.R1011 5'-most EST pmx700089969.h1

Seq. No. 288588

Contig ID 250941_1.R1011 5'-most EST xsy700209884.h1

Seq. No. 288589

Contig ID 250960_1.R1011 5'-most EST pmx700090058.h1

Method BLASTX
NCBI GI g2827715
BLAST score 366
E value 3.0e-35
Match length 88
% identity 80

NCBI Description (AL021684) receptor protein kinase - like protein

[Arabidopsis thaliana]

Seq. No. 288590

Contig ID 251028_1.R1011 5'-most EST pmx700090156.h1

Seq. No. 288591

Contig ID 251035_1.R1011 5'-most EST pmx700090165.h1

Method BLASTX
NCBI GI g2245131
BLAST score 291
E value 1.0e-26
Match length 103
% identity 57

NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No. 288592

Contig ID 251073_1.R1011 5'-most EST pmx700090220.h1

Method BLASTX
NCBI GI g3122914
BLAST score 475
E value 5.0e-48
Match length 101
% identity 86

NCBI Description VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS)

>gi_1890130 (U89986) valyl tRNA synthetase [Arabidopsis

thaliana]



Seq. No.	
Contig ID	
5'-most EST	

288593

251105 1.R1011 pmx700090260.hl

Seq. No. Contig ID 5'-most EST

288594

251130 1.R1011 pmx700090287.h1

Seq. No. Contig ID 5'-most EST 288595

251152 1.R1011 nbm700474034.h1

Seq. No. Contig ID 5'-most EST 288596

251157 1.R1011 $wen700\overline{3}34169.h1$

Seq. No. Contig ID 5'-most EST 288597 251162 1.R1011

wty700167980.h1

Seq. No. Contig ID 5'-most EST Method

288598

251263 1.R1011 pmx700090614.h1 BLASTX

NCBI GI g4559330 BLAST score 143 E value 4.0e-09 Match length 91 % identity

NCBI Description

(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. Contig ID 5'-most EST 288599

251289 1.R1011 xmt700265371.h1

Seq. No. Contig ID 5'-most EST 288600

251292 1.R1011 $pmx700\overline{0}90652.h1$

Seq. No. Contig ID 5'-most EST 288601

251335 1.R1011 pmx700090706.h1

Seq. No. Contig ID 5'-most EST 288602

251340 1.R1011 pmx700090712.h1

Seq. No. Contig ID

288603

251421 1.R1011 afb700380808.h1

5'-most EST Seq. No.

288604

Contig ID 5'-most EST Method

251440 1.R1011 xsy700212291.h1

BLASTX NCBI GI g3659909 BLAST score



E value 3.0e-65 Match length 169 % identity 69

NCBI Description (AF020715) histidyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.

288605

Contig ID 5'-most EST

251444_1.R1011 nbm700467169.h1

Seq. No.

288606

Contig ID 5'-most EST

251484_1.R1011 pmx700090890.h1

Seq. No.

288607

Contig ID 5'-most EST

251513_1.R1011 dhd700197972.h1

Seq. No.

288608

Contig ID 5'-most EST

251527_1.R1011 xmt700259541.h1

Seq. No.

288609

Contig ID 5'-most EST

251565_1.R1011 pmx700091007.h1

Seq. No.

288610

Contig ID 5'-most EST

251585_1.R1011 pmx700091030.h1

Method NCBI GI BLASTX q4506399

BLAST score
E value
Match length

270 1.0e-28 114

54

% identity NCBI Description

homolog of yeast Rael (Bharathi) mRNA-associated protein of

41 kDa (Kraemer) >gi_3122666_sp_P78406_RA1L_HUMAN MRNA-ASSOCIATED PROTEIN MRNP41 (RAE1 PROTEIN HOMOLOG) >gi_1903456 (U84720) mRNA export protein [Homo sapiens]

Seq. No.

288611

Contig ID 5'-most EST

251701_1.R1011 pmx700091173.h1

Method NCBI GI BLAST score BLASTX g4585871

BLAST score E value

333

Match length

6.0e-37 96

% identity

79

NCBI Description

(AC005850) Unknown protein [Arabidopsis thaliana]

Seq. No.

288612

Contig ID 5'-most EST

251714_1.R1011 yyf700350677.h1

Method NCBI GI BLAST score

E value

BLASTX g2911056

158 2.0e-10



Match length 86 % identity 45

NCBI Description (AL021961) hypothetical protein [Arabidopsis thaliana]

Seq. No. 288613

Contig ID 251715_1.R1011 5'-most EST xyt700346125.h1

Seq. No. 288614

Contig ID 251777_1.R1011 5'-most EST ymt700223758.h1

Seq. No. 288615

Contig ID 251833_1.R1011 5'-most EST uer700584244.h1

Seq. No. 288616

Contig ID 251861_1.R1011 5'-most EST pmx700091421.h1

Method BLASTX
NCBI GI g3402697
BLAST score 299
E value 4.0e-27
Match length 96
% identity 58

NCBI Description (AC004261) putative phosphatidylinositol-4-phosphate

5-kinase [Arabidopsis thaliana]

Seq. No. 288617

Contig ID 251876_1.R1011 5'-most EST pmx700091436.h1

Seq. No. 288618

Contig ID 251888_1.R1011 5'-most EST pmx700091451.h1

Seq. No. 288619

Contig ID 251890_1.R1011 5'-most EST pmx700091453.h1

Method BLASTX
NCBI GI g2244939
BLAST score 153
E value 1.0e-17
Match length 94
% identity 54

NCBI Description (297339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 288620

Contig ID 251894_1.R1011 5'-most EST pmx700091458.h1

Method BLASTX
NCBI GI g2145358
BLAST score 309
E value 1.0e-28
Match length 101
% identity 59

NCBI Description (Y10922) HD-Zip protein [Arabidopsis thaliana]



Contig ID 251917_1.R1011 5'-most EST pmx700091485.h1

Seq. No. 288622

Contig ID 251939_1.R1011 5'-most EST pmx700091514.h1

Method BLASTX
NCBI GI 94544402
BLAST score 466
E value 1.0e-46
Match length 134
% identity 65

NCBI Description (AC007047) putative leucine rich repeat protein

[Arabidopsis thaliana]

Seq. No. 288623

Contig ID 252040_1.R1011 5'-most EST pmx700091638.h1

Seq. No. 288624

Contig ID 252073_1.R1011 5'-most EST nbm700472501.h1

Method BLASTX
NCBI GI g4455203
BLAST score 186
E value 3.0e-14
Match length 205
% identity 30

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 288625

Contig ID 252134_1.R1011 5'-most EST pmx700091751.h1

Method BLASTX
NCBI GI g2501011
BLAST score 361
E value 1.0e-34
Match length 93
% identity 68

NCBI Description ISOLEUCYL-TRNA SYNTHETASE (ISOLEUCINE--TRNA LIGASE) (ILERS)

>gi_1652625_dbj_BAA17545_ (D90907) isoleucyl-tRNA

synthetase [Synechocystis sp.]

Seq. No. 288626

Contig ID 252152_1.R1011 5'-most EST mwy700441362.h1

Seq. No. 288627

Contig ID 252152 2.R1011 5'-most EST pmx700091777.h1

Seq. No. 288628

Contig ID 252216_1.R1011 5'-most EST pmx700091861.h1



288629 Seq. No. Contig ID 5'-most EST

252222 1.R1011 pmx700091868.hl

Seq. No. Contig ID 5'-most EST

288630 252241 1.R1011 pmx700091888.h1

Seq. No. Contig ID 5'-most EST

288631 252278 1.R1011 pmx700091942.hl

Seq. No. Contig ID 5'-most EST

288632 252344 1.R1011 $vmj700\overline{0}53750.r1$

Seq. No. Contig ID 5'-most EST 288633 252381 1.R1011 $vmj700\overline{0}53794.r1$

Method BLASTX NCBI GI g3482917 BLAST score 495 E value 3.0e-50 Match length 119 73 % identity

(AC003970) Similar to Glucose-6-phosphate dehydrogenases, NCBI Description gi 2276344, gi 2829880, gi 2352919 and others. [Arabidopsis

thaliana]

288634

Seq. No.

252391_1.R1011 Contig ID $vmj700\overline{0}53809.r1$ 5'-most EST

Seq. No. 288635

252394 1.R1011 Contig ID xsy700212859.h1 5'-most EST

Seq. No. Contig ID 288636 252403 1.R1011 ymt700218516.hl

5'-most EST BLASTX Method q1708972 NCBI GI BLAST score 245 E value 6.0e-21 Match length 79

% identity NCBI Description

(R)-MANDELONITRILE LYASE ISOFORM 3 PRECURSOR

(HYDROXYNITRILE LYASE 3) ((R)-OXYNITRILASE 3) >gi_1262279

(U51562) (R)-(+)-mandelonitrile lyase isoform MDL3 precursor [Prunus serotina] >gi 2343181 (AF013161) (R)-(+)-mandelonitrile lyase isoform MDL3 precursor

[Prunus serotina]

Seq. No. 288637

252423 1.R1011 Contig ID $ceu700\overline{4}28740.h1$ 5'-most EST



Contig ID 252477_1.R1011 5'-most EST ceu700424082.h1

Seq. No. 288639

Contig ID 252493_1.R1011 5'-most EST ymt700222295.h1

Seq. No. 288640

Contig ID 252500 1.R1011 5'-most EST ymt700218640.h1

Seq. No. 288641

Contig ID 252532_2.R1011 5'-most EST rvt700548946.h1

Method BLASTX
NCBI GI g2773249
BLAST score 155
E value 2.0e-10
Match length 62
% identity 44

NCBI Description (AF039707) glutamate carboxypeptidase II [Rattus

norvegicus]

Seq. No. 288642

Contig ID 252533_1.R1011 5'-most EST ymt700218683.h1

Seq. No. 288643

Contig ID 252590 1.R1011 5'-most EST ymt700218758.h1

Seq. No. 288644

Contig ID 252595_1.R1011 5'-most EST rvt700552987.h1

Method BLASTX
NCBI GI g1136434
BLAST score 345
E value 9.0e-33
Match length 89
% identity 63

NCBI Description (D80009) KIAA0187 [Homo sapiens]

Seq. No. 288645

Contig ID 252600_1.R1011 5'-most EST xyt700343368.h1

Seq. No. 288646

Contig ID 252614_1.R1011 5'-most EST rvt700549825.h1

Seq. No. 288647

Contig ID 252630_1.R1011 5'-most EST wty700172224.h1

Seq. No. 288648

Contig ID 252635 1.R1011

Match length

% identity

73

62



```
5'-most EST
                   ymt700218816.hl
Seq. No.
                   288649
Contig ID
                   252775 1.R1011
5'-most EST
                   ymt700218987.h1
Method
                   BLASTX
NCBI GI
                   q3096930
BLAST score
                   151
                   5.0e-10
E value
                   104
Match length
                   37
% identity
NCBI Description
                  (AL023094) Homeodomain - like protein [Arabidopsis
                   thaliana]
                   288650
Seq. No.
                   252806 1.R1011
Contig ID
5'-most EST
                   ymt700\overline{2}19029.h1
Seq. No.
                   288651
                   252836 1.R1011
Contig ID
5'-most EST
                   ymt700219063.h1
Method
                   BLASTX
                   g3337350
NCBI GI
BLAST score
                   473
E value
                   6.0e-50
Match length
                   139
% identity
                   72
NCBI Description (AC004481) putative permease [Arabidopsis thaliana]
                   288652
Seq. No.
                   252842 1.R1011
Contig ID
5'-most EST
                   wty700170544.hl
                   288653
Seq. No.
Contig ID
                   252847 1.R1011
5'-most EST
                   nbm700465756.h1
Seq. No.
                   288654
Contig ID
                   252889 1.R1011
5'-most EST
                   ymt700\overline{2}19132.h1
Method
                   BLASTX
NCBI GI
                   q3451075
BLAST score
                   227
E value
                   4.0e-19
Match length
                   79
% identity
                   58
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]
                   288655
Seq. No.
Contig ID
                   252935 1.R1011
5'-most EST
                   xmt700\overline{2}65656.h1
Method
                   BLASTX
NCBI GI
                   g1931649
BLAST score
                   220
E value
                   6.0e-18
```



NCBI Description (U95973) DNA helicase isolog [Arabidopsis thaliana]

Seq. No. - 288656

Contig ID 252977_1.R1011 5'-most EST rvt700549951.h1

Method BLASTX
NCBI GI g2244763
BLAST score 446
E value 2.0e-44
Match length 116
% identity 68

NCBI Description (Z97335) A6 anther-specific protein [Arabidopsis thaliana]

Seq. No. 288657

Contig ID 252978_1.R1011 5'-most EST ymt700219242.h1

Method BLASTX
NCBI GI g3859114
BLAST score 486
E value 4.0e-49
Match length 118
% identity 78

NCBI Description (AF031608) MS5-like protein [Arabidopsis thaliana]

Seq. No. 288658

Contig ID 253154_1.R1011 5'-most EST ymt700219466.h1

Seq. No. 288659

Contig ID 253218_1.R1011 5'-most EST ymt700219550.h1

Seq. No. 288660

Contig ID 253225_1.R1011 5'-most EST ceu700422648.h1

Seq. No. 288661

Contig ID 253279_1.R1011 5'-most EST rvt700549329.h1

Seq. No. 288662

Contig ID 253300 1.R1011 5'-most EST ymt700219646.h1

Method BLASTX
NCBI GI g4371279
BLAST score 175
E value 8.0e-13
Match length 102
% identity 36

NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 288663

Contig ID 253328_1.R1011 5'-most EST hvj700624622.h1

Seq. No. 288664

Contig ID 253359 1.R1011

Method

NCBI GI

E value Match length

BLAST score

BLASTX

184 4.0e-22

153

g2492681



```
ymt700219721.h1
5'-most EST
                    288665
Seq. No.
                    253392 1.R1011
Contig ID
5'-most EST
                    ymt700219761.h1
Method
                    BLASTX
                    g2088644
NCBI GI
BLAST score
                    385
                    3.0e-37
E value
                    123
Match length
% identity
                    56
NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]
                    288666
Seq. No.
                    253403 1.R1011
Contig ID
                    xdb700\overline{3}38655.h1
5'-most EST
                    BLASTX
Method
NCBI GI
                    g4204304
BLAST score
                    252
                    1.0e-21
E value
                    110
Match length
                    49
% identity
                    (AC003027) lcl_prt_seq No definition line found
NCBI Description
                    [Arabidopsis thaliana]
                    288667
Seq. No.
                    253417 1.R1011
 Contig ID
                    xmt700264224.h1
 5'-most EST
                    288668
 Seq. No.
                    253432 1.R1011
 Contig ID
                    ymt700219811.h1
 5'-most EST
 Seq. No.
                    288669
                    253598 1.R1011
 Contig ID
                    xsy700\overline{2}08945.h1
5'-most EST
 Seq. No.
                    288670
                    253657 1.R1011
 Contig ID
 5'-most EST
                    xmt700\overline{2}60342.h2
 Seq. No.
                    288671
 Contig ID
                    253658 1.R1011
 5'-most EST
                    hvj700621332.hl
                    288672
 Seq. No.
 Contig ID
                    253731 1.R1011
 5'-most EST
                    rvt700550817.h1
 Seq. No.
                    288673
 Contig ID
                    253762 1.R1011
                    nbm700475955.h1
 5'-most EST
```



```
% identity
                   PROBABLE COATOMER BETA SUBUNIT (BETA-COAT PROTEIN)
NCBI Description
                   (BETA-COP) >gi 1432173 (U62960) CopB [Dictyostelium
                   discoideum]
Seq. No.
                   288674
                   253823 1.R1011
Contig ID
                   ymt700\overline{2}20295.h1
5'-most EST
                   BLASTX
Method
                   g477094
NCBI GI
BLAST score
                   203
                   6.0e-16
E value
                   75
Match length
                   60
% identity
                   STE11 protein kinase homolog NPK1 - common tobacco
NCBI Description
                   288675
Seq. No.
                   253827 1.R1011
Contig ID
5'-most EST
                   ymt700220304.h1
                   BLASTX
Method
NCBI GI
                   g1707017
                   393
BLAST score
                   2.0e-38
E value
                   87
Match length
                   87
% identity
                  (U78721) RNA helicase isolog [Arabidopsis thaliana]
NCBI Description
                   288676
Seq. No.
                   253844 1.R1011
Contig ID
                   ymt700\overline{2}20322.h1
5'-most EST
                   288677
Seq. No.
                   253916 1.R1011
Contig ID
5'-most EST
                   ymt700\overline{2}20409.h1
                   288678
Seq. No.
                   253940 1.R1011
Contig ID
                   ymt700\overline{2}20439.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4006825
BLAST score
                   192
E value
                   1.0e-14
                   82
Match length
% identity
                    44
                   (AC005970) G9a-like protein [Arabidopsis thaliana]
NCBI Description
```

253959 1.R1011 Contig ID 5'-most EST $ymt700\overline{2}20460.h1$

288680 Seq. No.

254017 1.R1011 Contig ID 5'-most EST ymt700221302.hl

Seq. No. 288681

Contig ID 254052 1.R1011 bdu700382769.h1 5'-most EST



```
Method BLASTX
NCBI GI g1076725
BLAST score 155
E value 2.0e-10
Match length 79
% identity 56
NCBI Description NADPH de:
>gi_6834
[Hordeum
```

BI Description NADPH dehydrogenase (EC 1.6.99.1) - barley >gi 683476 emb CAA59228 (X84738) NADPH dehydrogenase

[Hordeum vulgare]

Seq. No. 288682

Contig ID 254054_1.R1011 5'-most EST xmt700266682.h1

Seq. No. 288683

Contig ID 254065_1.R1011 5'-most EST ceu700426203.h1

Seq. No.

288684

Contig ID 254219_1.R1011 5'-most EST ymt700220779.h1

Seq. No. 288685

Contig ID 254358_1.R1011 5'-most EST ymt700220960.h1

Method BLASTX
NCBI GI g2244749
BLAST score 554
E value 5.0e-57
Match length 147
% identity 67

NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 288686

Contig ID 254364_1.R1011 5'-most EST ymt700220969.h1

Method BLASTX
NCBI GI g2997589
BLAST score 516
E value 9.0e-53
Match length 109
% identity 90

NCBI Description (AF020813) glucose-6-phosphate/phosphate-translocator

precursor [Zea mays]

Seq. No. 288687

Contig ID 254423_1.R1011 5'-most EST ymt700221044.h1

Seq. No. 288688

Contig ID 254520 1.R1011 5'-most EST yyf700349616.h1

Seq. No. 288689

Contig ID 254609_1.R1011 5'-most EST ymt700223805.h1

Method BLASTX



```
g4153873
NCBI GI
                   163
BLAST score
                   2.0e-11
E value
Match length
                   77
                   45
% identity
NCBI Description
                   (AC004918) similar to weel-like protein kinase; similar to
                   P30291 (PID:g1351419) [Homo sapiens]
                   288690
Seq. No.
                   254704 1.R1011
Contig ID
5'-most EST
                   ymt700\overline{2}21409.h1
Method
                   BLASTX
                   g1091678
NCBI GI
BLAST score
                   355
                   8.0e-34
E value
                   123
Match length
                   59
% identity
                   activator-like transposable element [Pennisetum glaucum]
NCBI Description
Seq. No.
                   288691
                   254710 1.R1011
Contig ID
                   ymt700221416.h1
5'-most EST
Seq. No.
                   288692
                   254736 1.R1011
Contig ID
                   ymt700\overline{2}21449.h1
5'-most EST
                   288693
Seq. No.
                   254829 1.R1011
Contig ID
                   ymt700\overline{2}21568.h2
5'-most EST
                   BLASTX
Method
                   g2737882
NCBI GI
BLAST score
                   384
E value
                   3.0e-37
                   105
Match length
                   67
% identity
NCBI Description
                   (U46014) polyphenol oxidase [Saccharum sp.]
                   288694
Seq. No.
                   254837 1.R1011
Contig ID
5'-most EST
                   xmt700\overline{2}66336.h1
Seq. No.
                   288695
Contig ID
                   254851 1.R1011
5'-most EST
                   hbs701185111.h1
                   BLASTX
Method
NCBI GI
                   q4006861
BLAST score
                   450
E value
                   8.0e-45
Match length
                   137
% identity
```

NCBI Description

Contig ID 254885 1.R1011 5'-most EST nbm700476983.h1

(Z99707) tubulin-like protein [Arabidopsis thaliana]



Contig ID 254908_1.R1011 5'-most EST ymt700221684.h1

Seq. No. 288698

Contig ID 254931_1.R1011 5'-most EST ymt700221719.h1

Method BLASTN
NCBI GI g2832242
BLAST score 241
E value 1.0e-133
Match length 257
% identity 98

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 288699

Contig ID 254964_1.R1011 5'-most EST rvt700549823.h1

Seq. No. 288700

Contig ID 255062_1.R1011 5'-most EST xyt700347004.h1

Seq. No. 288701

Contig ID 255073_1.R1011 5'-most EST nbm700466155.h1

Method BLASTX
NCBI GI g1552169
BLAST score 478
E value 8.0e-48
Match length 234
% identity 42

NCBI Description (D42138) PIG-B [Homo sapiens]

Seq. No. 288702

Contig ID 255099_1.R1011 5'-most EST xmt700265848.h1

Seq. No. 288703

Contig ID 255110_1.R1011 5'-most EST xmt700258744.h1

Seq. No. 288704

Contig ID 255119_1.R1011 5'-most EST xsy700211981.h1

Method BLASTX
NCBI GI g3522937
BLAST score 309
E value 1.0e-28
Match length 69
% identity 72

NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]

Seq. No. 288705

Contig ID 255152_1.R1011 5'-most EST ymt700222035.h1

Method BLASTX



NCBI GI g399213 BLAST score 241 E value 1.0e-20 Match length 88 % identity 60

NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG

CD4B PRECURSOR >gi_100190_pir__B35905 CD4B protein - tomato

>gi 170435 (M32604) ATP-dependent protease (CD4B)

[Lycopersicon esculentum]

Seq. No. 288706

Contig ID 255184_1.R1011 5'-most EST xsy700210568.h1

Method BLĀSTX
NCBI GI g417488
BLĀST score 631
E value 5.0e-66
Match length 133
% identity 87

NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE

H) >gi_100452_pir__A40995 starch phosphorylase (EC 2.4.1.1) H - potato >gi 169473 (M69038) alpha-glucan phosphorylase

type H isozyme [Solanum tuber sum]

Seq. No. 288707

Contig ID 255310_1.R1011 5'-most EST ymt700222228.h1

Method BLASTX
NCBI GI g4539334
BLAST score 146
E value 2.0e-09
Match length 40
% identity 62

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 288708

Contig ID 255354_2.R1011 5'-most EST rvt700553157.h1

Seq. No. 288709

Contig ID 255393_1.R1011 5'-most EST vux700157806.h1

Method BLASTX
NCBI GI 9400983
BLAST score 476
E value 6.0e-48
Match length 107
% identity 81

NCBI Description 50S RIBOSOMAL PROTEIN L11, CHLOROPLAST PRECURSOR (CL11)

>gi_279648_pir__R5SP11 ribosomal protein L11 precursor spinach >gi_21313_emb_CAA39950_ (X56615) ribosomal protein

L11 [Spinacia oleracea]

Seq. No. 288710

Contig ID 255525 1.R1011 5'-most EST ymt700222560.h1

NCBI Description

oleracea]



```
Seq. No.
                   288711
Contig ID
                  255543 1.R1011
5'-most EST
                  ceu700\overline{421913.h1}
Method
                  BLASTX
NCBI GI
                  g1652057
BLAST score
                  140
                   9.0e-09
E value
Match length
                   65
% identity
NCBI Description
                  (D90902) hypothetical protein [Synechocystis sp.]
                  288712
Seq. No.
Contig ID
                  255559 1.R1011
5'-most EST
                  hbs701184517.h1
Method
                  BLASTX
NCBI GI
                  q4522009
BLAST score
                  226
E value
                   6.0e-38
Match length
                   145
                   51
% identity
NCBI Description (AC007069) unknown protein [Arabidopsis thaliana]
                   288713
Seq. No.
Contig ID
                   255607 1.R1011
5'-most EST
                  ymt700222669.h1
Seq. No.
                   288714
Contig ID
                   255648 1.R1011
5'-most EST
                  xmt700258737.h1
Seq. No.
                   288715
Contig ID
                   255657 1.R1011
5'-most EST
                   rvt700553159.h1
Method
                  BLASTX
NCBI GI
                   g1369852
BLAST score
                   313
E value
                   9.0e-29
Match length
                   148
% identity
                   48
NCBI Description
                   (L46702) kinesin heavy chain-like protein [Solanum
                   tuberosum]
                   288716
Seq. No.
                   255701 1.R1011
Contig ID
5'-most EST
                   ymt700222819.hl
Seq. No.
                   288717
                   255781 1.R1011
Contig ID
5'-most EST
                   vux700157453.h1
Method
                  BLASTX
NCBI GI
                   g1924972
BLAST score
                   538
                   4.0e-55
E value
                   139
Match length
% identity
                   76
                   (U52048) polyribonucleotide phophorylase [Spinacia
```



```
288718
Seq. No.
Contig ID
                  255818 1.R1011
5'-most EST
                  ymt700222968.h1
Method
                  BLASTX
NCBI GI
                  q586761
BLAST score
                  177
E value
                  7.0e-13
Match length
                  110
                  37
% identity
NCBI Description
                  HYPOTHETICAL 83.1 KD PROTEIN IN COB-ATPA INTERGENIC REGION
                  (ORF 732) >gi 282783 pir S25995 hypothetical protein 732 -
                  liverwort (Marchantia polymorpha) mitochondrion >gi_786228
                  (M68929) ORF732 [Marchantia polymorpha]
Seq. No.
                  288719
Contig ID
                  255875 1.R1011
5'-most EST
                  ymt700223050.h1
Method
                  BLASTX
NCBI GI
                  g1653089
BLAST score
                  242
E value
                  2.0e-20
                  103
Match length
% identity
                  (D90911) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                  288720
Contig ID
                  255914 1.R1011
5'-most EST
                  wuj700282006.h1
Method
                  BLASTX
NCBI GI
                  q1170619
BLAST score
                  470
E value
                  4.0e-47
Match length
                  150
% identity
NCBI Description
                  KINESIN-LIKE PROTEIN A >gi 479594 pir S34830
                  kinesin-related protein katA - Arabidopsis thaliana
                  >gi 303502 dbj BAA01972 (D11371) kinesin-like motor
                  protein heavy chain [Arabidopsis thaliana]
                  >gi 2911084 emb CAA17546.1 (AL021960) kinesin-related
                  protein katA [Arabidopsis thaliana]
Seq. No.
                  288721
                  255932 1.R1011
Contig ID
5'-most EST
                  xmt700264329.h1
Method
                  BLASTX
NCBI GI
                  g1362615
BLAST score
                  269
                  6.0e-24
E value
Match length
                  91
                  57
% identity
NCBI Description
                  iswi protein - fruit fly (Drosophila melanogaster)
```

Contig ID 255941_1.R1011 5'-most EST ymt700223126.h1

>gi 439197 (L27127) ISWI protein [Drosophila melanogaster]



```
288723
Seq. No.
Contig ID
                  255954 1.R1011
5'-most EST
                  ymt700223140.h1
Method
                  BLASTX
NCBI GI
                  q3152613
BLAST score
                  218
                   9.0e-18
E value
                   105
Match length
                   45
% identity
                  (AC004482) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   288724
Seq. No.
Contig ID
                   255958 1.R1011
5'-most EST
                  nbm700470979.h1
Seq. No.
                   288725
Contig ID
                   255992 1.R1011
5'-most EST
                   ymt700223187.h1
                   288726
Seq. No.
Contig ID
                   256076 1.R1011
                   wty700165882.h1
5'-most EST
                   288727
Seq. No.
Contig ID
                   256132 1.R1011
5'-most EST
                   nbm700476276.h1
Method
                   BLASTX
NCBI GI
                   g2981463
BLAST score
                   269
E value
                   7.0e-24
Match length
                   97
% identity
                   51
                   (AF052663) gamma-tubulin interacting protein [Xenopus
NCBI Description
                   laevis]
Seq. No.
                   288728
                   256169 1.R1011
Contig ID
5'-most EST
                   gw1700612850.hl
                   288729
Seq. No.
                   256182 1.R1011
Contig ID
5'-most EST
                   xyt700345584.h1
Method
                   BLASTX
                   g3123908
NCBI GI
                   406
BLAST score
                   8.0e-40
E value
                   118
Match length
% identity
                   65
                   (AF038392) pre-mRNA splicing factor [Homo sapiens]
NCBI Description
Seq. No.
                   288730
```

Contig ID 256238_1.R1011 5'-most EST ymt700223563.h1

Seq. No. 288731

Contig ID 256324_2.R1011



```
5'-most EST
                   rvt700551917.h1
Method
                   BLASTX
NCBI GI
                   q3676069
BLAST score
                   359
E value
                   2.0e-34
Match length
                   83
% identity
NCBI Description (Y17899) ERG protein [Antirrhinum majus]
                   288732
Seq. No.
Contig ID
                   256382 1.R1011
5'-most EST
                   ymt700\overline{2}23682.h1
                   BLASTX
Method
NCBI GI
                   q4585979
BLAST score
                   168
E value
                   6.0e-15
Match length
                   86
% identity
                   58
                   (AC005287) Similar to ABC-transporter atp-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   288733
Seq. No.
                   256389 1.R1011
Contig ID
                   ymt700223691.h1
5'-most EST
Seq. No.
                   288734
Contig ID
                   256477 1.R1011
5'-most EST
                   uer700580522.h1
Seq. No.
                   288735
Contig ID
                   256482 1.R1011
5'-most EST
                   xyt700342443.h1
Seq. No.
                   288736
Contig ID
                   256515 1.R1011
5'-most EST
                   ymt700223849.h1
Seq. No.
                   288737
Contig ID
                   256565 1.R1011
5'-most EST
                   ymt700224424.h1
Seq. No.
                   288738
Contig ID
                   256582 1.R1011
5'-most EST
                   ymt700223926.h1
Seq. No.
                   288739
Contig ID
                   256619 1.R1011
5'-most EST
                   nbm700465028.h1
Seq. No.
                   288740
Contig ID
                   256633 1.R1011
```

5'-most EST $nbm700\overline{4}76258.h1$ Method BLASTX

g4455323 NCBI GI BLAST score 168 E value 5.0e-12 Match length 95



% identity NCBI Description

(AL035525) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No. Contig ID 288741

5'-most EST

256651 1.R1011 $ymt700\overline{2}24013.h1$

Method NCBI GI BLAST score BLASTX q2500542 221

E value Match length 5.0e-18

% identity

103 39

NCBI Description

PUTATIVE ATP-DEPENDENT RNA HELICASE YMR128W

>gi_1078577_pir__S53058 probable membrane protein YMR128w yeast (Saccharomyces cerevisiae) >gi_728667_emb_CAA88553_

(Z48622) unknown [Saccharomyces cerevisiae]

Seq. No.

288742

Contig ID 5'-most EST 256661 1.R1011 ymt700224026.h1

Seq. No. Contig ID 288743

5'-most EST

256674 1.R1011 $ymt700\overline{2}24041.h1$

Seq. No.

288744

Contig ID 5'-most EST 256677 1.R1011 $ymt700\overline{2}24044.h1$

BLASTX Method NCBI GI g1169128 199 BLAST score E value Match length

1.0e-23 62

% identity NCBI Description

SERINE/THREONINE-PROTEIN KINASE CTR1 >gi 166680 (L08789)

protein kinase [Arabidopsis thaliana] >gi 166682 (L08790)

protein kinase [Arabidopsis thaliana]

Seq. No.

Contig ID 5'-most EST 288745

256737 1.R1011 ymt700224117.h1

Seq. No.

288746

Contig ID 5'-most EST 256755 1.R1011 $xsy700\overline{2}07385.h1$

Seq. No.

288747

Contig ID 5'-most EST 256824 1.R1011 hbs701181145.hl

Seq. No.

288748

Contig ID 5'-most EST 256854 1.R1011 $xyt700\overline{3}44062.h1$

Seq. No. Contig ID 288749

257095 1.R1011

ymt700224577.h1 5'-most EST BLASTX Method g2821957 NCBI GI 374 BLAST score 3.0e-36 E value Match length 95 % identity (AB006691) spermidine synthase 2 [Hyoscyamus niger] NCBI Description 288750 Seq. No. 257109 1.R1011 Contig ID ymt700224601.hl 5'-most EST 288751 Seq. No. 257240 1.R1011 Contig ID ymt700224783.hl 5'-most EST BLASTX Method g1172633 NCBI GI BLAST score 184 8.0e-14 E value 55 Match length 62 % identity PROLIFERA PROTEIN >gi 675491 (L39954) contains MCM2/3/5 NCBI Description family signature; PROSITE; PS00847; disruption leads to early lethal phenotype; similar to MCM2/3/5 family, most similar to YBR1441 [Arabidopsis thaliana] 288752 Seq. No. 257270 1.R1011 Contig ID 5'-most EST ymt700224826.h1 288753 Seq. No. 257296 1.R1011 Contig ID xtj700378222.h1 5'-most EST 288754 Seq. No. 257353 1.R1011 Contig ID 5'-most EST $xyt700\overline{3}45347.h1$ BLASTX Method

Method BLASTX
NCBI GI g3650033
BLAST score 146
E value 3.0e-09
Match length 69
% identity 41

NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]

Seq. No. 288755

Contig ID 257383_1.R1011 5'-most EST ceu700427125.h1

Seq. No. 288756

Contig ID 257400_1.R1011 5'-most EST fdz701161128.h1

Seq. No. 288757

Contig ID 257479 1.R1011 5'-most EST vux700156403.h1



Contig ID 257482 1.R1011 5'-most EST vux700156407.h1

Seq. No. 288759

Contig ID 257488_1.R1011 5'-most EST vux700156870.h1

Method BLASTX
NCBI GI g102280
BLAST score 308
E value 2.0e-28
Match length 76
% identity 16

NCBI Description ubiquitin 19 - slime mold (Dictyostelium discoideum)

Seq. No. 288760

Contig ID 257495_1.R1011 5'-most EST gct701173468.h2

Seq. No. 288761

Contig ID 257526_1.R1011 5'-most EST vux700156469.h1

Seq. No. 288762

Contig ID 257548_1.R1011 5'-most EST vux700159435.h1

Seq. No. 288763

Contig ID 257551_1.R1011 5'-most EST vux700156517.h1

Method BLASTN
NCBI GI g924952
BLAST score 77
E value 2.0e-35
Match length 217
% identity 88

NCBI Description Triticum aestivum beta 1,3-glucanase (Glc1) mRNA, complete

cds

Seq. No. 288764

Contig ID 257598 1.R1011 5'-most EST gct701176493.h1

Seq. No. 288765

Contig ID 257610_1.R1011 5'-most EST vux700156621.h1

Seq. No. 288766

Contig ID 257700 1.R1011 5'-most EST vux700156762.h1

Method BLASTX
NCBI GI g2464865
BLAST score 290
E value 2.0e-26
Match length 80
% identity 65



NCBI Description (Z99707) pectinesterase like protein [Arabidopsis thaliana]

Seq. No. 288767

Contig ID 257704_1.R1011 5'-most EST vux700161346.h1

Seq. No. 288768

Contig ID 257820_1.R1011 5'-most EST vux700159716.h1

Seq. No. 288769

Contig ID 257840_1.R1011 5'-most EST pwr700451270.h1

Seq. No. 288770

Contig ID 257936_1.R1011 5'-most EST xsy700213336.h1

Seq. No. 288771

Contig ID 257963_1.R1011 5'-most EST vux700158688.h1

Seq. No. 288772

Contig ID 257996_1.R1011 5'-most EST vux700157182.h1

Method BLASTX
NCBI GI g4204304
BLAST score 210
E value 1.0e-16
Match length 117
% identity 39

NCBI Description (AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 288773

Contig ID 257997 1.R1011 5'-most EST vux700157183.h1

Seq. No. 288774

Contig ID 258028 1.R1011 5'-most EST fdz701161486.h1

Method BLASTX
NCBI GI g3522938
BLAST score 276
E value 3.0e-24
Match length 160
% identity 42

NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]

Seq. No. 288775

Contig ID 258030_1.R1011 5'-most EST gct701168774.h1

Method BLASTX
NCBI GI g2146739
BLAST score 294
E value 2.0e-26
Match length 122



 Seq. No.
 288776

 Contig ID
 258067_1.R1011

 5'-most EST
 wty700168187.h1

 Method
 BLASTX

NCBI GI g4490708 BLAST score 410 E value 6.0e-40 Match length 119 % identity 73

NCBI Description (AL035680) putative protein [Arabidopsis thaliana]

Seq. No. 288777 Contig ID 258070

Contig ID 258070_1.R1011 5'-most EST gct701179125.h1

Seq. No. 288778

Contig ID 258073 1.R1011 5'-most EST vux700157288.h1

Method BLASTX
NCBI GI g3080415
BLAST score 327
E value 2.0e-30
Match length 135
% identity 51

NCBI Description (AL022604) cysteine proteinase-like protein [Arabidopsis

thaliana]

Seq. No. 288779

Contig ID 258088 1.R1011 5'-most EST vux700157319.h1

Seq. No. 288780

Contig ID 258092 1.R1011 5'-most EST vux700\overline{1}57324.h1

Seq. No. 288781

Contig ID 258117_1.R1011 5'-most EST vux700157356.h1

Seq. No. 288782

Contig ID 258147_1.R1011 5'-most EST vux700157405.h1

Seq. No. 288783

Contig ID 258205 1.R1011 5'-most EST fdz701166120.h1

Seq. No. 288784

Contig ID 258214_1.R1011 5'-most EST rvt700551489.h1 Method BLASTX

Method BLASTX
NCBI GI g2135057
BLAST score 194



E value 8.0e-15 Match length 147 % identity 35

NCBI Description EB1 - human >gi 998357 (U24166) EB1 [Homo sapiens]

Seq. No. 288785

Contig ID 258231_1.R1011 5'-most EST vux700160966.h1

Seq. No. 288786

Contig ID 258255_1.R1011 5'-most EST mwy700440875.h1

Seq. No. 288787

Contig ID 258304_1.R1011 5'-most EST vux700157653.h1

Seq. No. 288788

Contig ID 258330_1.R1011 5'-most EST vux700161866.h1

Seq. No. 288789

Contig ID 258354_1.R1011 5'-most EST uer700578878.h1

Seq. No. 288790

Contig ID 258420_1.R1011 5'-most EST tfd700571921.h1

Seq. No. 288791

Contig ID 258429_1.R1011 5'-most EST vux700157842.h1

Seq. No. 288792

Contig ID 258444_1.R1011 5'-most EST tfd700569451.h2

Seq. No. 288793

Contig ID 258470_1.R1011 5'-most EST vfk700404767.h1

Method BLASTX
NCBI GI g4324470
BLAST score 182
E value 1.0e-13
Match length 93
% identity 45

NCBI Description (AF105010) LAG1Ce-1 [Caenorhabditis elegans]

Seq. No. 288794

Contig ID 258532_1.R1011 5'-most EST sem700930287.h1

Seq. No. 288795

Contig ID 258552_1.R1011 5'-most EST sem700930295.h1

Method BLASTX NCBI GI g2494223



BLAST score 163 E value 2.0e-11 Match length 53 % identity 55

NCBI Description

DYNEIN LIGHT CHAIN 1, CYTOPLASMIC >gi_1209059 (U32855) cytoplasmic dynein light chain 1 [Drosophila melanogaster] >gi_4097197 (U48846) 8kd dynein light chain [Drosophila melanogaster] >gi_4097201 (U48848) 8kd dynein light chain [Drosophila melanogaster]

Seq. No. 288796

Contig ID 258575_1.R1011 5'-most EST nbm700465002.h1

Method BLASTX
NCBI GI g1167953
BLAST score 146
E value 2.0e-09
Match length 82
% identity 37

NCBI Description (U43496) putative 32.6 kDa jasmonate-induced protein

[Hordeum vulgare] >gi_2465426 (AF021256) 32 kDa protein

[Hordeum vulgare]

Seq. No. 288797

Contig ID 258600_1.R1011 5'-most EST vux700158075.h1

Method BLASTX
NCBI GI g3914006
BLAST score 383
E value 3.0e-37
Match length 79
% identity 99

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi_1816588

(U85495) LON2 [Zea mays]

Seq. No. 288798

Contig ID 258635_1.R1011 5'-most EST uer700582970.h1

Method BLASTX
NCBI GI g3024871
BLAST score 259
E value 2.0e-22
Match length 117
% identity 46

NCBI Description HYPOTHETICAL 77.3 KD PROTEIN SLL0005

>gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis

sp.]

Seq. No. 288799

Contig ID 258738_1.R1011 5'-most EST fdz701158559.h1

Seq. No. 288800

Contig ID 258753_1.R1011 5'-most EST vux700158294.h1

Seq. No. 288801



```
258766 1.R1011
Contig ID
                  gct701170941.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4567310
BLAST score
                  217
                  7.0e-18
E value
Match length
                  55
% identity
                  80
                  (AC005956) unknown protein [Arabidopsis thaliana]
NCBI Description
                  288802
Seq. No.
                  258835 1.R1011
Contig ID
                  wty700170415.h1
5'-most EST
                   288803
Seq. No.
                   258936 1.R1011
Contig ID
                  wty700169601.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                   g3123155
BLAST score
                   184
E value
                   1.0e-13
                   143
Match length
                   29
% identity
                  HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN
NCBI Description
                   F55F8.5 IN CHROMOSOME I >gi_1707049 (U80447) similar to the
                   beta transducin family [Caenorhabditis elegans]
                   288804
Seq. No.
                   258995 1.R1011
Contig ID
                   hvj700622327.hl
5'-most EST
Seq. No.
                   288805
                   259009 1.R1011
Contig ID
                   ceu700429203.h1
5'-most EST
Seq. No.
                   288806
                   259023 1.R1011
Contiq ID
5'-most EST
                   vux700\overline{1}58689.h1
                   BLASTX
Method
                   q730431
NCBI GI
BLAST score
                   224
E value
                   1.0e-18
Match length
                   94
% identity
                   PERIODIC TRYPTOPHAN PROTEIN 2 >qi 626864 pir S44226 PWP2
NCBI Description
                   protein - yeast (Saccharomyces cerevisiae)
                   >qi 475231 emb CAA55558 (X78964) periodic tryptophan
                   protein 2 [Saccharomyces cerevisiae]
                   >gi 1907198 emb CAA42286 (X59720) YCR057c, len:923
                   [Saccharomyces cerevisiae]
```

Contig ID 25914 5'-most EST vux70 Method BLAST

259143_1.R1011 vux700159001.h1 BLASTX

NCBI GI g4249662 BLAST score 501



E value 9.0e-51 Match length 150 % identity 63

NCBI Description (AF089810) Altered Response to Gravity [Arabidopsis

thaliana]

Seq. No. 288808

Contig ID 259144_1.R1011 5'-most EST ceu700423858.h1

Seq. No. 288809

Contig ID 259238_1.R1011 5'-most EST vux700159151.h1

Method BLASTN
NCBI GI g433043
BLAST score 42
E value 2.0e-14
Match length 62
% identity 94

NCBI Description Zea mays W-22 clone PREM-1E retroelement PREM-1, partial

sequence

Seq. No. 288810

Contig ID 259254_1.R1011 5'-most EST vux700159175.h1

Method BLASTX
NCBI GI g2213632
BLAST score 394
E value 2.0e-38
Match length 105
% identity 63

NCBI Description (AC000103) F21J9.24 [Arabidopsis thaliana]

Seq. No. 288811

Contig ID 259272_1.R1011 5'-most EST rv1700456781.h1

Method BLASTX
NCBI GI g3157933
BLAST score 146
E value 4.0e-09
Match length 130
% identity 28

NCBI Description (AC002131) Contains similarity to box helicases gb_U29097

from C. elegans and to the ENBP1 gene product gb X95995

from Vicia sativa. [Arabidopsis thaliana]

Seq. No. 288812

Contig ID 259324_1.R1011 5'-most EST vux700160427.h1

Seq. No. 288813

Contig ID 259326_1.R1011 5'-most EST rvt700550614.h1

Seq. No. 288814

Contig ID 259351 1.R1011 5'-most EST hbs701186181.h1



```
288815
Seq. No.
                   259352 1.R1011
Contig ID
                  vux700159348.hl
5'-most EST
                   288816
Seq. No.
                   259355 1.R1011
Contig ID
5'-most EST
                   nwy700446049.h1
Seq. No.
                   288817
                   259395 1.R1011
Contig ID
                   vux700159425.h1
5'-most EST
Method
                   BLASTX
                   g3059131
NCBI GI
BLAST score
                   176
                   6.0e-13
E value
                   75
Match length
                   47
% identity
NCBI Description (AJ000478) cytochrome P450 [Helianthus tuberosus]
                   288818
Seq. No.
                   259429 1.R1011
Contig ID
                   tfd700571736.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4262225
BLAST score
                   157
E value
                   9.0e-11
                   53
Match length
% identity
                   51
                   (AC006200) putative phosphatidic acid phosphatase
NCBI Description
                   [Arabidopsis thaliana]
                   288819
Seq. No.
                   259450 1.R1011
Contig ID
                   ceu700\overline{4}29964.h1
5'-most EST
                   BLASTX
Method
                   g4406773
NCBI GI
                   204
BLAST score
                   2.0e-16
E value
                   57
Match length
                   63
% identity
                   (AC006836) putative cell division control protein 48
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   288820
                   259477 1.R1011
Contig ID
                   vux700159551.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3341679
                   328
BLAST score
                   6.0e-31
E value
Match length
                   81
                   78
% identity
```

NCBI Description

40185

[Arabidopsis thaliana]

(AC003672) dynamin-like protein phragmoplastin 12

% identity



```
259479 1.R1011
Contig ID
                   nbm700\overline{4}70690.h1
5'-most EST
                                      . P.
                   288822
Seq. No.
                   259539 1.R1011
Contig ID
                   gct701172425.hl
5'-most EST
                   288823
Seq. No.
                   259588 1.R1011
Contig ID
                   vux700159710.h1
5'-most EST
                   288824
Seq. No.
                   259617 1.R1011
Contig ID
                   vux700159748.hl
5'-most EST
                   288825
Seq. No.
                   259710 1.R1011
Contig ID
                   ceu700\overline{4}30201.h1
5'-most EST
                   288826
Seq. No.
                   259747 1.R1011
Contig ID
                   vux700159941.h1
5'-most EST
                   BLASTX
Method
                   g3021270
NCBI GI
BLAST score
                   160
                   3.0e-11
E value
Match length
                   46
                   54
% identity
                    (AL022347) serine/threonine kinase -like protein
NCBI Description
                    [Arabidopsis thaliana]
                   288827
Seq. No.
                   259799_1.R1011
Contig ID
                   vux700160012.h1
5'-most EST
                    288828
Seq. No.
                   259956 1.R1011
Contig ID
                    ypc700803779.h1
5'-most EST
                   BLASTX
Method
                    g1136432
NCBI GI
                    150
BLAST score
                    2.0e-09
E value
                    109
Match length
                    33
% identity
                   (D80008) KIAA0186 [Homo sapiens]
NCBI Description
                    288829
Seq. No.
                    259994 1.R1011
Contig ID
                    cjh700194047.hl
5'-most EST
                    BLASTX
Method
                    q2956717
NCBI GI
                    359
BLAST score
                    2.0e-34
E value
                    92
Match length
```

NCBI Description (Y09722) beta-carotene hydroxylase 2 [Capsicum annuum]



```
288830
Seq. No.
                  260058 1.R1011
Contig ID
                  vux700161962.hl
5'-most EST
                  BLASTX
Method
                  g3218543
NCBI GI
                  321
BLAST score
                  3.0e-30
E value
Match length
                  74
% identity
                   (AB004813) alternative oxidase [Oryza sativa]
NCBI Description
                  >gi_3218548_dbj_BAA28774_ (AB004865) alternative oxidase
                   [Oryza sativa]
                   288831
Seq. No.
                   260125 1.R1011
```

Contig ID

vux700160436.h1 5'-most EST

288832 Seq. No. 260170 1.R1011 Contig ID vux700160489.h1 5'-most EST

288833 Seq. No. 260238 1.R1011 Contig ID vux700160580.h1 5'-most EST

Seq. No. 288834 260245 1.R1011 Contig ID pwr700450151.hl 5'-most EST

Seq. No. 288835 260407 1.R1011 Contig ID rv1700457593.h1 5'-most EST BLASTX Method

g3355480 NCBI GI BLAST score 185 4.0e-14 E value 89 Match length % identity

(AC004218) Medicago nodulin N21-like protein [Arabidopsis NCBI Description thaliana]

288836 Seq. No. 260516 1.R1011 Contig ID vux700160959.h1 5'-most EST BLASTX Method g585452 NCBI GI

143 BLAST score 3.0e-09 E value 27 Match length % identity

MALATE OXIDOREDUCTASE (NAD), MITOCHONDRIAL 59 KD ISOFORM NCBI Description PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME)

(NAD-ME) >gi 1076666 pir A53318 malate dehydrogenase (decarboxylating) (EC 1.1.1.39) 59K chain precursor, mitochondrial - potato >gi_438131_emb_CAA80547_ (Z23002) precursor of the 59kDa subunit of the mitochondrial

NAD+-dependent malic enzyme [Solanum tuberosum]



```
288837
Seq. No.
                  260586 2.R1011
Contig ID
                  gct701168835.hl
5'-most EST
                  BLASTN
Method
                  g535242
NCBI GI
                  76
BLAST score
                  7.0e-35
E value
                  107
Match length
                   93
% identity
NCBI Description O.sativa L. (Indica cv.IR24) U3 snRNA gene promoter
                   288838
Seq. No.
                   260607 1.R1011
Contig ID
                   vux700161114.h1
5'-most EST
                   288839
Seq. No.
                   260645 1.R1011
Contig ID
                   vux700161168.hl
5'-most EST
                   288840
Seq. No.
                   260670 1.R1011
Contig ID
                   wty700172123.h1
5'-most EST
                   BLASTX
Method
                   q1483218
NCBI GI
                   369
BLAST score
                   1.0e-35
E value
                   137
Match length
                   53
% identity
                   (X99793) induced upon wounding stress [Arabidopsis
NCBI Description
                   thaliana]
                   288841
Seq. No.
                   260699 1.R1011
Contig ID
                   vux700161661.h1
5'-most EST
                   288842
Seq. No.
                   260719 1.R1011
Contig ID
5'-most EST
                   mwy700442608.hl
                   288843
Seq. No.
                   260734 1.R1011
Contig ID
                   zuv700355961.h1
5'-most EST
Method
                   BLASTN
                   q4512570
NCBI GI
                   133
BLAST score
                   1.0e-68
E value
                   161
Match length
 % identity
                   Saccharum officinarum gene for 5S rRNA, repeat unit
NCBI Description
                   288844
 Seq. No.
```

Contig ID 260779_1.R1011 5'-most EST vux700161353.h1

Seq. No. 288845

Contig ID 260786 1.R1011



```
nwy700447826.h1
5'-most EST
                   288846
Seq. No.
                   260921 1.R1011
Contig ID
5'-most EST
                   fdz701161120.hl
Method
                  BLASTN
                   q1840117
NCBI GI
                   75
BLAST score
                   5.0e-34
E value
                   267
Match length
                   88
% identity
                   Zea mays PIF-12 transposable element in r-1 (r-p) locus,
NCBI Description
                   complete sequence
                   288847
Seq. No.
                   260954 1.R1011
Contig ID
                   vux700161637.h1
5'-most EST
                   BLASTX
Method
                   g3335354
NCBI GI
                   282
BLAST score
                   2.0e-25
E value
                   93
Match length
% identity
                   (AC004512) This gene is continued from gene F5I14.1 from
NCBI Description
                   BAC sequence gb AC001229 from A. thaliana. EST gb_AA585814
                   comes from this gene. [Arabidopsis thaliana]
                   288848
Seq. No.
                   261017 1.R1011
Contig ID
5'-most EST
                   xsy700217932.h1
                   288849
Seq. No.
Contig ID
                   261024 1.R1011
                   hbs701181039.h1
5'-most EST
                   288850
Seq. No.
                   261205 1.R1011
Contig ID
                   vux700161931.h1
5'-most EST
                   288851
Seq. No.
                   261418 1.R1011
Contig ID
                   nbm700464966.hl
5'-most EST
                   288852
Seq. No.
                   261546 1.R1011
Contig ID
                   wty700\overline{1}65479.h1
5'-most EST
                   BLASTX
Method
                   g2833379
NCBI GI
                   306
BLAST score
                   4.0e-28
E value
```

79 Match length % identity 75

RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 1 (PHOSPHORIBOSYL NCBI Description PYROPHOSPHATE SYNTHETASE 1) (PRS I) >gi_1076397_pir__S51270 ribose-phosphate pyrophosphokinase (EC 2.7.6.1) -Arabidopsis thaliana >gi_633140_emb_CAA58717_ (X83764) phosphoribosyl diphosphate synthetase [Arabidopsis



thaliana] >gi_3608149 (AC005314) phosphoribosyl diphosphate synthetase [Arabidopsis thaliana]

Seq. No. 288853

Contig ID 261587 1.R1011 5'-most EST wty700172973.h1

Seq. No. 288854

Contig ID 261620_1.R1011 5'-most EST wty700162666.h1

Seq. No. 288855

Contig ID 261700_1.R1011 5'-most EST wty700162821.h1

Method BLASTX
NCBI GI g3879165
BLAST score 351
E value 3.0e-33
Match length 108
% identity 68

NCBI Description (Z36238) similar to yeast hypothetical 83.2 KD protein

(Swiss Prot accession number P25582) [Caenorhabditis

elegans]

Seq. No. 288856

Contig ID 261732_1.R1011 5'-most EST uer700578877.h1

Seq. No. 288857

Contig ID 261785_1.R1011 5'-most EST wty700167937.h1

Seq. No. 288858

Contig ID 261787_1.R1011 5'-most EST zuv700355025.h1

Seq. No. 288859

Contig ID 261823_1.R1011 5'-most EST wty700162979.h1

Seq. No. 288860

Contig ID 261832_1.R1011 5'-most EST xyt700346822.h1

Method BLASTX
NCBI GI g2244854
BLAST score 169
E value 6.0e-12
Match length 90
% identity 43

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 288861

Contig ID 261833_1.R1011 5'-most EST wty700162995.h1

Seq. No. 288862

Contig ID 261836 1.R1011



```
wty700163003.h1
5'-most EST
                  BLASTX
Method
                  g2104908
NCBI GI
                  587
BLAST score
                  8.0e-61
E value
                  157
Match length
                   78
% identity
                  (Y07632) potassium channel [Zea mays]
NCBI Description
                   288863
Seq. No.
                   261883 1.R1011
Contig ID
5'-most EST
                   wty700166988.hl
                   288864
Seq. No.
                   261948 1.R1011
Contig ID
                   hbs701185440.hl
5'-most EST
                   BLASTX
Method
                   g4585872
NCBI GI
                   333
BLAST score
                   3.0e - 31
E value
Match length
                   112
                   59
% identity
NCBI Description (AC005850) Hypothetical protein [Arabidopsis thaliana]
                   288865
Seq. No.
                   261982 1.R1011
Contig ID
                   rvt700549655.hl
5'-most EST
                   288866
Seq. No.
                   262015 1.R1011
Contig ID
5'-most EST
                   xyt700343883.h1
                   288867
Seq. No.
                   262040 1.R1011
Contig ID
5'-most EST
                   xmt700263289.h1
                   288868
Seq. No.
                   262107 1.R1011
Contig ID
                   wty700171944.hl
5'-most EST
                   288869
Seq. No.
Contig ID
                   262111 1.R1011
5'-most EST
                   wty700163451.hl
Method
                   BLASTX
                   q3341679
NCBI GI
BLAST score
                   298
                   2.0e-27
E value
                   77
Match length
 % identity
                   74
                   (AC003672) dynamin-like protein phragmoplastin 12
NCBI Description
                   [Arabidopsis thaliana]
 Seq. No.
```

Contig ID

288870

262230 1.R1011 5'-most EST

wty700163612.hl

Seq. No.



```
262235 1.R1011
Contig ID
                   wty700163617.h1
5'-most EST
                   BLASTX
Method
                   g2829871
NCBI GI
                   339
BLAST score
                   5.0e-32
E value
                   111
Match length
                   53
% identity
                  (AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   288872
Seq. No.
                   262298 1.R1011
Contig ID
                   rvt700549385.h1
5'-most EST
Seq. No.
                   288873
                   262320 1.R1011
Contig ID
                   wty700163738.h1
5'-most EST
                   BLASTN
Method
                   g22176
NCBI GI
                   65
BLAST score
                   4.0e-28
E value
                   85
Match length
                   47
% identity
NCBI Description Z.mays P gene
                   288874
Seq. No.
                   262325 1.R1011
Contig ID
                   wty700163743.hl
5'-most EST
                   288875
Seq. No.
                   262362 1.R1011
Contig ID
5'-most EST
                   hvj700\overline{6}20952.h1
                   288876
Seq. No.
Contig ID
                   262373 1.R1011
5'-most EST
                   nbm700\overline{4}65042.h1
                   288877
Seq. No.
                   262382_1.R1011
Contig ID
5'-most EST
                   ceu700422228.h1
                   BLASTX
Method
                   q1001478
NCBI GI
                   205
BLAST score
                   5.0e-16
E value
Match length
                   99
                   45
% identity
                   (D63999) hypothetical protein [Synechocystis sp.]
NCBI Description
                   288878
Seq. No.
                   262383 1.R1011
Contig ID
5'-most EST
                   nbm700477363.hl
```

Seq. No. 288879

Contig ID 262449_1.R1011 5'-most EST wty700163911.h1

Method BLASTX NCBI GI g551535



```
BLAST score
                   1.0e-10
E value
Match length
                   60
% identity
                   47
                   (U14134) transcription factor IIIA [Homo sapiens]
NCBI Description
                   288880
Seq. No.
                   262467 1.R1011
Contig ID
                   wty700163933.hl
5'-most EST
Method
                   BLASTX
                   g3885340
NCBI GI
BLAST score
                   282
                   1.0e-25
E value
Match length
                   77
% identity
                   66
                   (AC005623) unknown protein [Arabidopsis thaliana]
NCBI Description
                   288881
Seq. No.
                   262488 1.R1011
Contig ID
                   gct701176085.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g99650
BLAST score
                   183
                   8.0e-14
E value
Match length
                   82
% identity
                   41
                   major storage protein - Carolina poplar
NCBI Description
                   >gi_237633_bbs_59423 (S59422) major storage protein [poplar
                   trees, xylem ray cells, Peptide, 329 aa] [poplar trees]
Seq. No.
                   288882
                   262501 1.R1011
Contig ID
                   wty700\overline{1}71727.h1
5'-most EST
                   288883
Seq. No.
Contig ID
                   262583 1.R1011
5'-most EST
                   wty700164713.h1
                   288884
Seq. No.
                   262627 1.R1011
Contig ID
                   nbm700\overline{4}66018.h1
5'-most EST
                   BLASTX
Method
                   g3935168
NCBI GI
BLAST score
                   299
                   5.0e-27
E value
Match length
                   150
% identity
                   46
                   (AC004557) F17L21.11 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   288885
Contig ID
                   262680 1.R1011
                   wty700\overline{1}64218.h1
5'-most EST
```

Seq. No. 288886

Contig ID 262731_1.R1011 5'-most EST ceu700424332.h1

Method BLASTX

% identity

NCBI Description

45



```
q1170921
NCBI GI
BLAST score
                  187
E value
                  1.0e-14
Match length
                  70
% identity
                  47
                  S-ADENOSYLMETHIONINE: 2-DEMETHYLMENAQUINONE
NCBI Description
                  METHYLTRANSFERASE >qi 1074428 pir G64153 hypothetical
                  protein HI0508 - Haemophilus influenzae (strain Rd KW20)
                  >qi 1573489 (U32732)
                  S-adenosylmethionine: 2-demethylmenaquinone
                  methyltransferase (menG) [Haemophilus influenzae Rd]
                  288887
Seq. No.
Contig ID
                  262736 1.R1011
5'-most EST
                  xsy700210007.h1
Method
                  BLASTX
NCBI GI
                  q3341672
BLAST score
                   358
                   3.0e - 34
E value
                   111
Match length
% identity
                   61
                   (AC003672) putative heme A: farnesyltransferase, 5' partial
NCBI Description
                   [Arabidopsis thaliana]
                   288888
Seq. No.
                   262811 1.R1011
Contig ID
5'-most EST
                  wty700164417.hl
                  BLASTN
Method
NCBI GI
                   q3821780
BLAST score
                   36
                   9.0e-11
E value
Match length
                   36
                   100
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   288889
Seq. No.
Contig ID
                   262826 1.R1011
                   ypc700806277.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g22220
                   153
BLAST score
E value
                   5.0e-10
                   30
Match length
% identity
                   100
                  (X55723) 22 kD zein [Zea mays]
NCBI Description
Seq. No.
                   288890
                   262841 1.R1011
Contig ID
5'-most EST
                   wty700164455.hl
Method
                   BLASTX
                   g3128231
NCBI GI
BLAST score
                   171
E value
                   1.0e-12
Match length
                   74
```

40194

(AC004077) hypothetical protein [Arabidopsis thaliana]

>gi 3337370 (AC004481) hypothetical protein [Arabidopsis

% identity

NCBI Description

56

[Arabidopsis thaliana]



thaliana]

```
288891
Seq. No.
                   262917 1.R1011
Contig ID
5'-most EST
                   gct701168875.h1
Method
                  BLASTX
                   q3237304
NCBI GI
                   362
BLAST score
                   2.0e-34
E value
                   131
Match length
% identity
                   (U91561) pyridoxine 5'-phosphate oxidase [Rattus
NCBI Description
                   norvegicus]
                   288892
Seq. No.
                   263061 1.R1011
Contig ID
                   wty700164803.hl
5'-most EST
                   BLASTX
Method
                   q2058273
NCBI GI
                   166
BLAST score
                   4.0e-12
E value
Match length
                   49
                   69
% identity
NCBI Description (D83527) YK426 [Oryza sativa]
                   288893
Seq. No.
                   263086 1.R1011
Contig ID
                   wty700164845.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4038042
                   629
BLAST score
                   8.0e-66
E value
Match length
                   141
% identity
                   (AC005936) putative DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   288894
Seq. No.
                   263114 1.R1011
Contig ID
                   wty700167555.hl
5'-most EST
                   288895
Seq. No.
Contig ID
                   263129 1.R1011
                   wty700164915.hl
5'-most EST
Seq. No.
                   288896
                   263170 1.R1011
Contig ID
                   hvj700619583.hl
5'-most EST
                   BLASTX
Method
                   g2342690
NCBI GI
                   342
BLAST score
                   2.0e-32
E value
Match length
                   109
```

(ACO00106) Similar to Homo copine I (gb_U83246).



```
Seq. No.
                   263215 1.R1011
Contig ID
5'-most EST
                   wty700165062.h1
                   288898
Seq. No.
Contig ID
                   263232 1.R1011
5'-most EST
                   xdb700\overline{3}39384.h1
                   BLASTX
Method
NCBI GI
                   g1653245
BLAST score
                   212
E value
                   4.0e-17
Match length
                   90
% identity
                   47
                   (D90912) hypothetical protein [Synechocystis sp.]
NCBI Description
                   288899
Seq. No.
                   263233 1.R1011
Contig ID
5'-most EST
                   wty700171240.h1
                   288900
Seq. No.
Contig ID
                   263252_1.R1011
5'-most EST
                   wty700165861.h1
Method
                   BLASTX
                   g4432860
NCBI GI
BLAST score
                   218
                   1.0e-36
E value
Match length
                   175
% identity
                   46
NCBI Description
                   (AC006300) putative glucose-induced repressor protein
                   [Arabidopsis thaliana]
Seq. No.
                   288901
Contig ID
                   263285 1.R1011
5'-most EST
                   yyf700351145.hl
Seq. No.
                   288902
                   263354 1.R1011
Contig ID
5'-most EST
                   wen700333074.h1
Seq. No.
                   288903
                   263368 1.R1011
Contig ID
5'-most EST
                   xsy700211246.h1
Seq. No.
                   288904
Contig ID
                   263377 1.R1011
5'-most EST
                   wty700\overline{1}65357.h1
Seq. No.
                   288905
                   263431 1.R1011
Contig ID
5'-most EST
                   wty700170775.h1
                   288906
Seq. No.
```

263505 1.R1011 Contig ID 5'-most EST wty700171751.hl

Seq. No. 288907

263529 1.R1011 Contig ID



```
5'-most EST
                   rvt700549591.h1
Method
                   BLASTX
NCBI GI
                   q3738297
BLAST score
                   167
E value
                   6.0e-12
Match length
                   78
% identity
NCBI Description
                   (AC005309) unknown protein [Arabidopsis thaliana]
                   288908
Seq. No.
Contig ID
                   263551 1.R1011
5'-most EST
                   ceu700430248.h1
                   288909
Seq. No.
                   263609 1.R1011
Contig ID
5'-most EST
                   wty700165734.h1
Seq. No.
                   288910
                   263661 1.R1011
Contig ID
                   wen700\overline{3}36454.h1
5'-most EST
Method
                   BLASTX
                   g114089
NCBI GI
BLAST score
                   410
E value
                   6.0e-41
Match length
                   97
% identity
                   84
NCBI Description
                   RAS-RELATED PROTEIN ARA-4 >gi 81633 pir JS0641 GTP-binding
                   protein ara-4 - Arabidopsis thaliana
                   >gi_217839_dbj_BAA00831_ (D01026) small GTP-binding protein
                   [Arabidopsis thaliana] >gi 3763922 (AC004450) GTP-binding
                   protein [Arabidopsis thaliana]
Seq. No.
                   288911
Contig ID
                   263667 1.R1011
5'-most EST
                   wty700165825.hl
Seq. No.
                   288912
Contig ID
                   263695 1.R1011
5'-most EST
                   rvt700551763.h1
Method
                   BLASTX
NCBI GI
                   q2498882
BLAST score
                   284
E value
                   2.0e-25
Match length
                   139
% identity
NCBI Description
                   SPLICEOSOME ASSOCIATED PROTEIN 114 (SAP 114) (SF3A120)
                   >gi_2146975_pir__S60735 splicing factor SF3a 120K chain -
                   human >gi_899298 emb CAA59494 (X85237) human splicing factor [Homo sapiens] >gi_3212998 (AC004997) spliceosome
                   associated protein 114 (SF3a) [Homo sapiens]
```

288913 Seq. No. 263698 1.R1011 Contig ID 5'-most EST wty700165892.h1 Method BLASTX NCBI GI g4587556

BLAST score 523



E value 2.0e-53 Match length 123 % identity

73

(AC006577) Similar to gi_1653162 (p)ppGpp NCBI Description

3-pyrophosphohydrolase from Synechocystis sp genome gb D90911. EST gb W43807 comes from this gene.

[Arabidopsis thaliana]

Seq. No.

Contig ID 5'-most EST

288914 263760 1.R1011 wty700165945.hl

Method BLASTX NCBI GI g2911280 BLAST score 387 1.0e-37 E value Match length 103 % identity 69

NCBI Description (U73937) PK12 protein kinase [Nicotiana tabacum]

Seq. No.

288915

Contig ID 5'-most EST

263783_1.R1011 $wty700\overline{1}72467.h1$

Seq. No.

288916

Contig ID 5'-most EST

263803 1.R1011 $pwr700\overline{4}53451.h1$

Seq. No.

288917

Contig ID 5'-most EST

263841 1.R1011 xmt700258905.h1

Seq. No.

288918

Contig ID 5'-most EST 263872 1.R1011 ypc700805272.h1

Seq. No.

288919

Contig ID 5'-most EST 263968 1.R1011 wty700166245.h1

Seq. No.

288920

Contig ID 5'-most EST 264043 1.R1011 $nbm700\overline{4}76810.h1$

Seq. No.

288921

Contig ID 5'-most EST 264154 1.R1011 wty700166487.h1

Seq. No.

288922

Contig ID 5'-most EST 264289 1.R1011 wty700166681.h1

Seq. No.

288923

Contig ID

264292 1.R1011 $xmt700\overline{2}60906.h1$

5'-most EST

Seq. No. Contig ID 288924 264306 1.R1011

Seq. No.

Contig ID

288931

264444 1.R1011



```
5'-most EST
                  wty700166707.hl
Method
                  BLASTX
NCBI GI
                  q4567281
BLAST score
                  153
                  3.0e-10
E value
Match length
                  52
% identity
                  50
NCBI Description
                  (AC006841) unknown protein [Arabidopsis thaliana]
                  288925
Seq. No.
Contig ID
                  264309 1.R1011
5'-most EST
                  fdz701166294.h1
Seq. No.
                  288926
Contig ID
                  264332 1.R1011
5'-most EST
                  rvt700548873.h1
Method
                  BLASTX
                  g1076742
NCBI GI
BLAST score
                  786
E value
                  4.0e-84
Match length
                  173
% identity
                  88
NCBI Description cyclin - rice >gi_558621_emb_CAA57555_ (X82035) cyclin
                  [Oryza sativa]
Seq. No.
                  288927
                  264369_1.R1011
Contig ID
5'-most EST
                  nbm700472485.h1
Method
                  BLASTX
NCBI GI
                  q2281090
BLAST score
                  292
E value
                  2.0e-26
Match length
                  118
% identity
                  47
NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  288928
Contig ID
                  264398 1.R1011
5'-most EST
                  wty700166840.h1
Seq. No.
                  288929
Contig ID
                  264417 1.R1011
5'-most EST
                  gct701172649.h1
Method
                  BLASTX
NCBI GI
                  q3953470
BLAST score
                  226
E value
                  9.0e-19
Match length
                  82
% identity
                  49
NCBI Description (AC002328) F20N2.15 [Arabidopsis thaliana]
Seq. No.
                  288930
Contig ID
                  264426 1.R1011
5'-most EST
                  wty700166876.h1
```



```
5'-most EST
                   xmt700257282.h1
Method
                   BLASTX
                   a4249382
NCBI GI
                   244
BLAST score
                   3.0e-21
E value
                   62
Match length
% identity
                   69
                   (AC005966) Strong similarity to gi_3337350 F13P17.3
NCBI Description
                   putative permease from Arabidopsis thaliana BAC
                   gb AC004481. [Arabidopsis thaliana]
Seq. No.
                   288932
Contig ID
                   264462 1.R1011
                   pwf700321724.h1
5'-most EST
Method
                   BLASTX
                   q2145356
NCBI GI
BLAST score
                   486
E value
                   4.0e-49
Match length
                   136
% identity
                   68
                   (Y11122) HD-Zip protein [Arabidopsis thaliana] >gi 3132474
NCBI Description
                   (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]
Seq. No.
                   288933
                   264486 1.R1011
Contig ID
5'-most EST
                   wty700166980.h1
Seq. No.
                   288934
Contig ID
                   264493 1.R1011
5'-most EST
                   afb700\overline{3}81685.h1
                   288935
Seq. No.
Contig ID
                   264555 1.R1011
5'-most EST
                   xsy700\overline{2}09102.h1
                   288936
Seq. No.
Contig ID
                   264679 1.R1011
5'-most EST
                   xyt700346258.h1
                   288937
Seq. No.
                   264717 1.R1011
Contig ID
5'-most EST
                   rvt700550252.hl
Seq. No.
                   288938
                   264777 1.R1011
Contig ID
5'-most EST
                   wty700167383.h1
Seq. No.
                   288939
                   264779 1.R1011
Contig ID
5'-most EST
                   wty700168840.h1
                   BLASTX
Method
NCBI GI
                   g4508069
```

Method BLASTX
NCBI GI g4508069
BLAST score 334
E value 2.0e-31
Match length 104
% identity 61

NCBI Description (AC005882) 12246 [Arabidopsis thaliana]



288940 Seq. No. Contig ID 264863 1.R1011 5'-most EST wty700167489.hl Method BLASTX NCBI GI g4038035 BLAST score 170 E value 2.0e-12 47 Match length 74 % identity NCBI Description (AC005936) putative DNA-binding protein [Arabidopsis thaliana] Seq. No. 288941 Contig ID 264937 1.R1011 5'-most EST wty700172920.h1 Method BLASTX g3250675 NCBI GI BLAST score 157 E value 9.0e-11 Match length 88 40 % identity NCBI Description (AL024486) putative protein [Arabidopsis thaliana] 288942 Seq. No. Contig ID 264982 1.R1011 5'-most EST wty700172131.h1 Seq. No. 288943 Contig ID 265032 1.R1011 5'-most EST wty700171763.hl Seq. No. 288944 265038 1.R1011 Contig ID 5'-most EST wty700167733.hl Method BLASTX NCBI GI q118390 BLAST score 590 E value 3.0e-61 Match length 144 % identity 79 NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC) >gi 2144526 pir DCZMP pyruvate decarboxylase (EC 4.1.1.1) - maize >gi 22395 emb CAA42120 (X59546) pyruvate decarboxylase [Zea mays] 288945 Seq. No. Contig ID 265059 1.R1011 5'-most EST tfd700569434.h2

Seq. No. 288946

Contig ID 265083 1.R1011 5'-most EST gwl700617306.h1

Method BLASTX
NCBI GI g3834302
BLAST score 384
E value 2.0e-37



Match length 83
% identity 88
NCBI Description (AC005679) Similar to gb_D45384 vacuolar H+-pyrophosphatase from Oryza sativa. ESTs gb_F14272 and gb_F14273 come from this gene. [Arabidopsis thaliana]

 Seq. No.
 288947

 Contig ID
 265144_1.R1011

 5'-most EST
 wty700167919.h1

Seq. No. 288948 Contig ID 265154_1.R1011

5'-most EST wty700167895.h1

Seq. No. 288949

Contig ID 265174_1.R1011 5'-most EST uer700578849.h1

 Seq. No.
 288950

 Contig ID
 265248 1.R1011

 5'-most EST
 wty700171813.h1

 Mathed
 BLASTY

Method BLASTX
NCBI GI g3688177
BLAST score 393
E value 4.0e-38
Match length 107
% identity 64

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 288951

Contig ID 265264 1.R1011 5'-most EST ypc700807164.h1

Method BLASTX
NCBI GI g3859944
BLAST score 165
E value 9.0e-12
Match length 45
% identity 71

NCBI Description (AF084570) FKBP12 interacting protein [Arabidopsis

thaliana]

Seq. No. 288952

Contig ID 265392_1.R1011 5'-most EST wty700168221.h1

Seq. No. 288953

Contig ID 265403_1.R1011 5'-most EST wen700332987.h1

Seq. No. 288954

Contig ID 265616 1.R1011 5'-most EST wty700168555.h1

Method BLASTX
NCBI GI g4455156
BLAST score 386
E value 2.0e-37
Match length 104



288955

Contig ID 265668_1.R1011
5'-most EST yyf700349611.h1
Method BLASTX
NCBI GI g586655
BLAST score 167

E value 5.0e-12
Match length 81
% identity 48

Seq. No.

NCBI Description ZINC-TRANSPORTING ATPASE (ZN(II)-TRANSLOCATING P-TYPE

ATPASE) >gi_1073528_pir__S47688 hypothetical protein o732 - Escherichia coli >gi_466605 (U00039) No definition line

found [Escherichia coli] >gi_1789879 (AE000422)

zinc-transporting ATPase [Escherichia coli]

Seq. No. 288956

Contig ID 265702_1.R1011 5'-most EST wty700168665.h1

Seq. No. 288957

Contig ID 265707_1.R1011 5'-most EST wty700168672.h1

Seq. No. 288958

Contig ID 265716_1.R1011 5'-most EST fdz701165301.h1

Method BLASTX
NCBI GI g135449
BLAST score 150
E value 1.0e-16
Match length 46
% identity 100

NCBI Description TUBULIN BETA-1 CHAIN >gi 100932 pir S14701 tubulin beta-1

chain - maize $>gi_295851$ _emb_CAA370 $\overline{60}$ _ (X52878) beta 1

tubulin [Zea mays]

Seq. No. 288959

Contig ID 265815_1.R1011 5'-most EST wty700168820.h1

Seq. No. 288960

Contig ID 265820_1.R1011 5'-most EST ceu700425201.h1

Method BLASTX
NCBI GI g2129629
BLAST score 215
E value 6.0e-18
Match length 51
% identity 75

NCBI Description L-ascorbate peroxidase (EC 1.11.1.11) - Arabidopsis thaliana >gi_1332439_emb_CAA66640_ (X98003) ascorbate peroxidase [Arabidopsis thaliana] >gi_1523791_emb_CAA66926_

(X98276) L-ascorbate peroxidase [Arabidopsis thaliana]



>gi_2444019 (U69138) ascorbate peroxidase 3 [Arabidopsis
thaliana] >gi_2924511_emb_CAA17765.1_ (AL022023)
L-ascorbate peroxidase [Arabidopsis thaliana]

 Seq. No.
 288961

 Contig ID
 265984_1.R1011

 5'-most EST
 wty700169060.h1

Seq. No. 288962

Contig ID 266006_1.R1011 5'-most EST xsy700217755.h1

Seq. No. 288963

Contig ID 266035_1.R1011 5'-most EST wty700169125.h1

Seq. No. 288964

Contig ID 266110_1.R1011 5'-most EST wty700169243.h1

Seq. No. 288965

Contig ID 266148_2.R1011 5'-most EST xsy700209966.h1

Method BLASTX
NCBI GI g3201541
BLAST score 226
E value 3.0e-23
Match length 100
% identity 49

NCBI Description (AJ005077) TCTR2 protein [Lycopersicon esculentum]

Seq. No. 288966

Contig ID 266150_1.R1011 5'-most EST nbm700473533.h1

Seq. No. 288967

Contig ID 266176_1.R1011 5'-most EST wty700169340.h1

Seq. No. 288968

Contig ID 266216_1.R1011 5'-most EST xyt700344723.h1

Method BLASTX
NCBI GI g4585878
BLAST score 218
E value 1.0e-17
Match length 71

% identity 55

NCBI Description (AC005850) Unknown protein [Arabidopsis thaliana]

Seq. No. 288969

Contig ID 266308_1.R1011 5'-most EST hvj700622101.h1

Seq. No. 288970

Contig ID 266441 1.R1011 5'-most EST yyf700350662.h1



Seq.	No.	
Conti	g :	ΙD
5'-mo	st	EST

288971

266480 1.R1011 xyt700344307.h1

Seq. No. Contig ID 5'-most EST 288972

266486 1.R1011 wty700172967.hl

Seq. No. Contig ID 5'-most EST 288973

266500 1.R1011 wty700169811.hl

Seq. No.

288974

Contig ID 266505 1.R1011 5'-most EST wty700172419.h1 Method BLASTX

NCBI GI q4559333 BLAST score 387 E value 1.0e-37 Match length 121 % identity 60

NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.

Contig ID 5'-most EST 288975

266506 1.R1011 wty700169819.hl

Seq. No.

Contig ID 5'-most EST 288976

266592 1.R1011 $wty700\overline{1}69961.h1$

Seq. No.

Contig ID 5'-most EST 288977 266628 1.R1011

kem700611578.h1

Seq. No.

288978

Contig ID 5'-most EST

266695 1.R1011 wty700170095.h1

Seq. No.

288979

Contig ID 5'-most EST 266699 1.R1011 nbm700471894.hl

Seq. No.

288980

Contig ID 5'-most EST 266716 1.R1011 xsy700209812.h1

Seq. No.

288981

Contig ID 5'-most EST

% identity

266785_1.R1011 wty700170251.h1

Method NCBI GI BLAST score E value Match length BLASTX q4039155 150 7.0e-10

59 46



NCBI Description (AF104258) putative copper-inducible 35.6 kDa protein [Festuca rubra]

Seq. No. 288982

Contig ID 266793_1.R1011 5'-most EST wty700170264.h1

Seq. No. 288983

Contig ID 266865_1.R1011 5'-most EST nwy700446246.h1

Seq. No. 288984

Contig ID 266936_1.R1011 5'-most EST wty700170464.h1

Seq. No. 288985

Contig ID 267054_1.R1011 5'-most EST wty700170740.h1

Seq. No. 288986

Contig ID 267100_1.R1011 5'-most EST wty700170801.h1 Method BLASTX

Method BLASTX
NCBI GI 94263522
BLAST score 155
E value 3.0e-10
Match length 108
% identity 36

NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No. 288987

Contig ID 267103_1.R1011 5'-most EST wty700170805.h1

Seq. No. 288988

Contig ID 267130_1.R1011 5'-most EST gct701178808.h1

Method BLASTX
NCBI GI g2911082
BLAST score 174
E value 1.0e-12
Match length 123
% identity 33

NCBI Description (AL021960) hypothetical protein [Arabidopsis thaliana]

Seq. No. 288989

Contig ID 267183_1.R1011 5'-most EST wty700172018.h1

Seq. No. 288990

Contig ID 267298_1.R1011 5'-most EST wty700171288.h1

Method BLASTX
NCBI GI g1171130
BLAST score 203
E value 2.0e-16
Match length 76



```
% identity
                  (U24657) putative O-methyltransferase [Myxococcus xanthus]
NCBI Description
Seq. No.
                   288991
                   267425 1.R1011
Contig ID
                  wty700171311.hl
5'-most EST
                   288992
Seq. No.
                   267431 1.R1011
Contig ID
                   wty700171318.hl
5'-most EST
                   BLASTX
Method
                   g3757524
NCBI GI
                   147
BLAST score
                   2.0e-09
E value
Match length
                   82
% identity
                   38
                   (AC005167) tetracycline transporter-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   288993
Seq. No.
                   267449 1.R1011
Contig ID
                   xsy700217628.hl
5'-most EST
                   288994
Seq. No.
                   267545 1.R1011
Contig ID
                   yyf700\overline{3}52510.h1
5'-most EST
                   BLASTX
Method
                   g3776023
NCBI GI
                   262
BLAST score
                   2.0e-23
E value
                   70
Match length
                   71
% identity
                   (AJ010473) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   288995
Seq. No.
                   267644_1.R1011
Contig ID
5'-most EST
                   wty700171623.hl
                   288996
Seq. No.
                   267802 1.R1011
Contig ID
                   wty700171835.hl
5'-most EST
                   288997
Seq. No.
Contig ID
                   267855 1.R1011
5'-most EST
                   ceu700434594.h1
                   BLASTX
Method
                   g4467124
NCBI GI
                   234
BLAST score
E value
                   2.0e-19
                   143
Match length
```

Seq. No. 288998

% identity

NCBI Description

Contig ID 267882 1.R1011 5'-most EST fdz701158990.h2

(AL035538) hypothetical protein [Arabidopsis thaliana]

E value

Match length

6.0e-24

161



```
288999
Seq. No.
                  267950 1.R1011
Contig ID
                  hbs701183280.hl
5'-most EST
                  BLASTX
Method
                  q4006864
NCBI GI
BLAST score
                  234
                  2.0e-19
E value
Match length
                  88
% identity
                  (Z99707) nucleoporin-like protein [Arabidopsis thaliana]
NCBI Description
                  289000
Seq. No.
                  267954 1.R1011
Contig ID
                  gct701168593.hl
5'-most EST
Seq. No.
                   289001
                   267956 1.R1011
Contig ID
                   wty700172074.h1
5'-most EST
                   289002
Seq. No.
                   268020 1.R1011
Contig ID
                   wty700172168.hl
5'-most EST
                   289003
Seq. No.
                   268049 1.R1011
Contig ID
                   hbs701183506.h1
5'-most EST
Method
                   BLASTX
                   g2914697
NCBI GI
BLAST score
                   155
                   2.0e-10
E value
                   94
Match length
                   37
% identity
                   (AC003974) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   289004
Seq. No.
                   268065 1.R1011
Contig ID
                   mwy700441361.hl
5'-most EST
                   BLASTX
Method
                   q3250676
NCBI GI
                   443
BLAST score
                   6.0e-44
E value
                   164
Match length
                   49
% identity
                   (AL024486) putative protein [Arabidopsis thaliana]
NCBI Description
                   289005
Seq. No.
                   268130 1.R1011
Contig ID
                   gct701176288.h1
5'-most EST
                   289006
Seq. No.
 Contig ID
                   268140 1.R1011
                   ceu700431812.hl
 5'-most EST
                   BLASTX
Method
                   g4539314
 NCBI GI
 BLAST score
                   273
```



```
% identity
NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]
                   289007
Seq. No.
                   268208 1.R1011
Contig ID
                   wty700172454.hl
5'-most EST
                   289008
Seq. No.
                   268246 1.R1011
Contig ID
5'-most EST
                   cjh700193525.hl
                   289009
Seq. No.
                   268274 1.R1011
Contig ID
                   gct701174501.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1255951
BLAST score
                   303
                   6.0e-28
E value
                   73
Match length
                   75
% identity
                   (X96932) PS60 [Nicotiana tabacum]
NCBI Description
                   289010
Seq. No.
                   268344 1.R1011
Contig ID
                   uer700\overline{5}77789.h1
5'-most EST
                   BLASTX
Method
                   g1653935
NCBI GI
BLAST score
                   188
                   2.0e-14
E value
                   76
Match length
                   51
% identity
NCBI Description (D90917) hypothetical protein [Synechocystis sp.]
                   289011
Seq. No.
                   268492 1.R1011
Contig ID
                   wty700172872.h1
5'-most EST
                   289012
Seq. No.
                   268499 1.R1011
Contig ID
                   xmt700\overline{2}65478.h1
 5'-most EST
                   BLASTX
Method
                    g4038035
NCBI GI
BLAST score
                    223
                   2.0e-18
E value
                    80
Match length
                    55
 % identity
                   (AC005936) putative DNA-binding protein [Arabidopsis
 NCBI Description
                    thaliana]
```

289013 Seq. No.

268570 1.R1011 Contig ID tfd700569621.h1 5'-most EST

289014 Seq. No.

268722 1.R1011 Contig ID cjh700193062.h1 5'-most EST

BLASTX Method



```
NCBI GI g2829911
BLAST score 169 .
E value 5.0e-12
Match length 94
% identity 23
NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]
```

Seg. No. 289015

 Seq. No.
 289015

 Contig ID
 268740_1.R1011

 5'-most EST
 cjh700193124.h1

Seq. No. 289016

Contig ID 268757_1.R1011 5'-most EST ypc700805353.h1

Seq. No. 289017

Contig ID 268895_1.R1011 5'-most EST cjh700193526.h1

Seq. No. 289018

Contig ID 268935_1.R1011 5'-most EST cjh700193627.h1

Method BLASTX
NCBI GI g1707017
BLAST score 330
E value 3.0e-31
Match length 78
% identity 78

NCBI Description (U78721) RNA helicase isolog [Arabidopsis thaliana]

Seq. No. 289019

Contig ID 268958_1.R1011 5'-most EST kem700611424.h1

Method BLASTN
NCBI GI g1864000
BLAST score 251
E value 1.0e-139
Match length 289
% identity 41

NCBI Description Maize DNA for Fd III, complete cds

Seq. No. 289020

Contig ID 269053 1.R1011 5'-most EST cjh700193928.h1

Seq. No. 289021

Contig ID 269264 1.R1011 5'-most EST ceu700433303.h1

Seq. No. 289022

Contig ID 269314_1.R1011 5'-most EST wen700336514.h1

Seq. No. 289023

Contig ID 269392 1.R1011 5'-most EST cjh700194734.h1

Method BLASTX



NCBI GI g100940 BLAST score 235 E value 5.0e-20 Match length 83 % identity 61

NCBI Description zein zA1 - maize

Seq. No. 289024

Contig ID 269553 1.R1011 5'-most EST xsy700217995.h1

Seq. No. 289025

Contig ID 269617_1.R1011 5'-most EST cjh700195251.h1

Seq. No. 289026

Contig ID 269664_1.R1011 5'-most EST xyt700342934.h1

Method BLASTX
NCBI GI g2196672
BLAST score 301
E value 1.0e-27
Match length 64
% identity 92

NCBI Description (Y08807) HMGd1 [Zea mays]

Seq. No. 289027

Contig ID 269767 1.R1011 5'-most EST xsy700207689.h1

Method BLASTX
NCBI GI g4557060
BLAST score 235
E value 7.0e-20
Match length 100
% identity 51

NCBI Description (AC007154) putative chromosome-associated polypeptide, 5'

partial [Arabidopsis thaliana]

Seq. No. 289028

Contig ID 269801_1.R1011 5'-most EST cjh700195693.h1

Method BLASTX
NCBI GI 94490310
BLAST score 359
E value 5.0e-35
Match length 127
% identity 62

NCBI Description (AL035678) somatic embryogenesis receptor-like kinase-like

protein [Arabidopsis thaliana]

Seq. No. 289029

Contig ID 269853_1.R1011 5'-most EST cjh700195815.h1

Seq. No. 289030

Contig ID 270041 1.R1011 5'-most EST cjh700196255.h1



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289031
Seq. No.
                   270262 1.R1011
Contig ID
                  cjh700\overline{1}96812.h1
5'-most EST
                   289032
Seq. No.
                   270324_1.R1011
Contig ID
                   cjh700196965.hl
5'-most EST
                   289033
Seq. No.
                   270366 1.R1011
Contig ID
                   wen700\overline{3}35607.h1
5'-most EST
                   289034
Seq. No.
                   270427 1.R1011
Contig ID
                   cjh700197217.h1
5'-most EST
                   BLASTX
Method
                   g407942
NCBI GI
                   170
BLAST score
                   2.0e-12
E value
                   79
Match length
                   43
% identity
NCBI Description (U02496) epoxide hydrolase [Solanum tuberosum]
                   289035
Seq. No.
                   270471 1.R1011
Contig ID
                   xsy700\overline{2}09707.h1
5'-most EST
                   289036
Seq. No.
                   270495 1.R1011
Contig ID
                   xyt700347377.h1
5'-most EST
                   BLASTN
Method
                   g3057119
NCBI GI
                   42
BLAST score
                   2.0e-14
E value
                   114
Match length
                   84
% identity
NCBI Description Zea mays starch synthase DULL1 (dull1) mRNA, complete cds
                   289037
Seq. No.
                   270518 1.R1011
Contig ID
                   xyt700346343.h1
5'-most EST
                   289038
Seq. No.
Contig ID
                   270521 1.R1011
5'-most EST
                   cjh700197450.h1
                   289039
Seq. No.
                   270619 1.R1011
Contig ID
5'-most EST
                   cjh700197745.h1
```

Seq. No. 289040

Contig ID 270652_1.R1011 5'-most EST wen700334309.h1

Seq. No. 289041

Contig ID 271015_1.R1011



```
xmt700263640.h1
5'-most EST
                   BLASTX
Method
                   q2104535
NCBI GI
                   255
BLAST score
                   1.0e-22
E value
                   68
Match length
                   71
% identity
                  (AF001308) T10M13.13 [Arabidopsis thaliana]
NCBI Description
                   289042
Seq. No.
                   271080 1.R1011
Contig ID
                   xsy700207588.h1
5'-most EST
                   BLASTX
Method
                   g4006878
NCBI GI
BLAST score
                   521
                   4.0e-53
E value
                   141
Match length
% identity
                   66
                  (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
NCBI Description
                   289043
Seq. No.
                   271118 1.R1011
Contig ID
                   fdz701166848.h1
5'-most EST
                   BLASTX
Method
                   g115132
NCBI GI
                   185
BLAST score
                   4.0e-14
E value
                   87
Match length
                   40
% identity
                   HOMEOTIC GENE REGULATOR (BRAHMA PROTEIN)
NCBI Description
                   >gi_283699_pir__A42091 transcriptional activator SNF2/SWI2
                   homolog brm - fruit fly (Drosophila melanogaster)
                   >gi 157012 (M85049) brahma protein [Drosophila
                   melanogaster]
                   289044
Seq. No.
Contig ID
                   271155 1.R1011
                   xsy700\overline{2}07730.h1
5'-most EST
                   289045
Seq. No.
                   271256 1.R1011
Contig ID
                   xsy700207889.h1
5'-most EST
                   BLASTX
Method
                   q3157941
NCBI GI
BLAST score
                   285
                   2.0e-25
E value
                   91
Match length
                   59
% identity
                   (AC002131) Contains similarity to hypothetical protein
NCBI Description
                   gb U95973 from A. thaliana. [Arabidopsis thaliana]
                   289046
Seq. No.
                   271300 1.R1011
Contia ID
                   xsy700\overline{2}08579.h1
5'-most EST
                   BLASTX
Method
```

g2388577

165

NCBI GI BLAST score



E value 5.0e-12 Match length 54 % identity 61

NCBI Description (AC000098) Similar to Arabidopsis putative ion-channel

PID:g2262157 (gb_AC002329). [Arabidopsis thaliana]

Seq. No. 289047

Contig ID 271317_1.R1011 5'-most EST xsy700207990.h1

Seq. No. 289048

Contig ID 271336_1.R1011 5'-most EST ypc700802115.h1

Method BLASTX
NCBI GI g2648032
BLAST score 456
E value 3.0e-50
Match length 135
% identity 69

NCBI Description (AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No. 289049

Contig ID 271368 1.R1011 5'-most EST xsy700208060.h1

Seq. No. 289050

Contig ID 271390_1.R1011 5'-most EST nbm700465203.h1

Seq. No. 289051

Contig ID 271402_1.R1011 5'-most EST xsy700208103.h1

Seq. No. 289052

Contig ID 271436_1.R1011 5'-most EST xsy700208147.h1

Method BLASTX
NCBI GI g2827139
BLAST score 625
E value 2.0e-65
Match length 128
% identity 87

NCBI Description (AF027172) cellulose synthase catalytic subunit

[Arabidopsis thaliana] >gi_4049343_emb_CAA22568_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis

thaliana]

Seq. No. 289053

Contig ID 271490_1.R1011 5'-most EST xsy700208219.h1

Seq. No. 289054

Contig ID 271751_1.R1011 5'-most EST xyt700343632.h1

Seq. No. 289055

Contig ID 271831_1.R1011



```
5'-most EST
                   xsy700208731.hl
                   289056
Seq. No.
Contig ID
                   271834 1.R1011
5'-most EST
                   xsy700\overline{2}08734.h1
Seq. No.
                   289057
                   271834 2.R1011
Contig ID
5'-most EST
                   xmt700\overline{2}57909.h1
Seq. No.
                   289058
Contig ID
                   271840 1.R1011
5'-most EST
                   xsy700208740.hl
                   BLASTX
Method
                   g1922246
NCBI GI
BLAST score
                    347
                    7.0e-33
E value
Match length
                    93
% identity
                    71
                   (Y10086) putative dehydrogenase [Arabidopsis thaliana]
NCBI Description
                    289059
Seq. No.
Contig ID
                    271936 1.R1011
5'-most EST
                   xsy700208867.h1
                    289060
Seq. No.
                    271954 1.R1011
Contig ID
5'-most EST
                    xsy700\overline{2}08888.h1
                    289061
Seq. No.
                    271958 1.R1011
Contig ID
5'-most EST
                    kem700\overline{6}10790.h1
Seq. No.
                    289062
Contig ID
                    271981 1.R1011
                    xsy700208923.hl
5'-most EST
Seg. No.
                    289063
Contig ID
                    272040 1.R1011
                    hbs701184169.h1
5'-most EST
Method
                    BLASTX
                    g2072626
NCBI GI
                    205
BLAST score
E value
                    4.0e-16
Match length
                    46
                    78
% identity
                    (Y12904) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    >gi 3281856 emb CAA19751 (AL031004) Transcription factor
```

. ¥-

 Seq. No.
 289064

 Contig ID
 272054_1.R1011

 5'-most EST
 xsy700209012.h1

 Method
 BLASTX

 NCBI GI
 g2827469

 BLAST score
 225

E value

1.0e-18

4

II homolog [Arabidopsis thaliana]



Match length 37 % identity

(AF044255) NOSA [Dictyostelium discoideum] NCBI Description

Seq. No. Contig ID 289065

BLASTX

5'-most EST

272082 1.R1011 xsy700209053.h1

Method NCBI GI BLAST score E value Match length

g1805254 415 7.0e-44 104

% identity NCBI Description

88 (U62622) monogalactosyldiacylglycerol synthase [Cucumis

sativus]

Seq. No.

289066

Contig ID 5'-most EST

272092 1.R1011 mwy700438453.hl

Seq. No.

289067

Contig ID 5'-most EST

272117 1.R1011 $xsy700\overline{2}09108.h1$

Seq. No.

289068

Contig ID 5'-most EST 272136 1.R1011 xmt700267941.h1

Seq. No. Contig ID 289069

272172 1.R1011 $xsy700\overline{2}09172.h1$ 5'-most EST

Seq. No.

289070

Contig ID 5'-most EST 272196 1.R1011 $xsy700\overline{2}09207.h1$

Seq. No.

289071

Contig ID 5'-most EST

272231 1.R1011 rvt700552849.h1

Seq. No.

289072

BLASTX

Contig ID 5'-most EST 272340 1.R1011 $xsy700\overline{2}09389.h1$

Method NCBI GI BLAST score E value

150 1.0e-09

g3860273

Match length % identity

54 48

NCBI Description

(AC005824) hypothetical protein [Arabidopsis thaliana] >qi 4314398 gb AAD15608 (AC006232) hypothetical protein

[Arabidopsis thaliana]

Seq. No.

289073

Contig ID 5'-most EST 272597 1.R1011 $xsy700\overline{2}09717.h1$



 Seq. No.
 289074

 Contig ID
 272693 1.R1011

 5'-most EST
 xsy700209848.h1

Seq. No. 289075

Contig ID 272731_1.R1011 5'-most EST xsy700209894.h1

Method BLASTN
NCBI GI g4512215
BLAST score 134
E value 2.0e-69
Match length 277
% identity 91

NCBI Description Zea mays ZmRR1 mRNA for response regulator, complete cds

Seq. No. 289076

Contig ID 272861_1.R1011 5'-most EST xsy700210105.h1

Seq. No. 289077

Contig ID 273069_1.R1011 5'-most EST rv1700458594.h1

Method BLASTX
NCBI GI g1402886
BLAST score 423
E value 7.0e-42
Match length 103
% identity 76

NCBI Description (X98130) unknown [Arabidopsis thaliana]

Seq. No. 289078

Contig ID 273070_1.R1011 5'-most EST xdg700405230.h1

Seq. No. 289079

Contig ID 273102_1.R1011 5'-most EST xsy700210427.h1

Seq. No. 289080

Contig ID 273174 1.R1011 5'-most EST xsy700210547.h1

Method BLASTX
NCBI GI g2765140
BLAST score 356
E value 2.0e-50
Match length 117
% identity 75

NCBI Description (Y11931) 1-phosphatidylinositol-4,5-bisphosphate

phosphodiesterase [Nicotiana rustica]

Seq. No. 289081

Contig ID 273295_1.R1011 5'-most EST mwy700440019.h1

Seq. No. 289082

Contig ID 273415 1.R1011 5'-most EST xsy700210862.h1



```
BLASTX
Method
                  q3065835
NCBI GI
                   156
BLAST score
                   2.0e-10
E value
                   56
Match length
% identity
                   55
                   (AF058800) putative methyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   289083
Seq. No.
                   273668 2.R1011
Contig ID
5'-most EST
                   fdz701161853.hl
Method
                   BLASTX
                   g2618725
NCBI GI
BLAST score
                   154
E value
                   4.0e-13
Match length
                   59
% identity
                   71
NCBI Description (U49074) IAA18 [Arabidopsis thaliana]
                   289084
Seq. No.
Contig ID
                   273683 1.R1011
5'-most EST
                   xsy700211261.h1
                   289085
Seq. No.
                   273687 1.R1011
Contig ID
                   rv1700458540.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3080415
BLAST score
                   344
E value
                   1.0e-32
Match length
                   101
% identity
                   (AL022604) cysteine proteinase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   289086
Seq. No.
                   273738 1.R1011
Contig ID
                   xsy700\overline{2}11337.h1
5'-most EST
                   BLASTX
Method
                   g3461814
NCBI GI
BLAST score
                   315
                   4.0e-29
E value
                   107
Match length
                   59
% identity
                   (AC004138) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   289087
Seq. No.
                   273781 1.R1011
Contig ID
                   afb700381940.h1
5'-most EST
Seq. No.
                   289088
```

Contig ID 273854 1.R1011 5'-most EST yne700378696.hl

289089 Seq. No.

273969_1.R1011 Contig ID



```
5'-most EST xsy700211646.h1

Method BLASTX

NCBI GI g1771158

BLAST score 231

E value 5.0e-19

Match length 160
% identity 32

NCBI Description (Y07861) MFP1 protein [Lycopersicon esculentum]
```

Seq. No. 289090

Contig ID 273998_1.R1011 5'-most EST xsy700211681.h1

Seq. No. 289091

Contig ID 274124 1.R1011 5'-most EST xsy700211855.h1

Method BLASTX
NCBI GI g4558659
BLAST score 271
E value 6.0e-30
Match length 145
% identity 48

NCBI Description (AC007063) unknown protein [Arabidopsis thaliana]

Seq. No. 289092

Contig ID 274323_1.R1011 5'-most EST xsy700212133.h1

Seq. No. 289093

Contig ID 274355 1.R1011 5'-most EST nbm700469225.h1

Seq. No. 289094

Contig ID 274453_1.R1011 5'-most EST nbm700469819.h1

Seq. No. 289095

Contig ID 274463_1.R1011 5'-most EST tfd700569945.h1

Seq. No. 289096

Contig ID 274469_1.R1011 5'-most EST nbm700473932.h1

Seq. No. 289097

Contig ID 274719 1.R1011 5'-most EST xsy700212719.h1

Seq. No. 289098

Contig ID 274744_1.R1011 5'-most EST fdz701163036.h1 Method BLASTX

 NCBI GI
 g1001311

 BLAST score
 455

 E value
 2.0e-45

 Match length
 149

 % identity
 58



275040 1.R1011

```
(D64006) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                  289099
                  274926_1.R1011
Contig ID
                  xsy700212995.h1
5'-most EST
                  289100
Seq. No.
```

xsy700213142.hl 5'-most EST BLASTX Method g4098238 NCBI GI BLAST score 141 7.0e-09 E value

Match length 63 % identity 48

Contig ID

NCBI Description (U76384) o-methyltransferase [Triticum aestivum]

289101 Seq. No.

275070 1.R1011 Contig ID xdb700342119.hl 5'-most EST

289102 Seq. No.

275111 1.R1011 Contig ID xsy700213232.h1 5'-most EST

BLASTX Method g3608154 NCBI GI BLAST score 218 7.0e-18 E value 104 Match length 45 % identity

NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

289103 Seq. No.

275118 1.R1011 Contig ID gct701169318.hl 5'-most EST

BLASTX Method NCBI GI g2462745 147 BLAST score 1.0e-09 E value Match length 91 % identity 38

(AC002292) Hypothetical protein [Arabidopsis thaliana] NCBI Description

289104 Seq. No.

275136 1.R1011 Contig ID 5'-most EST hbs701182124.h1

Seq. No. 289105

275144 1.R1011 Contig ID 5'-most EST xsy700213273.hl

289106 Seq. No.

275166_1.R1011 Contig ID 5'-most EST xsy700213310.h1

289107 Seq. No.

275327_1.R1011 Contig ID



```
5'-most EST xsy700213543.h1
```

Seq. No. 289109

Contig ID 275516_1.R1011 5'-most EST xmt700266828.h1

Seq. No. 289110

Contig ID 275756_1.R1011 5'-most EST zla700379928.h1

Seq. No. 289111

Contig ID 275764_1.R1011 5'-most EST nbm700466968.h1

Method BLASTX
NCBI GI g3687224
BLAST score 521
E value 3.0e-53
Match length 134
% identity 75

NCBI Description (AC005169) putative N-acetyl-gamma-glutamyl-phosphate

reductase [Arabidopsis thaliana]

Seq. No. 289112

Contig ID 275877_1.R1011 5'-most EST nbm700467111.h1

Method BLASTX
NCBI GI g2145356
BLAST score 257
E value 2.0e-22
Match length 95
% identity 60

NCBI Description (Y11122) HD-Zip protein [Arabidopsis thaliana] >gi_3132474

(AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]

Seq. No. 289113

Contig ID 275938_1.R1011 5'-most EST xsy700214440.h1

Seq. No. 289114

Contig ID 275959_1.R1011 5'-most EST xsy700214469.h1

Method BLASTX
NCBI GI g2914703
BLAST score 403
E value 3.0e-39
Match length 151
% identity 51

NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]

Seq. No. 289115

Contig ID 276006_1.R1011 5'-most EST xsy700214547.h1



```
Seq. No.
                   289116
                   276257 1.R1011
Contig ID
                  xsy700\overline{2}14924.h1
5'-most EST
                  BLASTX
Method
                   g3005983
NCBI GI
                   310
BLAST score
                   2.0e-28
E value
Match length
                   79
                   71
% identity
                  (Y14387) lycopene epsilon-cyclase [Lycopersicon esculentum]
NCBI Description
                   289117
Seq. No.
                   276433 1.R1011
Contig ID
5'-most EST
                   rv1700458450.h1
                   289118
Seq. No.
                   276519 1.R1011
Contig ID
                   nbm700476463.h1
5'-most EST
                   BLASTX
Method
                   g2739355
NCBI GI
                   480
BLAST score
                   4.0e-48
E value
Match length
                   122
                   70
% identity
                   (AC003972) pNORF1 [Homo sapiens] >gi_3328175 (AF074016)
NCBI Description
                   nonsense-mediated mRNA decay trans-acting factor [Homo
                   sapiens]
                   289119
Seq. No.
                   276619 1.R1011
Contig ID
                   nbm700\overline{4}71303.h1
5'-most EST
                   289120
Seq. No.
Contig ID
                   276620 1.R1011
5'-most EST
                   ypc700799028.h1
Seq. No.
                   289121
                   276646 1.R1011
Contig ID
5'-most EST
                   hvj700621555.h1
                   289122
Seq. No.
Contig ID
                   276693 1.R1011
5'-most EST
                   xsy700217488.h1
Seq. No.
                   289123
Contig ID
                   276747 1.R1011
5'-most EST
                   zuv700353260.h1
```

Method BLASTX g1942055 NCBI GI BLAST score 336 2:0e-31 E value Match length 94

% identity

67 NCBI Description Structure Of Nadph Dependent Thioredoxin Reductase

Seq. No.

289124

Contig ID

276829_1.R1011



```
5'-most EST
                   hbs701184611.hl
                   289125
Seq. No.
Contig ID
                   276834 1.R1011
5'-most EST
                   xsy700\overline{2}17694.h1
Seq. No.
                   289126
                   276876 1.R1011
Contig ID
5'-most EST
                   nwy700444979.hl
Seq. No.
                   289127
Contig ID
                   276896 1.R1011
5'-most EST
                   xsy700217779.hl
                   289128
Seq. No.
                   277066 1.R1011
Contig ID
5'-most EST
                   xmt700\overline{2}66821.h1
                   289129
Seq. No.
                   277078 1.R1011
Contig ID
5'-most EST
                   uwh700207171.hl
Seq. No.
                   289130
Contig ID
                   277094 1.R1011
                   xmt700\overline{2}65862.h1
5'-most EST
                   BLASTX
Method
                   q100876
NCBI GI
                   1722
BLAST score
E value
                   0.0e + 00
                   444
Match length
% identity
                   globulin-2 precursor - maize >gi_228310_prf__1802402A
NCBI Description
                   globulin 2 [Zea mays]
Seq. No.
                   289131
                   277121 1.R1011
Contig ID
                   rvt700552241.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4165089
BLAST score
                   178
                   7.0e-13
E value
Match length
                   119
% identity
                   36
                   (AF084480) Williams-Beuren syndrome deletion transcript 9
NCBI Description
                   homolog [Mus musculus]
Seq. No.
                   289132
                   277176 1.R1011
Contig ID
5'-most EST
                   xmt700\overline{2}58221.h1
                   289133
Seq. No.
```

Contig ID 5'-most EST

277183 1.R1011 $nbm700\overline{4}74918.h1$

Seq. No. Contig ID 5'-most EST 289134

277192 1.R1011 $xmt700\overline{2}57969.h1$



```
Method BLASTX
NCBI GI g4586244
BLAST score 224
E value 3.0e-18
Match length 131
% identity 41
```

NCBI Description (AL049640) putative protein [Arabidopsis thaliana]

Seq. No. 289135

Contig ID 277232_1.R1011 5'-most EST xmt700256819.h1

Seq. No. 289136

Contig ID 277239_1.R1011 5'-most EST xmt700261252.h1

Method BLASTX
NCBI GI g1710077
BLAST score 737
E value 3.0e-78
Match length 177
% identity 79

NCBI Description PEROXIREDOXIN (REHYDRIN HOMOLOG) (B15C)

>gi_2130029_pir__S60285 B15C protein - barley

>gi_471321_emb_CAA54066 (X76605) HvB15C [Hordeum vulgare]
>gi_1694833_emb_CAA65387 (X96551) peroxiredoxin [Hordeum

vulgare]

Seq. No. 289137

Contig ID 277239_2.R1011 5'-most EST xmt700264656.h1

Method BLASTX
NCBI GI g1710077
BLAST score 239
E value 3.0e-39
Match length 88
% identity 90

NCBI Description PEROXIREDOXIN (REHYDRIN HOMOLOG) (B15C)

>gi_2130029_pir__S60285 B15C protein - barley

>gi_471321_emb_CAA54066_ (X76605) HvB15C [Hordeum vulgare]
>gi_1694833_emb_CAA65387_ (X96551) peroxiredoxin [Hordeum

vulgare]

Seq. No. 289138

Contig ID 277303 1.R1011 5'-most EST ceu700423777.h1

Method BLASTX
NCBI GI g2244999
BLAST score 225
E value 2.0e-18
Match length 90
% identity 60

NCBI Description (Z97341) similarity to phaseolin G-box binding protein PG2

[Arabidopsis thaliana]

Seq. No. 289139

Contig ID 277312 1.R1011 5'-most EST xmt700256950.h1



```
Seq. No.
                   289140
                   277333 1.R1011
Contig ID
                   xmt700257010.h1
5'-most EST
                   BLASTX
Method
                   q691752
NCBI GI
BLAST score
                   224
                   2.0e-18
E value
                   84
Match length
% identity
                   55
NCBI Description
                  (D29803) preproMP27-MP32 [Cucurbita sp.]
Seq. No.
                   289141
                   277372 1.R1011
Contig ID
                   qw1700617436.h1
5'-most EST
                   BLASTX
Method
                   q1703227
NCBI GI
BLAST score
                   491
                   1.0e-49
E value
                   136
Match length
% identity
                   ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
NCBI Description
                   TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                   (ALAAT-2) >gi_629770_pir__S42535 alanine transaminase (EC
                   2.6.1.2) - barley >gi_469148_emb_CAA81231_ (Z26322) alanine
                   aminotransferase [Hordeum vulgare]
                   289142
Seq. No.
Contig ID
                   277376 1.R1011
                   xmt700\overline{2}57078.h1
5'-most EST
                   BLASTX
Method
                   q2735017
NCBI GI
BLAST score
                   349
E value
                   3.0e-33
Match length
                   98
% identity
                   61
                   (U82481) KI domain interacting kinase 1 [Zea mays]
NCBI Description
Seq. No.
                   289143
                   277389 1.R1011
Contig ID
                   nbm700\overline{4}67070.h1
5'-most EST
                   289144
Seq. No.
                   277401 1.R1011
Contig ID
                   xmt700\overline{2}64666.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q168508
BLAST score
                   371
                   0.0e + 00
E value
Match length
                   444
                   96
% identity
                   Maize oleosin KD18 (KD18; L2) gene, complete cds
NCBI Description
```

Seq. No. 289145

Contig ID 277403_1.R1011 5'-most EST xmt700262929.h1



```
289146
Seq. No.
                   277409 1.R1011
Contig ID
                   xmt700\overline{2}65750.h1
5'-most EST
                   BLASTX
Method
                   g691752
NCBI GI
                   386
BLAST score
                   3.0e-37
E value
Match length
                   99
                   66
% identity
                  (D29803) preproMP27-MP32 [Cucurbita sp.]
NCBI Description
                   289147
Seq. No.
                   277413 1.R1011
Contig ID
                   xmt700\overline{2}65754.h1
5'-most EST
                   289148
Seq. No.
                   277435 1.R1011
Contig ID
5'-most EST
                   ltv700479662.h1
                   289149
Seq. No.
                   277436_1.R1011
Contig ID
                   xmt700257196.h1
5'-most EST
                   289150
Seq. No.
                   277446 1.R1011
Contig ID
                   nbm700476492.h1
5'-most EST
                   BLASTX
Method
                   g2270994
NCBI GI
                   362
BLAST score
                   1.0e-34
E value
                   90
Match length
                   68
% identity
                   (AF004809) Ca+2-binding EF hand protein [Glycine max]
NCBI Description
                   289151
Seq. No.
Contig ID
                   277447 1.R1011
                   xmt700267629.h1
5'-most EST
                   BLASTX
Method
                   q3694807
NCBI GI
BLAST score
                   522
                   4.0e-53
E value
                   171
Match length
% identity
                   (AF055898) alanine aminotransferase [Zea mays]
NCBI Description
                   289152
Seq. No.
                   277498 1.R1011
Contig ID
                   xmt700257331.h1
5'-most EST
                   289153
Seq. No.
                   277506 1.R1011
Contig ID
```

gct701174216.h1 5'-most EST

289154 Seq. No.

277541 1.R1011 Contig ID hbs701185949.h1 5'-most EST



```
289155
Seq. No.
                    277561 1.R1011
Contig ID
                    xmt700\overline{2}68091.h1
5'-most EST
                    BLASTN
Method
                    q687246
NCBI GI
                    218
BLAST score
E value
                    1.0e-119
                    246
Match length
% identity
                    97
                    Zea mays oil body protein 17 kDa oleosin (ole17) gene,
NCBI Description
                    complete cds
                    289156
Seq. No.
Contig ID
                    277605 1.R1011
                    gw1700\overline{6}15154.h1
5'-most EST
Method
                    BLASTX
                    g2745900
NCBI GI
BLAST score
                    265
                    3.0e-23
E value
                    93
Match length
                    54
% identity
                   (AF039405) arsenite-translocating ATPase [Mus musculus]
NCBI Description
                    289157
Seq. No.
                    277619 1.R1011
Contig ID
                    xmt700\overline{2}62858.h1
5'-most EST
                    BLASTX
Method
NCBI GI
                    q99921
BLAST score
                    151
E value
                    8.0e-12
Match length
                    67
% identity
                    63
                    hypothetical protein - soybean >gi 18591_emb_CAA42636_
NCBI Description
                    (X60033) auxin-responsive GH3 product [Glycine max]
Seq. No.
                    289158
                    277706 1.R1011
Contig ID
                    xmt700\overline{2}57773.h1
5'-most EST
                    289159
Seq. No.
                    277718 1.R1011
Contig ID
                    hbs701184314.h1
5'-most EST
Seq. No.
                    289160
                    277739 1.R1011
Contig ID
                    xmt700\overline{2}63624.h1
5'-most EST
                    289161
Seq. No.
                    277746 1.R1011
Contig ID
                    xmt700\overline{2}61667.h1
5'-most EST
                    289162
Seq. No.
```

277760 1.R1011 Contig ID 5'-most EST xmt700262576.h1 BLASTX

Method g1707074 NCBI GI BLAST score 253



E value 9.0e-22 Match length 125 % identity 42

NCBI Description

(U80450) M01E11.2 [Caenorhabditis elegans]

Seq. No. 289163

Contig ID 277761_1.R1011 5'-most EST xmt700261288.h1

Seq. No. 289164

Contig ID 277776_1.R1011 5'-most EST xmt700257889.h1

Method BLASTN
NCBI GI g167005
BLAST score 34
E value 1.0e-09
Match length 70
% identity 87

NCBI Description Hordeum vulgare chloroplast beta-ketoacyl-ACP sythase I isozyme (Kas12) gene, exons 1 through 7 and complete cds

Seq. No. 289165

Contig ID 277778_1.R1011 5'-most EST ypc700799059.h1

Method BLASTX
NCBI GI g4468981
BLAST score 308
E value 1.0e-28
Match length 85
% identity 64

NCBI Description (AL035605) formamidase-like protein [Arabidopsis thaliana]

Seq. No. 289166

Contig ID 277796_1.R1011 5'-most EST xtd700282268.h2

Seq. No. 289167

Contig ID 277890_1.R1011 5'-most EST xdb700340315.h1

Method BLASTX
NCBI GI g4006897
BLAST score 213
E value 5.0e-17
Match length 78
% identity 56

NCBI Description (Z99708) globulin-like protein [Arabidopsis thaliana]

Seq. No. 289168

Contig ID 277894 1.R1011 5'-most EST xmt700258079.h1

Seq. No. 289169

Contig ID 277901_1.R1011 5'-most EST xmt700259393.h1

Seq. No. 289170

Contig ID 277913_1.R1011



5'-most EST xmt700258111.h1

Seq. No. 289171

Contig ID 277948_2.R1011 5'-most EST xmt700258155.h1

Method BLASTX
NCBI GI g3776025
BLAST score 388
E value 8.0e-38
Match length 97
% identity 80

NCBI Description (AJ010474) RNA helicase [Arabidopsis thaliana]

Seq. No. 289172

Contig ID 278002_1.R1011 5'-most EST xmt700259019.h1

Method BLASTX
NCBI GI 94105683
BLAST score 338
E value 9.0e-44
Match length 106
% identity 85

NCBI Description (AF049892) unknown [Oryza sativa] >gi_4105692 (AF050155)

embryo-specific protein [Oryza sativa subsp. indica]

Seq. No. 289173

Contig ID 278038_1.R1011 5'-most EST fdz701165778.h1

Method BLASTX
NCBI GI g4587565
BLAST score 154
E value 2.0e-10
Match length 51
% identity 59

NCBI Description (AC006550) Similar to rab28 protein gb X59138 from Zea

mays. EST gb AA042774 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 289174

Contig ID 278127_1.R1011 5'-most EST xmt700266971.h1

Seq. No. 289175

Contig ID 278131_1.R1011 5'-most EST xmt700258412.h1

Seq. No. 289176

Contig ID 278138_1.R1011 5'-most EST gwl700613230.h1

Seq. No. 289177

Contig ID 278180_1.R1011 5'-most EST xmt700258505.h1

Seq. No. 289178

Contig ID 278200 1.R1011 5'-most EST xmt700258529.h1

Seq. No.



	Acceptance of the second of th
Seq. No.	289179
Contig ID	278217 1.R1011
5'-most EST	fdz701163696.h1
Seq. No.	289180
Contig ID	278231_1.R1011
5'-most EST	xmt700258573.h1
Seq. No.	289181
Contig ID	278274 1.R1011
5'-most EST	xmt700258639.h1
Seq. No.	289182
Contig ID	278387_1.R1011
5'-most EST	xmt700258805.h1

Seq. No.	289183
Contig ID	278413 1.R1011
5'-most EST	xmt700264134.h

Seq. No.	289184
Contig ID	278419 1.R1011
5'-most EST	$xmt700\overline{2}58852.h1$

Seq. No.	289185
Contig ID	278454 1.R1011
5'-most EST	fdz701165922.h1
Method	BLASTX
NCBI GI	g1945283
BLAST score	314
E value	3.0e-29
Match length	62
% identity	89

NCBI	Description	(Y11351)	myb	factor	[Oryza	sativa]	

289186

Contig ID	278506 <u>1.R1011</u>
5'-most EST	xyt700346603.h1
Seq. No.	289187
Contig ID	278508_1.R1011
5'-most EST	xmt700263970.h1
Seq. No.	289188
Contig ID	278508_2.R1011
5'-most EST	fdz701161728.h1
Seq. No.	289189

Contig ID 278523_1.R1011
5'-most EST xmt700259032.h1
Method BLASTN
NCBI GI g687246
BLAST score 221
E value 1.0e-121
Match length 237
% identity 99



NCBI Description Zea mays oil body protein 17 kDa oleosin (ole17) gene, complete cds

Seq. No. 289190

Contig ID 278531_1.R1011 5'-most EST afb700380914.h1

Seq. No. 289191

Contig ID 278532_1.R1011 5'-most EST yyf700349671.h1

Method BLASTX
NCBI GI g4510401
BLAST score 265
E value 1.0e-22
Match length 127
% identity 46

NCBI Description (AC006587) putative general negative regulator of

transcription [Arabidopsis thaliana]

Seq. No. 289192

Contig ID 278562_1.R1011 5'-most EST hvj700622506.h1

Seq. No. 289193

Contig ID 278820_1.R1011 5'-most EST xmt700259691.h1

Method BLASTX
NCBI GI g4006848
BLAST score 272
E value 1.0e-30
Match length 117
% identity 62

NCBI Description (AJ131433) selenocysteine methyltransferase [Astragalus

bisulcatus]

Seq. No. 289194

Contig ID 278917_1.R1011 5'-most EST xmt700260177.h1

Method BLASTX
NCBI GI g3914212
BLAST score 376
E value 2.0e-36
Match length 104
% identity 70

NCBI Description 5-OXOPROLINASE (5-OXO-L-PROLINASE) (PYROGLUTAMASE)

(5-OPASE) >gi_1732065 (U70825) 5-oxo-L-prolinase [Rattus

norvegicus]

Seq. No. 289195

Contig ID 278925_1.R1011 5'-most EST fdz701158487.h1

Method BLASTX
NCBI GI g732174
BLAST score 321
E value 1.0e-29
Match length 141
% identity 49



NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE K03H1.2 >gi_3878176_emb_CAA82662_ (Z29560) similar to DEAH subfamily RNA helicases, especially yeast pre-mRNA splicing factors 22 and 16; cDNA EST EMBL:D27770 comes from this gene; cDNA EST EMBL: D27769 comes from this gene; cDNA EST EMBL: D36247 comes from this ...

>qi 4249768 qb AAD13795 (AF120269) sex determination

protein MOG-1 [Caenorhabditis elegans]

289196 Seq. No.

278960 1.R1011 Contig ID $xmt700\overline{2}60321.h2$ 5'-most EST

289197 Seq. No.

278993 1.R1011 Contig ID $xmt700\overline{2}60389.h2$ 5'-most EST

289198 Seq. No.

279106 1.R1011 Contig ID $nbm700\overline{4}68937.h1$ 5'-most EST

BLASTX Method g2864624 NCBI GI BLAST score 181 3.0e-13E value Match length 105 % identity 37

(AL021811) putative protein [Arabidopsis thaliana] NCBI Description

289199 Seq. No.

279131 1.R1011 Contig ID 5'-most EST $xmt700\overline{2}60738.h1$

289200 Seq. No.

Contig ID 279177 1.R1011 $xmt700\overline{2}60917.h1$ 5'-most EST

289201 Seq. No.

279190 1.R1011 Contig ID $xmt700\overline{2}60943.h1$ 5'-most EST

Seq. No. 289202

279238 1.R1011 Contig ID 5'-most EST $xmt700\overline{2}64302.h1$

Seq. No. 289203

279276 1.R1011 Contig ID 5'-most EST xmt700261135.h1

Seq. No. 289204

279289 1.R1011 Contig ID 5'-most EST xmt700261160.h1

Method BLASTX NCBI GI q82410 BLAST score 315 E value 4.0e-31 Match length 107 % identity 69



NCBI Description peroxidase (EC 1.11.1.7) BP1 precursor - barley >gi_167081 (M73234) peroxidase BP 1 [Hordeum vulgare]

Seq. No. 289205

Contig ID 279294_1.R1011 5'-most EST xmt700261168.h1

Seq. No. 289206

Contig ID 279353_1.R1011 5'-most EST xmt700266053.h1 Method BLASTX

NCBI GI g2632129
BLAST score 151
E value 1.0e-09
Match length 71
% identity 38

NCBI Description (AJ222589) poly(ADP-ribose) polymerase [Zea mays]

Seq. No. 289207

Contig ID 279366_1.R1011 5'-most EST afb700381623.h1

Method BLASTX
NCBI GI g4006880
BLAST score 165
E value 1.0e-11
Match length 58
% identity 71

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 289208

Contig ID 279376_1.R1011 5'-most EST rv1700453938.h1

Method BLASTX
NCBI GI g4263770
BLAST score 514
E value 3.0e-52
Match length 154
% identity 62

NCBI Description (AC006218) unknown protein [Arabidopsis thaliana]

Seq. No. 289209

Contig ID 279378_1.R1011 5'-most EST xmt700261326.h1

Seq. No. 289210

Contig ID 279427_1.R1011 5'-most EST nbm700475677.h1

Seq. No. 289211

Contig ID 279462_1.R1011 5'-most EST hbs701183560.h1

Seq. No. 289212

Contig ID 279547_1.R1011 5'-most EST xmt700261668.h1

Seq. No. 289213



Contig ID 279588_1.R1011 5'-most EST 1tv700479535.h1

Method BLASTX
NCBI GI g3335169
BLAST score 346
E value 7.0e-33
Match length 94
% identity 70

NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]

>gi_4455197_emb_CAB36520_ (AL035440) embryo-specific

protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No. 289214

Contig ID 279722_1.R1011 5'-most EST xmt700262470.h1

Seq. No. 289215

Contig ID 279757 1.R1011 5'-most EST xmt700262142.h1

Method BLASTX
NCBI GI g1351410
BLAST score 583
E value 2.0e-60
Match length 136
% identity 74

NCBI Description VACUOLAR PROCESSING ENZYME PRECURSOR (VPE)

>gi 511938 dbj BAA06030 (D28876) cysteine proteinase

[Glycine max]

Seq. No. 289216

Contig ID 279781_1.R1011 5'-most EST fdz701164942.h1

Seq. No. 289217

Contig ID 279789_1.R1011 5'-most EST xmt700266632.h1

Seq. No. 289218

Contig ID 279845_1.R1011 5'-most EST xmt700262309.h1

Seq. No. 289219

Contig ID 280172_1.R1011 5'-most EST xmt700262821.h1

Seq. No. 289220

Contig ID 280220 1.R1011 5'-most EST fdz701166461.h1

Seq. No. 289221

Contig ID 280254_1.R1011 5'-most EST xmt700266381.h1

Seq. No. 289222

Contig ID 280328_1.R1011 5!-most EST xmt700266208.h1



Seq. No. 289223

Contig ID 280344 1.R1011 5'-most EST xmt700263082.h1

Seq. No. 289224

Contig ID 280384_1.R1011 5'-most EST xmt700263159.h1

Method BLASTX
NCBI GI g4539005
BLAST score 196
E value 2.0e-15
Match length 68
% identity 63

NCBI Description (AL049481) putative oxidoreductase [Arabidopsis thaliana]

Seq. No. 289225

Contig ID 280440_1.R1011 5'-most EST gct701167784.h1

Seq. No. 289226

Contig ID 280465_1.R1011 5'-most EST xmt700263278.h1

Method BLASTX
NCBI GI g4505941
BLAST score 267
E value 3.0e-23
Match length 147
% identity 41

NCBI Description polymerase (RNA) II (DNA directed) polypeptide B (140kD)

>gi 401012 sp P30876 RPB2 HUMAN DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE (RNA POLYMERASE II SUBUNIT 2) (RPB2)
>gi 346349 pir S28976 DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain - human >gi 254869 bbs 112657 RNA polymerase II second largest subunit, RNA polymerase B second largest subunit [human, HeLa cells, Peptide, 1174 aa] >gi 36122 emb CAA45124 (X63563) RNA polymerase II 140

kDa subunit [Homo sapiens]

Seq. No. 289227

Contig ID 280487_1.R1011 5'-most EST xmt700267466.h1

Method BLASTX
NCBI GI g2147484
BLAST score 217
E value 6.0e-21
Match length 101
% identity 62

NCBI Description homeotic protein - Phalaenopsis sp >gi_1173622 (U34743)

homeobox protein [Phalaenopsis sp. 'hybrid SM9108']

Seq. No. 289228

Contig ID 280491_1.R1011 5'-most EST nbm700466701.h1

Seq. No. 289229

Contig ID 280497_1.R1011 5'-most EST nbm700476190.h1



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Seq. No.
                   289230
                   280504 1.R1011
Contig ID
5'-most EST
                   gwl700613353.hl
                   BLASTX
Method
NCBI GI
                   g4324597
BLAST score
                   312
E value
                   3.0e-28
Match length
                   237
                   41
% identity
NCBI Description
                   (AF106324) sodium proton exchanger Nhx1 [Arabidopsis
                   thaliana]
                   289231
Seq. No.
                   280505 1.R1011
Contig ID
5'-most EST
                   xmt700267072.h1
Seq. No.
                   289232
                   280507 1.R1011
Contig ID
                   xmt700\overline{2}66171.h1
5'-most EST
                   BLASTX
Method
                   g691752
NCBI GI
BLAST score
                   333
E value
                   3.0e-31
                   129
Match length
% identity
                   56
                  (D29803) preproMP27-MP32 [Cucurbita sp.]
NCBI Description
Seq. No.
                   289233
Contig ID
                   280540 1.R1011
                   xmt700267608.h1
5'-most EST
                   289234
Seq. No.
                   280551 1.R1011
Contig ID
5'-most EST
                   xmt700\overline{2}63420.h1
Method
                   BLASTX
                   q3724087
NCBI GI
BLAST score
                   418
E value
                   4.0e-41
Match length
                   104
% identity
                   75
                   (AJ011840) 1-deoxyxylulose 5-phosphate synthase
NCBI Description
                    [Catharanthus roseus]
                   289235
Seq. No.
                   280597 1.R1011
Contig ID
                   fdz701\overline{1}64132.h1
5'-most EST
                   289236
Seq. No.
Contig ID
                   280614 1.R1011
5'-most EST
                   ypc700804863.hl
```

Seq. No. Contig ID 289237

280662 1.R1011 xmt700263690.h1 5'-most EST

Method BLASTX NCBI GI g1046377



BLAST score 194 E value 6.0e-15 Match length 58 % identity 55

NCBI Description (S78994) copper amine oxidase {C-terminal} {EC 1.4.3.6}

[lentil, seedling, Peptide Partial, 224 aa] [Lens

culinaris]

Seq. No. 289238

Contig ID 280669_1.R1011 5'-most EST rv1700457446.h1

Method BLASTX
NCBI GI g4335722
BLAST score 474
E value 1.0e-47
Match length 128
% identity 66

NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No. 289239

Contig ID 280689_1.R1011 5'-most EST gwl700618450.h2

Seq. No. 289240

Contig ID 280730_1.R1011 5'-most EST nbm700471854.h1

Seq. No. 289241

Contig ID 280731_1.R1011 5'-most EST xmt700263787.h1

Seq. No. 289242

Contig ID 280756_1.R1011 5'-most EST fdz701163137.h1

Seq. No. 289243

Contig ID 280769_1.R1011 5'-most EST xmt700263864.h1

Seq. No. 289244

Contig ID 280811_1.R1011 5'-most EST xmt700263927.h1

Seq. No. 289245

Contig ID 280875_1.R1011 5'-most EST nwy700446408.h1

Seq. No. 289246

Contig ID 280884_1.R1011 5'-most EST kem700611087.h1

Method BLASTX
NCBI GI g2244971
BLAST score 225
E value 3.0e-25
Match length 96
% identity 64

NCBI Description (Z97340) hypothetical protein [Arabidopsis thaliana]



 Seq. No.
 289247

 Contig ID
 280926_1.R1011

 5'-most EST
 xmt700264101.h1

Seq. No. 289248

Contig ID 280992_1.R1011 5'-most EST pwr700451435.h1

Seq. No. 289249

Contig ID 281025_1.R1011 5'-most EST xmt700264271.h1 Method BLASTX

NCBI GI g3176687
BLAST score 388
E value 1.0e-37
Match length 97
% identity 73

NCBI Description (AC003671) Strong similarity to trehalose-6-phosphate

synthase homolog from A. thaliana chromosome 4 contig gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and gb_R64855 come from this gene. [Arabidopsis thaliana]

Seq. No. 289250

Contig ID 281069_1.R1011 5'-most EST rvt700549465.h1

Method BLASTX
NCBI GI g4558672
BLAST score 253
E value 7.0e-26
Match length 147
% identity 49

NCBI Description (AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis

thaliana]

Seq. No. 289251

Contig ID 281242_1.R1011 5'-most EST xmt700264546.h1

Method BLASTX
NCBI GI g431162
BLAST score 246
E value 4.0e-21
Match length 104
% identity 54

NCBI Description (D21822) ORF [Lilium longiflorum]

Seq. No. 289252

Contig ID 281369_1.R1011 5'-most EST xmt700264709.h1

Seq. No. 289253

Contig ID 281378 2.R1011 5'-most EST fdz701161357.h1

Seq. No. 289254

Contig ID 281408_1.R1011 5'-most EST gct701173338.h2



a	37 -	200255
Seq.	NO.	289255

281411 1.R1011 Contig ID 5'-most EST xmt700264764.h1

Seq. No. 289256

281434 1.R1011 Contig ID 5'-most EST $xmt700\overline{2}66806.h1$

Seq. No. 289257

Contig ID 281480 1.R1011 5'-most EST $xmt700\overline{2}64859.h1$

289258 Seq. No.

281508 1.R1011 Contig ID $xmt700\overline{2}64901.h1$ 5'-most EST

Seq. No. 289259

281710 1.R1011 Contig ID 5'-most EST yyf700349425.h1

Seq. No. 289260

Contig ID 281909 1.R1011 5'-most EST ypc700801033.h1

Seq. No. 289261

281918 1.R1011 Contig ID 5'-most EST $xmt700\overline{2}65541.h1$

Seq. No. 289262

281922 1.R1011 Contig ID 5'-most EST $xmt700\overline{2}65546.h1$ BLASTX

Method g3482916 NCBI GI BLAST score 162 3.0e-11E value Match length 102

% identity 33

NCBI Description (AC003970) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 289263

282015 1.R1011 Contig ID 5'-most EST yyf700350879.hl

289264 Seq. No.

282159 1.R1011 Contig ID 5'-most EST $xmt700\overline{2}65933.h1$

Seq. No. 289265

282172 1.R1011 Contig ID 5'-most EST $xmt700\overline{2}65951.h1$

Seq. No. 289266

Contig ID 282174 1.R1011 5'-most EST yyf700349082.h1

Seq. No. 289267

Contig ID 5'-most EST	282201_1.R1011 xmt700265990.h1
Seq. No. Contig ID 5'-most EST	289268 282211 1.R1011 xmt700266009.h1
Seq. No. Contig ID 5'-most EST	289269 282298_1.R1011 xmt700266120.h1
Seq. No. Contig ID 5'-most EST	289270 282430_1.R1011 xmt700266296.h1
Seq. No. Contig ID 5'-most EST	289271 282506_1.R1011 xmt700266417.h1
Seq. No. Contig ID 5'-most EST	289272 282520_1.R1011 ceu700431981.h1
Seq. No. Contig ID 5'-most EST	289273 282522_1.R1011 xmt700266436.h1
Seq. No. Contig ID 5'-most EST	289274 282647_1.R1011 nwy700444441.h1
Seq. No. Contig ID 5'-most EST	289275 282670_1.R1011 hvj700623215.h1
Seq. No. Contig ID 5'-most EST	289276 282674_2.R1011 hbs701182121.h1
Seq. No. Contig ID 5'-most EST	289277 282777_1.R1011 fdz701163675.h1
Seq. No. Contig ID 5'-most EST	289278 282806_1.R1011 hbs701186252.h1
Seq. No. Contig ID 5'-most EST	289279 282839_1.R1011 xmt700266913.h1

289279 282839_1.R1011 xmt700266913.h1 289280 282979_1.R1011 xmt700267140.h1

Seq. No. 289281 Contig ID 283020_1.R1011

Seq. No.
Contig ID
5'-most EST



5'-most EST hbs701181990.h1

Method BLASTX
NCBI GI g3738230
BLAST score 272
E value 7.0e-24
Match length 77

Match length 77 % identity 64

NCBI Description (AB007790) DREB2A [Arabidopsis thaliana]

>gi_4126706_dbj_BAA36705_ (AB016570) DREB2A [Arabidopsis

thaliana]

Seq. No. 289282

Contig ID 283025_1.R1011 5'-most EST fdz701158803.h1

Seq. No. 289283

Contig ID 283028_1.R1011 5'-most EST zuv700355514.h1

Method BLASTX
NCBI GI g1742800
BLAST score 149
E value 9.0e-10
Match length 98
% identity 39

NCBI Description (D90814) ORF_ID:o322#7; similar to [SwissProt Accession

Number Q06373 [Escherichia coli]

Seq. No. 289284

Contig ID 283038_1.R1011 5'-most EST xmt700267266.h1

Method BLASTN
NCBI GI g21892
BLAST score 78
E value 6.0e-36
Match length 133
% identity 90

NCBI Description T.aestivum (clone pTAU1.3) U1 snRNA

Seq. No. 289285

Contig ID 283092_1.R1011 5'-most EST xmt700267286.h1

Seq. No. 289286

Contig ID 283102_1.R1011 5'-most EST xmt700267305.h1

Seq. No. 289287

Contig ID 283174_1.R1011 5'-most EST hbs701186172.h1

Seq. No. 289288

Contig ID 283274_1.R1011 5'-most EST xmt700267602.h1

Method BLASTX
NCBI GI g4586244
BLAST score 387
E value 2.0e-37



Match length 112 % identity 68

NCBI Description (AL049640) putative protein [Arabidopsis thaliana]

Seq. No. 289289

Contig ID 283410_1.R1011 5'-most EST rvt700550221.h1

Seq. No. 289290

Contig ID 283418_1.R1011 5'-most EST pwr700452089.h1

Seq. No. 289291

Contig ID 283484_1.R1011 5'-most EST xmt700267960.h1

Seq. No. 289292

Contig ID 283496_1.R1011 5'-most EST zuv700356285.h1

Method BLASTX
NCBI GI g2500142
BLAST score 295
E value 8.0e-27
Match length 117
% identity 53

NCBI Description PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2)

>gi_2313254_gb_AAD07236.1_ (AE000537) peptide chain release

factor RF-2 (prfB) [Helicobacter pylori 26695]

Seq. No. 289293

Contig ID 283533 1.R1011 5'-most EST xmt700268041.h1

Seq. No. 289294

Contig ID 283669 1.R1011 5'-most EST wen700331869.h1

Seq. No. 289295

Contig ID 283708_1.R1011 5'-most EST xtj700378135.h1

Seq. No. 289296

Contig ID 283767_1.R1011 5'-most EST wen700332011.h1

Method BLASTN
NCBI GI g4505010
BLAST score 195
E value 1.0e-106
Match length 308
% identity 91

NCBI Description Homo sapiens lysyl oxidase-like 2 (LOXL2) mRNA

>gi 1890107 gb U89942 HSU89942 Human lysyl oxidase-related

protein (WS9-14) mRNA, complete cds

Seq. No. 289297

Contig ID 283793 1.R1011 5'-most EST gct701176265.h1



Seq. No. 289298

Contia ID 283889 1.R1011 5'-most EST nwy700444650.h1

BLASTN Method NCBI GI q5016088 BLAST score 244 E value 1.0e-135 Match length 409 96 % identity

NCBI Description Homo sapiens actin, beta (ACTB) mRNA

>gi 28251 emb X00351 HSAC07 Human mRNA for beta-actin

289299 Seq. No.

Contig ID 283983 1.R1011 5'-most EST wen700332371.hl

Seq. No. 289300

284006 1.R1011 Contig ID 5'-most EST pwr700450033.h2

BLASTX Method q127148 NCBI GI BLAST score 447 E value 1.0e-47 Match length 96 98 % identity

MYOSIN LIGHT CHAIN ALKALI, SMOOTH-MUSCLE ISOFORM (MLC3SM) NCBI Description

(LC17B) (LC17-GI) >gi_108819_pir__ S13671 myosin catalytic light chain A - bovine >gi_1360691_pir__ MOHU6N myosin alkali light chain 6, nonmuscle form - human

>gi_578_emb_CAA38721_ (X54977) 17,000 dalton myosin light
chain [Bos taurus] >gi_189018 (M22919) non-muscle myosin

light chain [Homo sapiens]

Seq. No. 289301

284017 1.R1011 Contig ID $wen700\overline{3}32431.h1$ 5'-most EST

Method BLASTX q132653 NCBI GI 544 BLAST score 7.0e-56 E value 108 Match length % identity 98

60S RIBOSOMAL PROTEIN L12 >gi_71213_pir__R7RT12 ribosomal NCBI Description

protein L12 - rat >gi_57680_emb_CAA37581_ (X53504)

ribosomal protein L12 [Rattus rattus]

289302 Seq. No.

284041 1.R1011 Contig ID pwr700449743.h2 5'-most EST

BLASTX Method NCBI GI g31092 BLAST score 733 8.0e-87 E value Match length 166 99 % identity

NCBI Description (X16869) elongation factor 1-alpha (AA 1-462) [Homo



sapiens]

289303 Seq. No. 284056 1.R1011 Contig ID 5'-most EST bdu700382713.h1 Method BLASTX NCBI GI g127397 BLAST score 172 1.0e-12 E value Match length 61 56 % identity

METALLOTHIONEIN-II (MT-II) >gi_72158_pir__SMHU2
metallothionein 2 - human >gi_37121_emb_CAA23841_ (V00594)
reading frame metallothionein [Homo sapiens] NCBI Description

>gi 263507 bbs 122344 (S52379) metallothionein-II, MT-II [human, astrocytoma U373MG cell line, Peptide, 61 aa] [Homo sapiens] >gi_386863 (J00271) metallothionein II [Homo sapiens] >gi_1495466_emb_CAA65915_ (X97260) Metallothionein

2 [Homo sapiens] >gi 223529 prf 0811253A metallothionein

II [Homo sapiens]

289304 Seq. No.

Contig ID 284062 1.R1011 5'-most EST pwr700453014.h1

Method BLASTX g116509 NCBI GI BLAST score 241 2.0e-28 E value Match length 90 % identity 80

CALCYCLIN (PROLACTIN RECEPTOR ASSOCIATED PROTEIN) (PRA) NCBI Description

(GROWTH FACTOR-INDUCIBLE PROTEIN 2A9) (S100 CALCIUM-BINDING

PROTEIN A6) >gi_71752_pir__BCHUY calcyclin - human

>gi 179766 (J02763) calcyclin [Homo sapiens] >gi_179768 (M18981) put. calcyclin; putative [Homo sapiens] >gi 183098

(M14300) 2A9 peptide [Homo sapiens]

289305 Seq. No.

Contig ID 284106 1.R1011 5'-most EST yyf700348201.h1

Seq. No. 289306

Contig ID 284157 1.R1011 5'-most EST zla700380106.h1

Seq. No. 289307

Contig ID 284190 1.R1011 5'-most EST bdu700382730.h1

Method BLASTX NCBI GI q1374698 BLAST score 240 8.0e-21 E value 68 Match length % identity 71

(D83032) nuclear protein, NP220 [Homo sapiens] NCBI Description

Seq. No. 289308

5'-most EST

Seq. No.

Contig ID



```
284237 1.R1011
Contig ID
5'-most EST
                   wen700332876.h1
                   289309
Seq. No.
                   284245 1.R1011
Contig ID
5'-most EST
                   wen700336227.h1
Seq. No.
                   289310
                   284246 1.R1011
Contig ID
5'-most EST
                   yyf700347722.h1
Method
                   BLASTX
NCBI GI
                   q4506593
BLAST score
                   344
E value
                   1.0e-32
Match length
                   88
                   76
% identity
                   ribosomal protein L10 >gi_4506603_ref_NP_002939.1_pRPL15
NCBI Description
                   ribosomal protein L15 >gi 414587 (L25899) ribosomal protein
                   L10 [Homo sapiens]
                   289311
Seq. No.
Contig ID
                   284413 1.R1011
5'-most EST
                   rv1700456562.h1
Method
                   BLASTX
NCBI GI
                   q4503797
BLAST score
                   329
E value
                   1.0e-30
Match length
                   65
% identity
                   100
                   ferritin, light polypeptide >gi 182518 (M10119) ferritin
NCBI Description
                   light subunit [Homo sapiens]
Seq. No.
                   289312
                   284430 1.R1011
Contig ID
                   wen700333283.hl
5'-most EST
                   289313
Seq. No.
                   284461 1.R1011
Contig ID
                   wen700\overline{3}33232.h1
5'-most EST
Method
                   BLASTX
                   g306553
NCBI GI
BLAST score
                   1020
E value
                   1.0e-111
Match length
                   214
                   93
% identity
NCBI Description
                   (L13802) ribosmal protein small subunit [Homo sapiens]
Seq. No.
                   289314
                   284509 1.R1011
Contig ID
5'-most EST
                   wen700\overline{3}33306.h1
Seq. No.
                   289315
                   284526 1.R1011
Contig ID
```

40245

 $wen700\overline{3}33327.h1$

284530_1.R1011



5'-most EST wen700333334.h1 Method BLASTX q4539351 NCBI GI 298 BLAST score E value 4.0e-27 Match length 129 47 % identity NCBI Description (AL035539) putative protein [Arabidopsis thaliana] 289317 Seq. No. Contig ID 284538 1.R1011 5'-most EST wen700333352.h1 Seq. No. 289318 Contig ID 284596 1.R1011 yyf700350335.h1 5'-most EST BLASTX Method NCBI GI g132827 BLAST score 372 5.0e-36 E value Match length 81 % identity 89 NCBI Description 60S RIBOSOMAL PROTEIN L26 >gi_71312_pir__R5RT26 ribosomal protein L26 - rat >gi_57692 emb CAA32801 (X14671) rpl 26 (AA 1-145) [Rattus rattus] >gi_226411_prf__1511091A ribosomal protein L26 [Rattus norvegicus] 289319 Seq. No. Contig ID 284643 1.R1011 5'-most EST nwy700443948.h1 Method BLASTX NCBI GI q198578 BLAST score 469 E value 3.0e-47Match length 94 % identity 98 NCBI Description (M76762) ribosomal protein [Mus musculus] Seq. No. 289320 Contig ID 284650 1.R1011 5'-most EST pwr700449673.h1 Method BLASTX NCBI GI g133043 BLAST score 378 E value 1.0e-36 Match length 80 % identity 94 NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN PO (L10E) >gi 71139 pir R5MS10 acidic ribosomal protein P0 - mouse >gi 50026 emb CAA33338 (X15267) PO protein [Mus musculus]

289321 Seq. No.

284694 1.R1011 Contig ID zuv700354406.h1 5'-most EST

Method BLASTX NCBI GI g121665 BLAST score 499



E value Match length 94 98 % identity

GLUTATHIONE PEROXIDASE (GSHPX-1) (CELLULAR GLUTATHIONE NCBI Description

PEROXIDASE) >qi 4467837 emb CAB37833 (Y00483) glutathione

peroxidase [Homo sapiens]

289322 Seq. No.

284752 1.R1011 Contig ID pwr700449776.h2 5'-most EST

Method BLASTX NCBI GI q2119204 BLAST score 758 1.0e-80 E value 165 Match length 93 % identity

vimentin - human >qi 37850 emb CAA39600 (X56134) vimentin NCBI Description

[Homo sapiens]

289323 Seq. No.

284762 1.R1011 Contig ID wen700333707.h1 5'-most EST

Method BLASTX NCBI GI q4506701 BLAST score 725 6.0e-77 E value 143 Match length 98 % identity

NCBI Description

ribosomal protein S23 >gi_730647_sp_P39028_RS23_HUMAN 40S RIBOSOMAL PROTEIN S23 >gi_543449_pir__S41955 ribosomal protein S23 - rat >gi_631360_pir__S42105 ribosomal protein S23, cytosolic - human >gi_414349_dbj_BAA03400__(D14530) ribosomal protein [Homo sapiens] >gi 453281 emb CAA54584

(X77398) ribosomal protein S23 [Rattus norvegicus]

Seq. No. 289324

285001 1.R1011 Contig ID zuv700354640.h1 5'-most EST

Method BLASTX NCBI GI g2340104 BLAST score 167 7.0e-12 E value Match length 38 % identity 79

(AC002476) Very similar and perhaps identical to NCBI Description

Hs-CUL-4B.; 80-100% similarity to partial sequence U58091

(PID:g1381150). [Homo sapiens]

289325 Seq. No.

285051 1.R1011 Contig ID yyf700347590.h1 5'-most EST

289326 Seq. No.

285205 1.R1011 Contig ID 5'-most EST xyt700342555.h1

BLASTX Method NCBI GI g4504345



BLAST score 727 E value 3.0e-77 Match length 142 % identity 99 NCBI Description hemoglo

hemoglobin, alpha 1 >gi_4504347_ref_NP_000549.1_pHBA2_hemoglobin, alpha 2 >gi_122412_sp_P01922_HBA_HUMAN
HEMOGLOBIN ALPHA CHAIN >gi_2134629_pir___T58217 hemoglobin
alpha 1 chain - chimpanzee >gi_2134630_pir__I78575
hemoglobin alpha 2 chain - chimpanzee

>gi_3891440_pdb_1BZ1_A Chain A, Hemoglobin (Alpha + Met)
Mutant >gi_3891442_pdb_1BZ1_C Chain C, Hemoglobin (Alpha +
Met) Mutant >gi_28547_emb_CAA23748_ (V00488) alpha globin
[Homo sapiens] >gi_28558_emb_CAA23752_ (V00493) reading
frame alpha-globin [Homo sapiens] >gi_38223_emb_CAA25044_

(X00226) alpha1-globin [Pan troglodytes]

>gi_38225_emb_CAA25045_ (X00227) alpha2-globin [Pan
troglodytes] >gi_386764 (J00153) hba2 alpha globin [Homo
sapiens] >gi_386765 (J00153) hba1 alpha globin [Homo

sapiens] >gi_1817577_emb_CAB06554_ (Z84721) alpha-globin 1

[Homo sapiens] >gi 1817578 emb CAB06555 (Z84721) alpha-globin 2 [Homo sapiens] >gi 3859550 (AF09763)

alpha-globin 2 [Homo sapiens] >gi_3859550 (AF097635) alpha-2 globin [Homo sapiens] >gi_4038450 (AF105974) alpha

one globin [Homo sapiens]

Seq. No. 289327

Contig ID 285262_1.R1011 5'-most EST wen700334620.h1

Seq. No. 289328

Contig ID 285408_1.R1011 5'-most EST wen700334950.h1

Method BLASTX
NCBI GI g1076715
BLAST score 297
E value 3.0e-27
Match length 67
% identity 78

NCBI Description abscisic acid-induced protein HVA22 - barley >q1 404589

(L19119) A22 [Hordeum vulgare]

Seq. No. 289329

Contig ID 285459_1.R1011 5'-most EST wen700335053.h1

Method BLASTX
NCBI GI g3080740
BLAST score 205
E value 7.0e-19
Match length 83
% identity 61

NCBI Description (U77366) pasticcino 1-D [Arabidopsis thaliana]

Seq. No. 289330

Contig ID 285467_1.R1011 5'-most EST wen700335072.h1

Method BLASTX NCBI GI g4008577 BLAST score 220



E value Match length 130 % identity

(AL034491) conserved hypothetical protein NCBI Description

[Schizosaccharomyces pombe]

Seq. No. 289331

285557 1.R1011 Contig ID 5'-most EST nwy700446696.hl

Method BLASTX NCBI GI q132848 BLAST score 255 E value 7.0e-27 65 Match length 93 % identity

60S RIBOSOMAL PROTEIN L23A >gi_279654_pir__R3RT3A ribosomal protein L23a - rat >gi_57690_emb_CAA46336_ (X65228) ribosomal protein L23a [Rattus rattus] >gi_1399086 (U43701) ribosomal protein L23a [Homo sapiens] >gi_2739452 NCBI Description

(AF001689) ribosomal protein L23A [Homo sapiens]

289332 Seq. No.

Contig ID 285645 1.R1011 5'-most EST wen700335416.h1

289333 Seq. No.

285679 1.R1011 Contig ID 5'-most EST $nbm700\overline{4}69008.h1$

289334 Seq. No.

285691 1.R1011 Contig ID 5'-most EST nbm700475108.h1

Method BLASTX NCBI GI q3142303 BLAST score 323 4.0e-30 E value Match length 94 % identity 63

NCBI Description (AC002411) Strong similarity to MRP-like ABC transporter

gb U92650 from A. thaliana and canalicular multi-drug resistance protein gb L49379 from Rattus norvegicus.

[Arabidopsis thaliana]

Seq. No. 289335

285731 1.R1011 Contig ID 5'-most EST xdb700338906.h1

289336 Seq. No.

285755 1.R1011 Contig ID $xdb700\overline{3}38672.h1$ 5'-most EST

BLASTX Method NCBI GI g2213632 BLAST score 178 3.0e-13 E value 77 Match length 49 % identity

NCBI Description (AC000103) F21J9.24 [Arabidopsis thaliana]



```
289337
Seq. No.
Contig ID
                   285758 1.R1011
                   wen700\overline{3}35628.h1
5'-most EST
                   289338
Seq. No.
Contig ID
                   285774 1.R1011
                   ceu700429323.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g507273
BLAST score
                   194
                   9.0e-15
E value
Match length
                   91
% identity
                   46
                   (L27052) probably expressed; ORFA; putative [Leishmania
NCBI Description
                   infantum]
                   289339
Seq. No.
Contig ID
                   285783 1.R1011
5'-most EST
                   wen700\overline{3}35673.h1
                   289340
Seq. No.
                   285795 1.R1011
Contig ID
5'-most EST
                   xdb700337056.h1
Seq. No.
                   289341
                   285809 1.R1011
Contig ID
5'-most EST
                   xdb700338778.h1
Seq. No.
                   289342
Contig ID
                   285814 1.R1011
                   wen700335726.h1
5'-most EST
Method
                   BLASTN
                   g609289
NCBI GI
BLAST score
                   118
E value
                   5.0e-60
Match length
                   154
                   95
% identity
NCBI Description
                   Z.mays cultivar (LG11) ROA mRNA for replication origin
                   activator protein
Seq. No.
                   289343
Contig ID
                   285880 1.R1011
5'-most EST
                   wen700335866.h1
Method
                   BLASTN
NCBI GI
                   q466266
BLAST score
                   59
E value
                   1.0e-24
Match length
                   224
% identity
                   93
```

NCBI Description Mus musculus c57bl6 metallothionein IV (MTIV) gene,

complete cds

Seq. No. 289344

Contig ID 285897_1.R1011 5'-most EST yyf700351111.h1

Method BLASTX



NCBI GI g2829612 BLAST score 175 E value 7.0e-13 Match length 90 % identity 42

NCBI Description HYPOTHETICAL 30.8 KD PROTEIN SLL0818

>gi 1653197 dbj BAA18113 (D90911) hypothetical protein

[Synechocystis sp.]

Seq. No. 289345

Contig ID 285929_1.R1011 5'-most EST wen700335979.h1

Seq. No. 289346

Contig ID 285990_1.R1011 5'-most EST wen700336136.h1

Seq. No. 289347

Contig ID 286025_1.R1011 5'-most EST xtj700377708.h1

Method BLASTX
NCBI GI g4506593
BLAST score 378
E value 1.0e-36
Match length 95
% identity 78

NCBI Description ribosomal protein L10 >gi_4506603_ref_NP_002939.1_pRPL15_

ribosomal protein L15 >gi_414587 (L25899) ribosomal protein

L10 [Homo sapiens]

Seq. No. 289348

Contig ID 286164_1.R1011 5'-most EST gwl700615724.h1

Method BLASTX
NCBI GI g114773
BLAST score 561
E value 1.0e-57
Match length 119
% identity 88

NCBI Description BETA-2-MICROGLOBULIN PRECURSOR >gi_70065_pir__MGHUB2

beta-2-microglobulin precursor - human

>gi_2118697_pir__I36963 beta-2-microglobulin - chimpanzee >gi_2118698_pir__I37063 beta-2-microglobulin - gorilla >gi_176827 (M30683) beta-2-microglobulin [Pan troglodytes] >gi_177065 (M30684) beta-2-microglobulin [Gorilla gorilla] >gi_4038733_dbj_BAA35182_ (AB021288) beta 2-microglobulin

[Homo sapiens]

Seq. No. 289349

Contig ID 286165_1.R1011 5'-most EST wen700336474.h1

Seq. No. 289350

Contig ID 286335_1.R1011 5'-most EST wen700336753.h1

Seq. No. 289351



```
Contia ID
                   286390 1.R1011
5'-most EST
                   wen700\overline{3}36839.h1
                   BLASTN
Method
NCBI GI
                   q4519628
BLAST score
                   138
                   5.0e-72
E value
Match length
                   178
% identity
                   94
                   Homo sapiens mRNA for oxidative-stress responsive 1,
NCBI Description
                   complete cds
Seq. No.
                   289352
Contig ID
                   286405 1.R1011
5'-most EST
                   wen700\overline{3}36863.h1
                   289353
Seq. No.
                   286415 1.R1011
Contig ID
5'-most EST
                   wen700\overline{3}36877.h1
                   289354
Seq. No.
                   286430 1.R1011
Contig ID
5'-most EST
                   wen700\overline{3}36905.h1
Seq. No.
                   289355
Contig ID
                   286506_1.R1011
                   fdz701158442.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   a4432840
BLAST score
                   147
E value
                   2.0e-09
Match length
                   66
% identity
                   45
NCBI Description
                   (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                   289356
                   286563 1.R1011
Contig ID
5'-most EST
                   rvt700553453.h1
Method
                   BLASTX
NCBI GI
                   g2194121
BLAST score
                   175
                   7.0e-20
E value
                   107
Match length
% identity
                   53
NCBI Description
                   (AC002062) Strong similarity to Arabidopsis cyclin delta-1
                    (gb ATCD1). EST gb ATTS4338 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   289357
                   286592 1.R1011
Contiq ID
5'-most EST
                   pwr700449160.h1
Method
                   BLASTX
```

q1706958 NCBI GI BLAST score 550 9.0e-57 E value Match length 105 % identity 92

NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]



```
Seq. No.
                          289358
Contig ID
                          286680 1.R1011
5'-most EST
                          pwr700451529.h1
                          289359
Seq. No.
Contig ID
                          286729 1.R1011
                          ceu700429683.h1
5'-most EST
                          BLASTX
Method
                          q1703127
NCBI GI
BLAST score
                          785
E value
                          6.0e-84
Match length
                          154
% identity
                          98
                          ACTIN, CYTOPLASMIC TYPE 8 >gi 537597 (M24770) actin
NCBI Description
                          [Xenopus laevis]
Seq. No.
                          289360
Contig ID
                          286773 1.R1011
                          rv1700456801.h1
5'-most EST
Method
                          BLASTX
                          g133978
NCBI GI
BLAST score
                          547
E value
                          2.0e-56
Match length
                          107
% identity
                          98
                          40S RIBOSOMAL PROTEIN S6 (PHOSPHOPROTEIN NP33)
NCBI Description
                          >gi_70932_pir__R3RTS6 ribosomal protein S6 - rat
>gi_70933_pir__R3MS6 ribosomal protein S6 - mouse
>gi_319910_pir__R3HU6 ribosomal protein S6 - human
>gi_36148_emb_CAA47719_ (X67309) ribosomal protein S6 [Homo
sapiens] >gi_54010_emb_CAA68430_ (Y00348) ribosomal protein
S6 [Mus musculus] >gi_206747 (M29358) ribosomal protein S6
[Pattus porvegious] >gi_307393_ (M77232) ribosomal protein
                          [Rattus norvegicus] >gi_307393 (M77232) ribosomal protein
S6 [Homo sapiens] >gi_1177549_emb_CAA90936_ (Z54209) rpS6
                          [Mus musculus]
Seq. No.
                          289361
Contig ID
                          286780 1.R1011
5'-most EST
                          xtj700377828.h1
Seq. No.
                          289362
                          286834 1.R1011
Contig ID
5'-most EST
                          yyf700348834.h1
Method
                          BLASTX
                          g3928096
NCBI GI
BLAST score
                          259
E value
                          1.0e-22
                          79
Match length
% identity
                          66
                          (AC005770) hypothetical protein [Arabidopsis thaliana]
```

Seq. No.

NCBI Description

289363

286883 1.R1011 Contig ID zvd700460678.hl 5'-most EST

Seq. No. 289364



Contig ID 286897_1.R1011 5'-most EST hbs701180756.h1

Seq. No. 289365

Contig ID 286907_1.R1011 5'-most EST jfc700968602.h1

Method BLASTX
NCBI GI g3687225
BLAST score 303
E value 1.0e-27
Match length 131
% identity 51

NCBI Description (AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No. 289366

Contig ID 286914_1.R1011 5'-most EST nbm700465503.h1

Seq. No. 289367

Contig ID 287024 1.R1011 5'-most EST uwn700281618.h1

Seq. No. 289368

Contig ID 287078_1.R1011 5'-most EST uwn700281718.h1

Seq. No. 289369

Contig ID 287096_1.R1011 5'-most EST xdb700342124.h1

Method BLASTX
NCBI GI g4415925
BLAST score 319
E value 2.0e-29
Match length 163
% identity 43

NCBI Description (AC006282) putative glucosyl transferase [Arabidopsis

thaliana]

Seq. No. 289370

Contig ID 287142_1.R1011 5'-most EST yne700378404.h1

Seq. No. 289371

Contig ID 287150_1.R1011 5'-most EST zuv700357434.h1

Seq. No. 289372

Contig ID 287213_1.R1011 5'-most EST gct701174201.h1

Seq. No. 289373

Contig ID 287244 1.R1011 5'-most EST rv1700458514.h1

Method BLASTX
NCBI GI g2529685
BLAST score 245
E value 8.0e-21



Match length 128 % identity 48

NCBI Description (AC002535) putative dimethyladenosine transferase [Arabidopsis thaliana]

Seq. No. 289374

Contig ID 287286_1.R1011 5'-most EST xdb700337260.h1

Seq. No. 289375

Contig ID 287292_1.R1011 5'-most EST yyf700351073.h1

Seq. No. 289376

Contig ID 287301_1.R1011 5'-most EST xdb700337286.h1 Method BLASTX

NCBI GI g4432846
BLAST score 237
E value 1.0e-19
Match length 74
% identity 64

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 289377

Contig ID 287305_1.R1011 5'-most EST hbs701180942.h1

Method BLASTN
NCBI GI g22371
BLAST score 219
E value 1.0e-120
Match length 272
% identity 96

NCBI Description Maize Mu4 transposable element DNA

Seq. No. 289378

Contig ID 287321 1.R1011 5'-most EST fdz701160506.h1

Seq. No. 289379

Contig ID 287357_1.R1011 5'-most EST xdb700337383.h1

Seq. No. 289380

Contig ID 287360_1.R1011 5'-most EST xdb700337389.h1

Seq. No. 289381

Contig ID 287441_1.R1011 5'-most EST xdb700337528.h1

Method BLASTX
NCBI GI g2829887
BLAST score 188
E value 2.0e-14
Match length 56
% identity 59

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]



Seq. No. 289383

Contig ID 287531_1.R1011 5'-most EST gct701178605.h1

Method BLASTX
NCBI GI g4138131
BLAST score 165
E value 2.0e-11
Match length 82
% identity 46

NCBI Description (AJ011828) NDX1 homeobox protein [Lotus japonicus]

Seq. No. 289384

Contig ID 287563 1.R1011 5'-most EST xdb700341991.h1

Seq. No. 289385

Contig ID 287565_1.R1011 5'-most EST rvt700552679.h1

Seq. No. 289386

Contig ID 287613_1.R1011 5'-most EST xdb700342157.h1

Seq. No. 289387

Contig ID 287613_2.R1011 5'-most EST xdb700342133.h1

Seq. No. 289388

Contig ID 287649_1.R1011 5'-most EST xdb700337856.h1

Seq. No. 289389

Contig ID 287686_1.R1011 5'-most EST nbm700465642.h1

Method BLASTX
NCBI GI g3046711
BLAST score 215
E value 2.0e-17
Match length 48
% identity 85

NCBI Description (AJ005334) replication factor C/activator 1 subunit [Cicer

arietinum]

Seq. No. 289390

Contig ID 287711_1.R1011 5'-most EST gct701168863.h1

Seq. No. 289391

Contig ID 287730_1.R1011 5'-most EST fdz701158967.h2

Seq. No. 289392

Contig ID 5'-most EST	287762_1.R1011 yne700378524.h1
Seq. No. Contig ID 5'-most EST	289393 287780_1.R1011 xdb700338078.h1
Seq. No. Contig ID 5'-most EST	289394 287785_1.R1011 xdb700338087.h1
Seq. No. Contig ID 5'-most EST	289395 287842_1.R1011 xdb700338294.h1
Seq. No. Contig ID 5'-most EST	289396 287876_1.R1011 xdb700338354.h1
Seg. No.	289397

Seq. No.	289397
Contig ID	287925 1.R1011
5'-most EST	rvt700552804.h1

Seq. No.	289398
Contig ID	288179 1.R1011
5'-most EST	xdb700339004.h1

Seq. No.	289399
Contig ID	288185 1.R1011
5'-most EST	xdb700341149.h1

Seq. No.	289400
Contig ID	288270 1.R1011
5'-most EST	$xdb700\overline{3}39145.h1$

Seq. No.	289401
Contig ID	288395 1.R1011
5'-most EST	xdb700339366.h1
Method	BLASTX
NCBI GI	g3377810
BLAST score	387
E value	9.0e-38
Match length % identity	94 76

% identity	76				
NCBI Description	(AF076275)	contains	similarity	to	glutaredoxins
	[Arabidops:	is thalian	na]		

Seq. No.	289402
Contig ID	288703 <u>1.R1011</u>
5'-most EST	xdb700339925.h1
Seq. No.	289403
Contig ID	288775 <u>1.R1011</u>
5'-most EST	tfd700574637.h1

Seq. No. 289404 Contig ID 288845_1.R1011



5'-most EST xdb700340195.

Seq. No. 289405

Contig ID 288847_1.R1011 5'-most EST xdb700340201.h1

Seq. No. 289406

Contig ID 288895_1.R1011 5'-most EST nbm700477939.h1

Seq. No. 289407

Contig ID 288916 1.R1011 5'-most EST fdz701165312.h1

Seq. No. 289408

Contig ID 288973 1.R1011 5'-most EST ceu700434284.h1

Method BLASTX
NCBI GI g4432822
BLAST score 158
E value 1.0e-10
Match length 66
% identity 52

NCBI Description (AC006593) hypothetical protein [Arabidopsis thaliana]

Seq. No. 289409

Contig ID 289016 1.R1011 5'-most EST xdb700342002.h1

Seq. No. 289410

Contig ID 289023_1.R1011 5'-most EST xdb700340620.h1

Seq. No. 289411

Contig ID 289027 1.R1011 5'-most EST xdb700340627.h1

Seq. No. 289412

Contig ID 289028 1.R1011 5'-most EST xdb700342029.h1

Seq. No. 289413

Contig ID 289032 1.R1011 5'-most EST nbm700466001.h1

Seq. No. 289414

Contig ID 289046_1.R1011 5'-most EST xdb700342062.h1

Seq. No. 289415

Contig ID 289051_1.R1011 5'-most EST xdb700342069.h1

Seq. No. 289416

Contig ID 289056_1.R1011 5'-most EST xdb700340679.h1



```
Seq. No.
                     289417
                    289063 1.R1011
Contig ID
                    pwr700451195.h1
5'-most EST
Method
                    BLASTX
NCBI GI
                    g4468310
BLAST score
                    303
                    1.0e-34
E value
Match length
                    90
% identity
                    90
NCBI Description
                    (AL031432) dJ465N24.1 (PUTATIVE novel protein similar to
                    predicted yeast and worm proteins) [Homo sapiens]
Seq. No.
                    289418
                    289096 1.R1011
Contig ID
5'-most EST
                    xdb700340752.h1
Method
                    BLASTX
NCBI GI
                    g4506145
BLAST score
                    644
E value
                    1.0e-124
Match length
                    236
% identity
                    93
                    protease, serine, 1 (trypsin 1)
NCBI Description
                    >gi_136408_sp_P07477_TRY1_HUMAN TRYPSINOGEN I PRECURSOR
>gi_88941_pir_A25852_trypsin (EC 3.4.21.4) I precursor -
human >gi_521216 (M22612) trypsinogen [Homo sapiens]
                    >gi 1552515 (U66061) trypsinogen A [Homo sapiens]
                    >gi 224981 prf 1205235A trypsinogen I [Homo sapiens]
                    289419
Seq. No.
                    289195 1.R1011
Contig ID
5'-most EST
                    ceu700427840.h1
Seq. No.
                    289420
                    289201 1.R1011
Contig ID
5'-most EST
                    xdb700\overline{3}40936.h1
Seq. No.
                    289421
                    289396 1.R1011
Contig ID
5'-most EST
                    xdb700341251.h1
                    BLASTN
Method
NCBI GI
                    g433039
BLAST score
                    67
                    2.0e-29
E value
Match length
                    83
                    95
% identity
NCBI Description
                    Zea mays W-22 clone PREM-1 retroelement PREM-1, partial
                    sequence
Seq. No.
                    289422
```

289493 1.R1011 Contig ID 5'-most EST xdb700341401.h1

Method BLASTX NCBI GI g1169199 BLAST score 326 E value 1.0e-30 Match length 71 % identity 83



NCBI Description

DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT102
>gi_479739_pir__S35271 hypothetical protein - Arabidopsis
thaliana >gi_166928 (L11368) [Arabidopsis thaliana
unidentified mRNA sequence, complete cds.], gene product
[Arabidopsis thaliana]

 Seq. No.
 289423

 Contig ID
 289501 1.R1011

 5'-most EST
 gwl700615079.h1

 Seq. No.
 289424

Contig ID 289851_1.R1011 5'-most EST xdb700342019.h1

 Seq. No.
 289425

 Contig ID
 289944_1.R1011

 5'-most EST
 xdb700342168.h1

 Seq. No.
 289426

 Contig ID
 289971 1.R1011

 5'-most EST
 yne700378411.h1

 Seq. No.
 289427

 Contig ID
 289989_1.R1011

 5'-most EST
 uer700578179.h1

 Seq. No.
 289428

 Contig ID
 290080_1.R1011

 5'-most EST
 gct701175995.h1

 Seq. No.
 289429

 Contig ID
 290111_2.R1011

 5'-most EST
 rvt700550912.h1

 Seq. No.
 289430

 Contig ID
 290186_1.R1011

 5'-most EST
 yne700378779.h1

 Seq. No.
 289431

 Contig ID
 290268_1.R1011

 5'-most EST
 yne700378946.h1

 Seq. No.
 289432

 Contig ID
 290439_1.R1011

 5'-most EST
 gct701172762.h2

 Seq. No.
 289433

 Contig ID
 290445_1.R1011

 5'-most EST
 yne700379377.h1

Seq. No. 289434 Contig ID 290449 1.R1011 5'-most EST yne700379383.h1

Seq. No. 289435 Contig ID 290517_1.R1011 5'-most EST xyt700342469.h1



Method BLASTX
NCBI GI g3927836
BLAST score 546
E value 8.0e-56
Match length 142
% identity 73

NCBI Description (AC005727) unknown protein [Arabidopsis thaliana]

Seq. No.
Contig ID
5'-most EST

289436 290572 1.R1011 vvh700281857.h2

Seq. No.
Contig ID
5'-most EST

289437 290613 1.R1011 nbm700475830.h1

Seq. No.
Contig ID
5'-most EST

289438 290655_1.R1011 vvh700281978.h2

Seq. No.
Contig ID
5'-most EST

289439 290692_1.R1011 xyt700343431.h1

Seq. No.
Contig ID
5'-most EST

290718_1.R1011 xyt700342271.h1

289440

Seq. No. Contig ID 5'-most EST 289441 290810_1.R1011 xyt700342403.h1

Method BLASTX
NCBI GI g4314391
BLAST score 181
E value 1.0e-13
Match length 90
% identity 51

NCBI Description (AC006232) unknown protein [Arabidopsis thaliana]

Seq. No. Contig ID 5'-most EST 289442 290891_1.R1011 xyt700342515.h1

Seq. No.
Contig ID
5'-most EST

289443 290935_1.R1011 yyf700347522.h1

Seq. No.
Contig ID
5'-most EST

289444

291042 1.R1011 xyt700342717.h1

Seq. No.

289445

Contig ID 5'-most EST

291145_1.R1011 hvj700622783.h1

Seq. No. Contig ID

289446

291171 1.R1011



zla700380593.h1 5'-most EST

BLASTX Method NCBI GI g127243 BLAST score 519 8.0e-53 E value 172 Match length 63 % identity

AUTONOMOUS TRANSPOSABLE ELEMENT EN-1 MOSAIC PROTEIN NCBI Description

(SUPPRESSOR-MUTATOR SYSTEM PROTEIN) (SPM)

>gi_320621_pir__S28365 gene 1 protein - maize transposon

 $En-\overline{1} > gi_1\overline{168640}$ (M25427) mosaic protein [Zea mays]

>gi 225007 prf 1206239C gene 1 [Zea mays]

Seq. No. 289447

291186 1.R1011 Contig ID 5'-most EST xyt700342938.hl

BLASTX Method g4097950 NCBI GI BLAST score 349 4.0e-33 E value Match length 121 58 % identity

(U72393) plant IF-like protein [Arabidopsis thaliana] NCBI Description

Seq. No. 289448

Contig ID 291202 1.R1011 5'-most EST pwr700448593.h1

BLASTX Method q1352363 NCBI GI BLAST score 869 7.0e-95 E value Match length 182 93 % identity

NCBI Description ELASTASE IIIA PRECURSOR (PROTEASE E)

>gi_220014_dbj_BAA00212_ (D00306) pancreatic protease E precursor [Homo sapiens] >gi_361780_prf__1410241A

pancreatic protease E isozyme [Homo sapiens]

289449 Seq. No.

Contig ID 291216 1.R1011 5'-most EST xyt700342982.h1

289450 Seq. No.

291231 1.R1011 Contig ID 5'-most EST yyf700349664.h1

289451 Seq. No.

Contig ID 291371 1.R1011 xyt700347214.hl 5'-most EST

Seq. No. 289452

291457 1.R1011 Contig ID xyt700343296.h1 5'-most EST

Method BLASTX NCBI GI g3935147 291 BLAST score 2.0e-26 E value



Match length 93 % identity 61

NCBI Description (AC005106) T25N20.11 [Arabidopsis thaliana]

Seq. No. 289453

Contig ID 291561_1.R1011 5'-most EST xyt700343440.h1

Method BLASTX
NCBI GI g4587512
BLAST score 324
E value 2.0e-30
Match length 88
% identity 70

NCBI Description (AC007060) Strong similarity to gi_2245113

glycerol-3-phosphate permease homolog from Arabidopsis thaliana BAC gb_Z97343 and a member of the PF_00083 Sugar

transporter family

Seq. No. 289454

Contig ID 291597_1.R1011 5'-most EST xyt700343508.h1

Method BLASTX
NCBI GI g2245096
BLAST score 217
E value 8.0e-18
Match length 64
% identity 67

NCBI Description (Z97343) inositol 2-dehydrogenase homolog [Arabidopsis

thaliana]

Seq. No. 289455

Contig ID 291599_1.R1011 5'-most EST zla700379975.h1

Seq. No. 289456

Contig ID 291612_1.R1011 5'-most EST xyt700343524.h1

Method BLASTX
NCBI GI 9746500
BLAST score 174
E value 2.0e-12
Match length 92
% identity 38

NCBI Description (U23515) weak similarity to lupus LA proteins

[Caenorhabditis elegans]

Seq. No. 289457

Contig ID 291626_1.R1011 5'-most EST xyt700343540.h1

Seq. No. 289458

Contig ID 291650_1.R1011 5'-most EST xyt700343572.h1

Seq. No. 289459

Contig ID 291736_2.R1011 5'-most EST yyf700348496.h1



Method BLASTX
NCBI GI g4204310
BLAST score 179
E value 2.0e-13
Match length 38
% identity 82

NCBI Description (AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No.
Contig ID
5'-most EST

289460 291772 1.R1011 gct701179034.h1

Seq. No.
Contig ID
5'-most EST

289461 291779_1.R1011 xyt700345430.h1

Seq. No. Contig ID

289462 291802 1.R1011 hbs701185920.h1

Seq. No.
Contig ID
5'-most EST

5'-most EST

289463 291850_1.R1011 xyt700343856.h1

Method BLASTN
NCBI GI g2655115
BLAST score 85
E value 4.0e-40
Match length 85

% identity 100

NCBI Description Zea mays Ca-5 mRNA, 3'UTR

Seq. No.
Contig ID
5'-most EST

289464 291856_1.R1011 uer700580239.h1

Seq. No.
Contig ID
5'-most EST

289465 291931_1.R1011 xyt700343965.h1

Seq. No.
Contig ID
5'-most EST

289466 292057_1.R1011 nbm700470064.h1

Seq. No.
Contig ID
5'-most EST

289467 292079_1.R1011 yyf700352241.h1

Seq. No.
Contig ID
5'-most EST

289468 292083 1.R1011 xyt700344168.h1

Seq. No.
Contig ID
5'-most EST

289469 292096_1.R1011 xyt700344186.h1

Seq. No. 289470



292176 1.R1011 Contig ID 5'-most EST zuv700354993.h1 289471 Seq. No. 292208 1.R1011 Contig ID 5'-most EST xyt700344364.h1 Seq. No. 289472 Contig ID 292275 1.R1011 5'-most EST zuv700354613.h1 Seq. No. 289473 Contig ID 292289 1.R1011 5'-most EST xyt700344512.h1 BLASTX Method NCBI GI g2262177 BLAST score 226 E value 5.0e-20 90 Match length % identity 56 (AC002329) hypothetical protein similar to T18A10.3 NCBI Description [Arabidopsis thaliana] Seq. No. 289474 292304 1.R1011 Contig ID 5'-most EST zuv700354754.h1 BLASTX Method NCBI GI a4490330 BLAST score 311 E value 7.0e-29 Match length 64 91 % identity NCBI Description (AL035656) splicing factor-like protein [Arabidopsis thaliana] 289475 Seq. No. 292371 1.R1011 Contig ID 5'-most EST zuv700356633.h1 Seq. No. 289476 292422 1.R1011 Contig ID 5'-most EST xyt700344772.h1 289477 Seq. No. 292527 1.R1011 Contig ID 5'-most EST pwr700449747.h2 Method BLASTX

NCBI GI g4506605 BLAST score 553 6.0e-57 E value 129 Match length 87 % identity NCBI Description

ribosomal protein L23 >gi 266927 sp P23131 RL23 HUMAN 60S RIBOSOMAL PROTEIN L23 (L17) >gi_71229_pir_R5RT23 ribosomal protein L23 - rat >gi 34194 emb CAA39417 (X55954) HL23 ribosomal protein [Homo sapiens] >gi 36126 emb CAA37023_

(X52839) ribosomal protein L17 [Homo sapiens]





>gi_57688_emb_CAA41177_ (X58200) ribosomal protein L23
[Rattus rattus]

Seq. No. 289478

Contig ID 292556_1.R1011 5'-most EST xyt700344954.h1

Seq. No. 289479

Contig ID 292570_1.R1011 5'-most EST xyt700344975.h1

Seq. No. 289480

Contig ID 292655_1.R1011 5'-most EST xyt700345512.h1

Seq. No. 289481

Contig ID 292693_1.R1011 5'-most EST zuv700353941.h1

Seq. No. 289482

Contig ID 292741 1.R1011 5'-most EST mwy700442060.h1

Seq. No. 289483

Contig ID 292802_1.R1011 5'-most EST xyt700345363.h1

Seq. No. 289484

Contig ID 292829_1.R1011 5'-most EST xyt700345412.h1

Seq. No. 289485

Contig ID 292866_1.R1011 5'-most EST yyf700349868.h1

Method BLASTX
NCBI GI g2865623
BLAST score 191
E value 1.0e-14
Match length 92
% identity 49

NCBI Description (AF045286)

GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase

[Arabidopsis thaliana]

Seq. No. 289486

Contig ID 292872_1.R1011 5'-most EST fdz701164790.h1

Method BLASTX
NCBI GI g1709971
BLAST score 365
E value 9.0e-43
Match length 92
% identity 100

NCBI Description 60S RIBOSOMAL PROTEIN L10A (CSA-19) >gi 531171 (U12404)

Csa-19 [Homo sapiens]

Seq. No. 289487



Contig ID 292918_1.R1011 5'-most EST yyf700348956.h1

Method BLASTX
NCBI GI g4557060
BLAST score 197
E value 1.0e-15
Match length 72

Match length 72 % identity 58

NCBI Description (AC007154) putative chromosome-associated polypeptide, 5'

partial [Arabidopsis thaliana]

Seq. No. 289488

Contig ID 292937_1.R1011 5'-most EST xyt700345571.h1 Method BLASTX

Method BLASTX
NCBI GI g3859568
BLAST score 301
E value 1.0e-27
Match length 65
% identity 83

NCBI Description (AF098752) unknown [Oryza sativa]

Seq. No. 289489

Contig ID 292963_1.R1011 5'-most EST xyt700345615.h1

Seq. No. 289490

Contig ID 292982_1.R1011 5'-most EST yyf700348043.h1

Seq. No. 289491

Contig ID 293070_1.R1011 5'-most EST xyt700345762.h1

Seq. No. 289492

Contig ID 293160_1.R1011 5'-most EST xyt700345895.h1

Seq. No. 289493

Contig ID 293243_1.R1011 5'-most EST xyt700346014.h1

Seq. No. 289494

Contig ID 293290 1.R1011 5'-most EST yyf700351022.h1

Seq. No. 289495

Contig ID 293329_1.R1011 5'-most EST xyt700346134.h1

Seq. No. 289496

Contig ID 293338_1.R1011 5'-most EST yyf700348408.h1

Method BLASTX
NCBI GI g4455231
BLAST score 338
E value 5.0e-32



Match length 92 % identity 67

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 289497

Contig ID 293364_1.R1011 5'-most EST xyt700346204.h1

Seq. No. 289498

Contig ID 293370_1.R1011 5'-most EST xyt700346212.h1

Method BLASTX
NCBI GI g2290770
BLAST score 153
E value 3.0e-10
Match length 89
% identity 33

NCBI Description (AF002163) delta-adaptin [Homo sapiens]

Seq. No. 289499

Contig ID 293373_1.R1011 5'-most EST xyt700346217.h1

Seq. No. 289500

Contig ID 293409_1.R1011 5'-most EST hvj700620330.h1

Seq. No. 289501

Contig ID 293446_1.R1011 5'-most EST yyf700352316.h1

Seq. No. 289502

Contig ID 293448_1.R1011 5'-most EST yyf700351980.h1

Seq. No. 289503

Contig ID 293463_1.R1011 5'-most EST yyf700351135.h1

Seq. No. 289504

Contig ID 293499_1.R1011 5'-most EST xyt700346385.h1

Seq. No. 289505

Contig ID 293559_1.R1011 5'-most EST xyt700346476.h1

Seq. No. 289506

Contig ID 293597_1.R1011 5'-most EST xyt700347332.h1 Method BLASTN

NCBI GI g1263159 BLAST score 34 E value 8.0e-10 Match length 66

% identity 88

NCBI Description O.sativa DNA for LRK2 gene



```
289507
Seq. No.
                  293635 1.R1011
Contig ID
                  xyt700\overline{3}46587.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1617270
BLAST score
                   319
                   4.0e-30
E value
Match length
                  73
% identity
                  84
                  (X94624) acyl-CoA synthetase [Brassica napus]
NCBI Description
Seq. No.
                   289508
                   293651 1.R1011
Contig ID
5'-most EST
                  xyt700346612.h1
Seq. No.
                   289509
                   293662 1.R1011
Contig ID
5'-most EST
                  yyf700348472.h1
Seq. No.
                   289510
Contig ID
                   293686 1.R1011
5'-most EST
                  yyf700348438.h1
Seq. No.
                   289511
                   293704 1.R1011
Contig ID
5'-most EST
                  xyt700346683.h1
Method
                  BLASTX
NCBI GI
                   g3702631
BLAST score
                   265
                   2.0e-23
E value
Match length
                   75
% identity
                   65
                   (AL031824) protein transport protein sec23 homolog
NCBI Description
                   [Schizosaccharomyces pombe]
                   289512
Seq. No.
                   293758 1.R1011
Contig ID
5'-most EST
                  yyf700350773.hl
Seq. No.
                   289513
                   293771 1.R1011
Contig ID
5'-most EST
                   xyt700346802.h1
Method
                   BLASTN
NCBI GI
                   g4558372
BLAST score
                   34
                   9.0e-10
E value
Match length
                   46
                   93
% identity
                  Mus musculus MRVI1 protein (Mrvi1) mRNA, complete cds
NCBI Description
```

Seq. No. 289514

Contig ID 29 5'-most EST yy

293820_1.R1011 yyf700348362.h1

Seq. No. 289515

Contig ID 294110 1.R1011



```
5'-most EST
                   uer700580176.hl
Method
                   BLASTX
NCBI GI
                   q4490738
BLAST score
                   286
E value
                   1.0e-25
Match length
                   107
% identity
                   52
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]
Seq. No.
                   289516
                   294205 1.R1011
Contig ID
5'-most EST
                   zla700379618.h1
                   289517
Seq. No.
                   294249 1.R1011
Contig ID
5'-most EST
                   zla700379674.h1
Seq. No.
                   289518
                   294253 1.R1011
Contig ID
5'-most EST
                   zla700379685.hl
                   BLASTX
Method
                   g2829918
NCBI GI
BLAST score
                   247
E value
                   6.0e-21
Match length
                   88
                   59
% identity
                   (AC002291) similar to "tub" protein gp_U82468_2072162
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   289519
                   294266 1.R1011
Contig ID
5'-most EST
                   zla700379709.h1
Seq. No.
                   289520
Contig ID
                   294298 1.R1011
5'-most EST
                   zla700379759.h1
                   289521
Seq. No.
Contig ID
                   294339 1.R1011
                   zla700379843.h1
5'-most EST
                   289522
Seq. No.
                   294369 1.R1011
Contig ID
5'-most EST
                   gw1700\overline{6}14788.h1
Seq. No.
                   289523
                   294474 1.R1011
Contig ID
                   uer700\overline{5}77517.h1
5'-most EST
                   BLASTX
Method
                   q3386621
NCBI GI
BLAST score
                   302
                   1.0e-27
E value
```

Match length 71 % identity 82

NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 289524



```
294603 1.R1011
Contig ID
5'-most EST
                   uer700\overline{5}82341.h1
Seq. No.
                    289525
                    294644 1.R1011
Contig ID
5'-most EST
                    zla700\overline{3}80682.h1
Seq. No.
                    289526
                    294737 1.R1011
Contig ID
                    afb700\overline{3}81680.h1
5'-most EST
Method
                    BLASTX
NCBI GI
                    g2500107
BLAST score
                    289
                    4.0e-26
E value
Match length
                    68
% identity
                    85
NCBI Description
                   DNA REPAIR PROTEIN RAD51 HOMOLOG >gi 1143810 (U22441)
                   LeRAD51 [Solanum lycopersicum]
Seq. No.
                    289527
                    294743 1.R1011
Contig ID
5'-most EST
                    kem700\overline{6}10719.h1
Seq. No.
                    289528
                    294754 1.R1011
Contig ID
5'-most EST
                   rvt700551766.h1
Seq. No.
                    289529
                    294784 1.R1011
Contig ID
5'-most EST
                    kem700\overline{6}10808.h1
Seq. No.
                    289530
                    294926 1.R1011
Contig ID
5'-most EST
                    fdz701163268.h1
Seq. No.
                    289531
                    294955 1.R1011
Contig ID
5'-most EST
                    kem700\overline{6}11125.h1
Seq. No.
                   289532
                    294967 1.R1011
Contig ID
5'-most EST
                   kem700<del>6</del>11149.h1
Seq. No.
                   289533
Contig ID
                    294969 1.R1011
5'-most EST
                   kem700611152.h1
Seq. No.
                   289534
Contig ID
                   294982 1.R1011
```

5'-most EST $kem700\overline{6}11178.h1$

Method BLASTX NCBI GI g4587678 BLAST score 171 E value 2.0e-12 Match length 86 % identity 11

NCBI Description (AC007197) putative disease resistance gene, 5' partial



[Arabidopsis thaliana]

Seq. No. 289535

Contig ID 295046_1.R1011 5'-most EST gwl700616385.h1

Seq. No. 289536

Contig ID 295054_1.R1011 5'-most EST rvt700553407.h1

Method BLASTN
NCBI GI g516551
BLAST score 249
E value 1.0e-138
Match length 284
% identity 98

NCBI Description Zea mays B73 cyclin IbZm mRNA, complete cds

Seq. No. 289537

Contig ID 295121_1.R1011 5'-most EST fdz701164125.h1

Method BLASTX
NCBI GI g3875345
BLAST score 192
E value 1.0e-14
Match length 86
% identity 48

% identity ...

NCBI Description (Z99771) cDNA EST EMBL:D33404 comes from this gene; cDNA

EST EMBL:D27028 comes from this gene; cDNA EST EMBL:D27027 comes from this gene; cDNA EST EMBL:D27026 comes from this gene; cDNA EST EMBL:D27025 comes from this gene; cDN... >gi_3877518_emb_CAA91339_ (Z66513) cDNA EST EMBL:D33404 comes from this gene; cDNA EST EMBL:D27028 comes from this gene; cDNA EST EMBL:D27028 comes from this gene; cDNA EST EMBL:D27025

comes from this gene; cDN

Seq. No. 289538

Contig ID 295134_1.R1011 5'-most EST ypc700801603.h1

Method BLASTX
NCBI GI g507273
BLAST score 158
E value 7.0e-11
Match length 87
% identity 38

NCBI Description (L27052) probably expressed; ORFA; putative [Leishmania

infantum]

Seq. No. 289539

Contig ID 295138_1.R1011 5'-most EST rvt700552212.h1

Seq. No. 289540

Contig ID 295189_1.R1011 5'-most EST kem700611549.h1

Seq. No. 289541



36

% identity

NCBI Description

```
Contig ID
                   295191 1.R1011
                   kem700611552.hl
5'-most EST
                   289542
Seq. No.
                   295192 1.R1011
Contig ID
5'-most EST
                   kem700\overline{6}11553.h1
Method
                   BLASTX
NCBI GI
                   q3228517
BLAST score
                   317
E value
                   2.0e-29
Match length
                   97
% identity
                   63
NCBI Description (AF007788) ETTIN [Arabidopsis thaliana]
                   289543
Seq. No.
                   295245 1.R1011
Contig ID
5'-most EST
                   kem700611744.h1
Method
                   BLASTX
                   g1363325
NCBI GI
                   230
BLAST score
                   4.0e-20
E value
                   87
Match length
% identity
                   60
NCBI Description
                   RNA helicase HEL117 - rat >gi_897915 (U25746) RNA helicase
                   [Rattus norvegicus]
                   289544
Seq. No.
Contig ID
                   295246 1.R1011
5'-most EST
                   kem700611648.h1
Seq. No.
                   289545
                   295287 1.R1011
Contig ID
5'-most EST
                   kem700611741.h1
Method
                   BLASTX
NCBI GI
                   g4007758
                   321
BLAST score
                   2.0e-29
E value
Match length
                   134
% identity
                   49
                   (AL034433) conserved hypothetical protein
NCBI Description
                   [Schizosaccharomyces pombe]
                   289546
Seq. No.
                   295290 1.R1011
Contig ID
5'-most EST
                   gct701179084.h1
                   289547
Seq. No.
                   295294 1.R1011
Contig ID
5'-most EST
                   nbm700471518.hl
Method
                   BLASTX
                   g2980767
NCBI GI
BLAST score
                   158
E value
                   1.0e-10
Match length
                   89
```

(AL022198) putative protein [Arabidopsis thaliana]



 Seq. No.
 289548

 Contig ID
 295345_1.R1011

 5'-most EST
 kem700611881.h1

Method BLASTX
NCBI GI g4510377
BLAST score 193
E value 5.0e-15
Match length 87
% identity 43

NCBI Description (AC007017) putative RNA helicase A [Arabidopsis thaliana]

Seq. No. 289550 Contig ID 295469

Contig ID 295469_1.R1011 5'-most EST kem700612216.h1

Seq. No. 289551

Contig ID 295478_1.R1011 5'-most EST uer700582473.h1

Seq. No. 289552

Contig ID 295481 1.R1011 5'-most EST kem700612078.h1

Method BLASTX
NCBI GI g4415912
BLAST score 296
E value 4.0e-27
Match length 80
% identity 69

NCBI Description (AC006282) putative protease [Arabidopsis thaliana]

Seq. No. 289553

Contig ID 295518_1.R1011 5'-most EST kem700612229.h1

Seq. No. 289554

Contig ID 295537 1.R1011 5'-most EST uer700582554.h1

Seq. No. 289555

Contig ID 295599_1.R1011 5'-most EST uer700579038.h1

Seq. No. 289556

Contig ID 295624_1.R1011 5'-most EST kem700612271.h1

Seq. No. 289557

Contig ID 295739 1.R1011 5'-most EST rvt700548517.h1

Seq. No. 289558

Contig ID 295741 1.R1011 5'-most EST rvt700548523.h1



```
289559
Seq. No.
                   295819 1.R1011
Contig ID
                  rvt700\overline{5}48672.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2143481
BLAST score
                   198
E value
                   2.0e-29
Match length
                   130
% identity
                   56
NCBI Description
                  homeotic gene regulator - mouse (fragment)
                   >gi_545018_bbs_142383 (S68108) homeotic gene regulator=brg1
                   [mice, embryo, erythroleukemia cell line CB7, Peptide
                   Partial, 1022 aa] [Mus sp.]
Seq. No.
                   289560
Contig ID
                   295859 1.R1011
5'-most EST
                  rvt700548736.h1
Seq. No.
                   289561
                  295919 1.R1011
Contig ID
5'-most EST
                  rvt700548925.h1
Seq. No.
                  289562
                   295948 1.R1011
Contig ID
                   qct701175127.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q4006909
BLAST score
                   330
E value
                   1.0e-30
                  107
Match length
% identity
                   63
NCBI Description
                  (Z99708) putative protein [Arabidopsis thaliana]
                   289563
Seq. No.
                  295988 1.R1011
Contig ID
5'-most EST
                  nbm700\overline{4}66067.h1
Method
                  BLASTX
NCBI GI
                  g4503453
BLAST score
                   214
                   2.0e-17
E value
Match length
                   42
                   100
% identity
NCBI Description
                  endothelial differentiation-related factor 1
                  >gi 3043445 emb CAA06446 (AJ005259) homologous to Bombyx
                  mori multiprotein bridging factor (EMBL: AB001078) [Homo
                  sapiens]
Seq. No.
                  289564
```

Contig ID 296002_1.R1011 5'-most EST gct701176156.h1

Seq. No. 289565

Contig ID 296010_1.R1011 5'-most EST rvt700550338.h1

Seq. No. 289566



Contig ID 296073_1.R1011 5'-most EST nbm700474339.h1

Seq. No. 289567

Contig ID 296147_1.R1011 5'-most EST rvt700550732.h1

Method BLASTN
NCBI GI g2832242
BLAST score 227
E value 1.0e-125
Match length 307
% identity 93

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 289568

Contig ID 296151_1.R1011 5'-most EST rvt700549309.h1

Seq. No. 289569

Contig ID 296199 1.R1011 5'-most EST rvt700549365.h1

Seq. No. 289570

Contig ID 296272_1.R1011 5'-most EST rvt700551295.h1

Seq. No. 289571

Contig ID 296304_1.R1011 5'-most EST rvt700549525.h1

Method BLASTX
NCBI GI g68406
BLAST score 215
E value 1.0e-29
Match length 75
% identity 77

NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) - tomato

Seq. No. 289572

Contig ID 296417_1.R1011 5'-most EST ceu700434043.h1

Seq. No. 289573

Contig ID 296426 1.R1011 5'-most EST rvt700549711.h1

Seq. No. 289574

Contig ID 296446 1.R1011 5'-most EST rvt700549752.h1

Seq. No. 289575

Contig ID 296462_1.R1011 5'-most EST rvt700549793.h1

Seq. No. 289576

Contig ID 296464_1.R1011 5'-most EST rvt700550921.h1



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Seq. No. 28957
```

Contig ID 296533_1.R1011 5'-most EST rvt700549887.h1

Method BLASTX
NCBI GI g4455359
BLAST score 693
E value 3.0e-73
Match length 151
% identity 91

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 289578

Contig ID 296542_1.R1011 5'-most EST hvj700619606.h1

Seq. No. 289579

Contig ID 296546_1.R1011 5'-most EST pwr700453414.h1

Seq. No. 289580

Contig ID 296568_1.R1011 5'-most EST nbm700468169.h1

Seq. No. 289581

Contig ID 296584_1.R1011 5'-most EST nbm700465540.h1

Method BLASTN
NCBI GI 94206305
BLAST score 132
E value 4.0e-68
Match length 232
% identity 89

NCBI Description Zea mays retrotransposon Cinful-1, complete sequence

Seq. No. 289582

Contig ID 296809_1.R1011 5'-most EST rvt700550309.h1

Method BLASTX
NCBI GI g3875246
BLAST score 308
E value 2.0e-28
Match length 87
% identity 64

NCBI Description (Z81490) similar to WD domain, G-beta repeats (2 domains);

cDNA EST EMBL: T00482 comes from this gene; cDNA EST

EMBL: T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gene;

Seq. No. 289583

Contig ID 296823 1.R1011 5'-most EST rvt700550707.h1

Seq. No. 289584

Contig ID 296840_1.R1011 5'-most EST ceu700422461.h1

Seq. No. 289585



Contig ID 296877 1.R1011 5'-most EST $nbm700\overline{4}64894.h1$ 289586 Seq. No. 296928 1.R1011 Contig ID 5'-most EST rvt700550475.h1 Method BLASTX q1350944 NCBI GI BLAST score 162 E value 2.0e-11 Match length 40 % identity 82 NCBI Description 40S RIBOSOMAL PROTEIN S17 289587 Seq. No. Contig ID 296932 1.R1011 5'-most EST rvt700550479.h1 Method BLASTX NCBI GI g2257568 BLAST score 200 E value 2.0e-15 Match length 68 % identity 51 NCBI Description (AB004539) basic transcription factor 2.35KD subunit [Schizosaccharomyces pombe] Seq. No. 289588 Contig ID 297127 1.R1011 5'-most EST rvt700550765.h1 Method BLASTN NCBI GI g5091496 BLAST score 41 E value 7.0e-14Match length 77 % identity 37 Oryza sativa genomic DNA, chromosome 6, clone P0680A03, NCBI Description complete sequence Seq. No. 289589 297168 1.R1011 Contig ID 5'-most EST rvt700550830.h1 Seq. No. 289590 297181 1.R1011 Contig ID 5'-most EST fdz701159644.h1 289591 Seq. No. Contig ID 297227 1.R1011 5'-most EST rvt700550928.h1 289592 Seq. No.

Contig ID 297241_1.R1011 5'-most EST nbm700465291.h1

Seq. No. 289593

Contig ID 297255_1.R1011 5'-most EST rvt700550972.h1



```
Method
NCBI GI
                  q2323410
BLAST score
                  201
E value
                  6.0e-16
Match length
                  84
                  48
% identity
NCBI Description (AF015913) Skb1Hs [Homo sapiens]
                  289594
Seq. No.
Contig ID
                  297341_1.R1011
5'-most EST
                  gct701176051.hl
Seq. No.
                  289595
                  297401 1.R1011
Contig ID
5'-most EST
                  nbm700464596.h1
                  289596
Seq. No.
Contig ID
                  297403 1.R1011
5'-most EST
                  nbm700464883.h1
Seq. No.
                  289597
                  297411 1.R1011
Contig ID
5'-most EST
                  rvt700551232.h1
Method
                  BLASTX
                  q4580395
NCBI GI
BLAST score
                  147
E value
                  1.0e-09
Match length
                  64
% identity
                  52
NCBI Description
                  (AC007171) putative kinesin-related protein [Arabidopsis
                  thaliana]
Seq. No.
                  289598
Contig ID
                  297421 1.R1011
5'-most EST
                  rvt700551233.h1
Seq. No.
                  289599
                  297504 1.R1011
Contig ID
5'-most EST
                  rvt700551371.h1
                  289600
Seq. No.
                  297642 1.R1011
Contig ID
5'-most EST
                  rvt700551582.h1
Method
                  BLASTX
                  g3367592
NCBI GI
BLAST score
                  369
                  1.0e-35
E value
Match length
                  89
```

74 % identity

(AL031135) putative protein [Arabidopsis thaliana] NCBI Description

289601 Seq. No.

Contig ID 297659 1.R1011 5'-most EST rvt700551614.h1

Seq. No. 289602 Contig ID

297685_1.R1011



```
5'-most EST
                   rvt700551654.h1
Seq. No.
                  289603
Contig ID
                  297722 1.R1011
5'-most EST
                  fdz701163159.hl
Seq. No.
                  289604
Contig ID
                  297784 1.R1011
5'-most EST
                  rvt700551818.hl
                  289605
Seq. No.
Contig ID
                  297798 1.R1011
5'-most EST
                  rvt700551836.h1
Method
                  BLASTX
NCBI GI
                  g3241943
                  197
BLAST score
                  2.0e-15
E value
                  81
Match length
% identity
                  49
NCBI Description
                 (AC004625) hypothetical protein [Arabidopsis thaliana]
                  289606
Seq. No.
Contig ID
                  297861_1.R1011
5'-most EST
                  uer700582338.hl
Seq. No.
                  289607
Contig ID
                  297892 1.R1011
5'-most EST
                  rvt700552678.h1
Seq. No.
                  289608
                  297907 1.R1011
Contig ID
5'-most EST
                  rvt700552011.h1
                  289609
Seq. No.
                  297913 1.R1011
Contig ID
                  tfd700572276.h1
5'-most EST
                  289610
Seq. No.
                  297945 1.R1011
Contig ID
5'-most EST
                  rvt700552075.h1
Seq. No.
                  289611
Contig ID
                  298106 1.R1011
5'-most EST
                  ymy700282421.h2
                  289612
Seq. No.
                  298107 1.R1011
Contig ID
5'-most EST
                  hbs701182602.h1
Method
                  BLASTX
NCBI GI
                  g2245119
BLAST score
                  291
                  3.0e-26
E value
```

Match length % identity

NCBI Description (Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No. 289613

92



2.0e-45

100

```
298124 1.R1011
Contig ID
5'-most EST
                  rvt700552535.h1
                   289614
Seq. No.
                   298125 1.R1011
Contig ID
                  nbm700477822.h1
5'-most EST
Method
                  BLASTX
                  g1491931
NCBI GI
BLAST score
                   452
```

% identity 80 NCBI Description (U52078) kinesin-like protein [Nicotiana tabacum]

 Seq. No.
 289615

 Contig ID
 298324 1.R1011

 5'-most EST
 rvt700552641.h1

 Method
 BLASTX

Method BLASTX
NCBI GI 94567283
BLAST score 384
E value 2.0e-37
Match length 95
% identity 69

E value

Match length

NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]

 Seq. No.
 289616

 Contig ID
 298352_1.R1011

 5'-most EST
 nbm700466568.h1

Method BLASTX
NCBI GI g1170619
BLAST score 392
E value 4.0e-38
Match length 123
% identity 63

NCBI Description KINESIN-LIKE PROTEIN A >gi_479594_pir__S34830

kinesin-related protein katA - Arabidopsis thaliana >gi_303502_dbj_BAA01972_ (D11371) kinesin-like motor

protein heavy chain [Arabidopsis thaliana]

>gi 2911084 emb CAA17546.1 (AL021960) kinesin-related

protein katA [Arabidopsis thaliana]

Seq. No. 289617

Contig ID 298408_1.R1011 5'-most EST rvt700552762.h1

Seq. No. 289618

Contig ID 298419_1.R1011 5'-most EST rvt700552777.h1

Method BLASTX
NCBI GI g1076832
BLAST score 308
E value 2.0e-28
Match length 87
% identity 66

NCBI Description DEAD box protein - slime mold (Dictyostelium discoideum) (fragment) >gi_550329_emb_CAA57417_ (X81823) putative RNA

helicase [Dictyostelium discoideum]



```
289619
Seq. No.
                   298428 1.R1011
Contig ID
5'-most EST
                   rvt700552791.h1
Method
                   BLASTX
NCBI GI
                   q1091678
BLAST score
                   331
E value
                   3.0e-31
Match length
                   89
% identity
                   67
NCBI Description activator-like transposable element [Pennisetum glaucum]
Seq. No.
                   289620
                   298488 1.R1011
Contig ID
5'-most EST
                   rvt700552890.h1
Seq. No.
                   289621
                   298497 1.R1011
Contig ID
5'-most EST
                   rvt700552903.h1
Seq. No.
                   289622
Contig ID
                   298571 1.R1011
5'-most EST
                   rvt700553026.h1
Seq. No.
                   289623
                   298607 1.R1011
Contig ID
5'-most EST
                   fdz701163860.h1
Seq. No.
                   289624
                   298620 1.R1011
Contig ID
5'-most EST
                   rvt700553429.h1
Seq. No.
                   289625
Contig ID
                   298638 1.R1011
5'-most EST
                   rvt700553127.h1
Method
                   BLASTN
NCBI GI
                   g1917018
BLAST score
                   49
                   2.0e-18
E value
Match length
                   192
                   83
% identity
NCBI Description
                   Zea mays ribosomal protein S6 RPS6-1 (rps6-1) mRNA,
                   complete cds
                   289626
Seq. No.
                   298670_1.R1011
Contig ID
5'-most EST
                   nbm700\overline{4}69609.h1
Seq. No.
                   289627
Contig ID
                   298743 1.R1011
5'-most EST
                   rvt700553269.h1
```

Seq. No. 289628

Contig ID 298818 1.R1011 5'-most EST $nbm700\overline{4}76961.h1$

Seq. No. 289629



```
298832 1.R1011
Contig ID
5'-most EST
                    rvt700553409.h1
Seq. No.
                    289630
                    298854 1.R1011
Contig ID
5'-most EST
                    rvt700553445.h1
Method
                    BLASTX
NCBI GI
                    g3121829
BLAST score
                    140
E value
                    9.0e-09
Match length
                    62
% identity
                    42
NCBI Description
                    CHROMATIN ASSEMBLY FACTOR I P60 SUBUNIT (CAF-I 60 KD
                    SUBUNIT) >gi_2134915_pir__B56731 chromatin assembly factor
                    I p60 chain - human >gi_882260 (U20980) chromatin assembly
                    factor-I p60 subunit [Homo sapiens]
Seq. No.
                    289631
Contig ID
                    298921 1.R1011
5'-most EST
                    hvj700619502.h1
Method
                    BLASTX
NCBI GI
                    q1906830
BLAST score
                    410
                                                                    . .
E value
                    3.0e-40
Match length
                    119
% identity
                    74
NCBI Description
                   (Y11829) heat shock protein [Arabidopsis thaliana]
Seq. No.
                    289632
                    299026 1.R1011
Contig ID
5'-most EST
                    ceu700427123.hl
Method
                    BLASTX
NCBI GI
                    g136580
BLAST score
                    231
E value
                    3.0e-19
Match length
                    46
% identity
                    100
                   THYMOSIN BETA-4 >gi_111143_pir_ A37217 thymosin beta-4 -mouse >gi_54794_emb_CAA34187_ (X16053) thymosin beta-4a (AA
NCBI Description
                    1 - 50) [Mus musculus]
Seq. No.
                    289633
Contig ID
                    299075 1.R1011
5'-most EST
                   afb700380871.h1
Seq. No.
                   289634
Contig ID
                   299104 1.R1011
5'-most EST
                   afb700\overline{3}80927.h1
```

Seq. No. 289635

Contig ID 299151_1.R1011 5'-most EST afb700380995.h1

Seq. No. 289636

Contig ID 299446_1.R1011 5'-most EST afb700381463.h1



```
Seq. No. 289637
Contig ID 299476
```

Contig ID 299476_1.R1011 5'-most EST afb700381520.h1

Method BLASTX
NCBI GI g4558592
BLAST score 158
E value 8.0e-11
Match length 82
% identity 44

NCBI Description (AC006555) hypothetical protein [Arabidopsis thaliana]

Seq. No. 289638

Contig ID 299599_1.R1011 5'-most EST afb700381692.h1

Method BLASTN
NCBI GI 94454687
BLAST score 292
E value 1.0e-163
Match length 312
% identity 99

NCBI Description Homo sapiens FtsH homolog mRNA, complete cds

Seq. No. 289639

Contig ID 299626_1.R1011 5'-most EST gct701172720.h2

Seq. No. 289640

Contig ID 299648_1.R1011 5'-most EST rv1700458683.h1

Seq. No. 289641

Contig ID 299657_1.R1011 5'-most EST afb700381783.h1

Method BLASTX
NCBI GI g4505357
BLAST score 193
E value 1.0e-16
Match length 75
% identity 61

NCBI Description NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 (9kD,

MLRQ) >gi_2499333 sp_000483_NUML_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (COMPLEX I-MLRQ) (CI-MLRQ) >gi_1946692 (U94586) NADH:ubiquinone oxidoreductase MLRQ

subunit [Homo sapiens]

Seq. No. 289642

Contig ID 299665_1.R1011 5'-most EST afb700381795.h1

Seq. No. 289643

Contig ID 299823_1.R1011 5'-most EST nwy700448379.h1

Method BLASTX
NCBI GI g3335336
BLAST score 303
E value 1.0e-27
Match length 86



% identity 60

NCBI Description (AC004512) Contains similarity to DnaJ gene YM8520.10 gb_825566 from from S. cerevisiae cosmid gb_Z49705. ESTs gb_Z47720 and gb_Z29879 come from this gene. [Arabidopsis thaliana]

Seq. No. 289644

Contig ID 299833_1.R1011 5'-most EST yyf700348607.h1

Seq. No. 289645

Contig ID 299888_1.R1011 5'-most EST xtd700282312.h2

Method BLASTX
NCBI GI g3377813
BLAST score 178
E value 4.0e-13
Match length 57
% identity 53

NCBI Description (AF076275) No definition line found [Arabidopsis thaliana]

Seq. No. 289646

Contig ID 300045_1.R1011 5'-most EST gwl700615770.h1

Seq. No. 289647

Contig ID 300050_1.R1011 5'-most EST nbm700471471.h1

Seq. No. 289648

Contig ID 300324 1.R1011 5'-most EST ypc700806870.h1

Seq. No. 289649

Contig ID 300406_1.R1011 5'-most EST nbm700466250.h1

Seq. No. 289650

Contig ID 300473_1.R1011 5'-most EST yyf700348326.h1

Seq. No. 289651

Contig ID 300669_1.R1011 5'-most EST yyf700348584.h1

Seq. No. 289652

Contig ID 300746_1.R1011 5'-most EST yyf700348719.h1

Method BLASTX
NCBI GI g3451069
BLAST score 514
E value 3.0e-52
Match length 130
% identity 72

NCBI Description (AL031326) hypothetical protein [Arabidopsis thaliana]

Seq. No. 289653



```
301072 1.R1011
Contig ID
5'-most EST
                   yyf700349220.h1
                   289654
Seq. No.
Contig ID
                   301130 1.R1011
5'-most EST
                   yyf700349329.h1
                   289655
Seq. No.
Contig ID
                   301181_1.R1011
                   yyf700349401.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4490706
BLAST score
                   398
E value
                   8.0e-39
Match length
                   86
% identity
                   83
NCBI Description (AL035680) putative protein [Arabidopsis thaliana]
Seq. No.
                   289656
Contig ID
                   301237 1.R1011
5'-most EST
                   yyf700350005.hl
                   BLASTX
Method
NCBI GI
                   q2407790
BLAST score
                   273
                   2.0e-24
E value
                   92
Match length
% identity
NCBI Description (AF019910) grr1 [Glycine max]
                   289657
Seq. No.
Contig ID
                   301264 1.R1011
5'-most EST
                   yyf700349532.h1
                   289658
Seq. No.
Contig ID
                   301428_1.R1011
5'-most EST
                   yyf700349764.hl
Method
                   BLASTX
NCBI GI
                   q4455221
BLAST score
                   289
                   5.0e-26
E value
                   109
Match length
                   57
% identity
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                   289659
                   301521 1.R1011
Contig ID
                   yyf700\overline{3}49935.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3687230
BLAST score
                   497
E value
                   1.0e-50
Match length
                   98
```

90 % identity

NCBI Description (AC005169) hypothetical protein [Arabidopsis thaliana]

289660 Seq. No.

Contiq ID 301536 1.R1011



```
5'-most EST
                  hbs701181025.hl
                  289661
Seq. No.
                  301693 1.R1011
Contig ID
5'-most EST
                  yd1700405481.h1
Method
                  BLASTX
NCBI GI
                  q2708744
BLAST score
                  366
                  4.0e-35
E value
Match length
                  121
% identity
                  60
NCBI Description
                  (AC003952) putative Bop-like zinc finger protein
                  [Arabidopsis thaliana]
                  289662
Seq. No.
Contig ID
                  301815 1.R1011
5'-most EST
                  yyf700350369.h1
                  289663
Seq. No.
                  301964 1.R1011
Contig ID
5'-most EST
                  gw1700613954.h1
Seq. No.
                  289664
Contig ID
                  302046 1.R1011
5'-most EST
                  yyf700350691.h1
                  289665
Seq. No.
Contig ID
                  302137 1.R1011
5'-most EST
                  ceu700426365.hl
Method
                  BLASTX
NCBI GI
                  g2462911
BLAST score
                  521
E value
                  3.0e-53
Match length
                  135
% identity
                  67
                  (Z83832) UDP-glucose:sterol glucosyltransferase [Avena
NCBI Description
                  sativa]
Seq. No.
                  289666
                  302271 1.R1011
Contig ID
                  yyf700351036.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3914163
BLAST score
                  399
                  3.0e-39
E value
Match length
                  86
% identity
                  84
NCBI Description
                  NITRILASE 4 > gi 1171482 dbj BAA09645 (D63331) nitrilase
                  [Nicotiana tabacum]
                  289667
Seq. No.
                  302333 1.R1011
Contig ID
```

Method BIASTY

Method BLASTX
NCBI GI g2565010
BLAST score 267
E value 3.0e-23



Match length 97 % identity 55

NCBI Description (AC002983) putative microfibril-associated protein

[Arabidopsis thaliana] >gi_3377811 (AF076275) contains similarity to ATP synthase B/B' (Pfam: ATP-synt_B.hmm,

score: 11.71) [Arabidopsis thaliana]

Seq. No. 289668

Contig ID 302343_1.R1011 5'-most EST yyf700351142.h1

Seq. No. 289669

Contig ID 302596_1.R1011 5'-most EST yyf700351515.h1

Seq. No. 289670

Contig ID 302728_1.R1011 5'-most EST yyf700351703.h1

Seq. No. 289671

Contig ID 302735_1.R1011 5'-most EST yyf700351713.h1

Seq. No. 289672

Contig ID 302863_1.R1011 5'-most EST gct701169286.h1

Seq. No. 289673

Contig ID 302925_1.R1011 5'-most EST gwl700618234.h1

Seq. No. 289674

Contig ID 302936_1.R1011 5'-most EST nbm700464738.h1

Method BLASTX
NCBI GI g4249412
BLAST score 316
E value 3.0e-29
Match length 70
% identity 80

NCBI Description (AC006072) hypothetical protein [Arabidopsis thaliana]

Seq. No. 289675

Contig ID 303070_1.R1011 5'-most EST yyf700352208.h1

Method BLASTX
NCBI GI g3881810
BLAST score 147
E value 1.0e-09
Match length 63
% identity 48

NCBI Description (Z70783) similar to EF-hand calcium binding protein; cDNA

EST EMBL: C08700 comes from this gene [Caenorhabditis

elegans]

Seq. No. 289676

Contig ID 303151 1.R1011



5'-most EST

zuv700356167.h1

Seq. No.

289677

Contig ID 5'-most EST

303165_1.R1011 ceu700433571.h1

Seq. No.

289678

Contig ID 5'-most EST

303175_1.R1011 hbs701181962.h1

Seq. No.

289679

Contig ID 5'-most EST

303442_1.R1011 bdu700382365.h1

Seq. No.

289680

Contig ID 5'-most EST

303450 1.R1011 bdu700382268.h1

Seq. No.

289681

Contig ID 5'-most EST

303462_1.R1011 ypc700805333.h1

Seq. No.

289682

Contig ID 5'-most EST 303471_1.R1011 bdu700382252.h1

Method BLASTX NCBI GI g1946361 BLAST score 164

E value 1.0e-11 Match length 83

% identity 40

NCBI Description (U93215) C3HC4 zinc finger protein isolog [Arabidopsis

thaliana]

Seq. No. Contig ID

289683

Contig ID 303706_1.R1011 5'-most EST gct701178045.h1

Seq. No.

289684

Contig ID 5'-most EST

303744_1.R1011 bdu700382758.h1

Method BLASTX
NCBI GI g1707640
BLAST score 509
E value 7.0e-52
Match length 123
% identity 82

NCBI Description

(X98355) transcription factor GAMyb [Oryza sativa]

.....

Seq. No.

289685

Contig ID 5'-most EST

303760_1.R1011 bdu700382781.h1

Seq. No.

289686

Contig ID 5'-most EST

303892_1.R1011 zuv700352935.h1



```
Seq. No.
                   289687
Contig ID
                   303944 1.R1011
                   bdu700\overline{3}83072.h1
5'-most EST
Method
                   BLASTX
                   g2245032
NCBI GI
BLAST score
                   227
                   6.0e-19
E value
Match length
                   85
                   49
% identity
                   (Z97342) gibberellin oxidase homolog [Arabidopsis thaliana]
NCBI Description
                   289688
Seq. No.
                   304128 1.R1011
Contig ID
5'-most EST
                   ymy700\overline{2}82553.h2
Method
                   BLASTX
NCBI GI
                   q2342494
BLAST score
                   142
                   6.0e-12
E value
                   80
Match length
% identity
                   47
NCBI Description
                   (D14058) bromelain [Ananas comosus]
                   >gi 2463582 dbj BAA22543 (D38531) FB31 precursor (FB13
                   precursor) [Ananas comosus]
Seq. No.
                   289689
                   304266 1.R1011
Contig ID
5'-most EST
                   zuv700356015.h1
                   289690
Seq. No.
Contig ID
                   304399 1.R1011
5'-most EST
                   mwy700441403.h1
                   BLASTX
Method
                   g3874761
NCBI GI
BLAST score
                   266
E value
                   1.0e-23
Match length
                   89
                   54
% identity
NCBI Description
                   (Z71185) Similarity to yeast hypothetical protein Swiss
                   Prot accession number P28606. [Caenorhabditis elegans]
Seq. No.
                   289691
                   304402 1.R1011
Contig ID
5'-most EST
                   ceu700\overline{4}24651.h1
                   BLASTX
Method
                   g1170383
NCBI GI
BLAST score
                   371
                   6.0e-36
E value
Match length
                   75
```

% identity 99

HEAT SHOCK PROTEIN HSP 90-ALPHA (HSP 86) >qi 495759 NCBI Description (L33676) heat shock protein 90A [Cricetulus griseus]

289692 Seq. No. Contig ID

304422 1.R1011 5'-most EST zuv700353018.h1

Seq. No. 289693



```
Contig ID
                   304521 1.R1011
                  zuv700353165.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4582787
BLAST score
                   600
                  2.0e-62
E value
                  122
Match length
                  92
% identity
NCBI Description (AJ012281) adenosine kinase [Zea mays]
                  289694
Seq. No.
                   304538 1.R1011
Contig ID
5'-most EST
                  zuv700\overline{3}56014.h1
Seq. No.
                  289695
                  304840 1.R1011
Contig ID
5'-most EST
                  zuv700355434.h1
                  BLASTN
Method
                   q3646129
NCBI GI
BLAST score
                  258
                  1.0e-143
E value
                  294
Match length
                   97
% identity
NCBI Description Homo sapiens mRNA for putative ATP(GTP)-binding protein,
                  partial
Seq. No.
                  289696
Contig ID
                   304883 1.R1011
5'-most EST
                  zuv700354326.h1
                   289697
Seq. No.
Contig ID
                   304937 1.R1011
5'-most EST
                   zuv700354416.h1
                  BLASTX
Method
NCBI GI
                   g4587550
BLAST score
                   169
E value
                   4.0e-12
Match length
                   53
% identity
                   66
NCBI Description
                   (AC006577) EST qb R64848 comes from this gene. [Arabidopsis
                   thaliana]
                   289698
Seq. No.
Contig ID
                   304978 1.R1011
5'-most EST
                   zuv700354493.h1
                   BLASTX
Method
NCBI GI
                   q4538906
```

BLAST score 200 E value 1.0e-25 Match length 91 % identity

(ALO49482) choline kinase GmCK2p-like protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 289699

304988 1.R1011 Contig ID zuv700354513.h1 5'-most EST



```
BLASTX
Method
                   g4581207
NCBI GI
BLAST score
                   233
                   5.0e-20
E value
                   57
Match length
                   77
% identity
                   (Y17914) cyclic nucleotide and calmodulin-regulated ion
NCBI Description
                   channel [Arabidopsis thaliana]
                   289700
Seq. No.
                   305012 1.R1011
Contig ID
                   zuv700\overline{3}55758.h1
5'-most EST
Seq. No.
                   289701
Contig ID
                   305071 1.R1011
5'-most EST
                   zuv700354663.hl
Method
                   BLASTX
NCBI GI
                   g1362162
BLAST score
                   201
                   6.0e-16
E value
                   57
Match length
                   67
% identity
                   beta-glucosidase BGQ60 precursor - barley >gi_804656
NCBI Description
                   (L41869) beta-glucosidase [Hordeum vulgare]
                   289702
Seq. No.
Contig ID
                   305221 1.R1011
5'-most EST
                   zuv700354914.h1
Seq. No.
                   289703
                   305257 1.R1011
Contig ID
                   zuv700354973.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3452263
BLAST score
                   488
E value
                   9.0e-52
Match length
                   122
% identity
                   83
                   (AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis
NCBI Description
                   thaliana]
                   289704
Seq. No.
                   305344 1.R1011
Contig ID
5'-most EST
                   hbs701181504.h1
                   289705
Seq. No.
                   305506 1.R1011
Contig ID
5'-most EST
                   zuv700\overline{3}55539.h1
```

289706 Seq. No.

Contiq ID 305547 1.R1011 5'-most EST zuv700355625.h1

Method BLASTX NCBI GI g4115377 BLAST score 262 E value 4.0e-42 Match length 129

```
% identity
NCBI Description
                  (AC005967) unknown protein [Arabidopsis thaliana]
                  289707
Seq. No.
                  305594 1.R1011
Contig ID
5'-most EST
                  uer700579822.hl
                  BLASTX
Method
NCBI GI
                  g3738297
BLAST score
                  146
                  2.0e-09
E value
Match length
                  94
                  39
% identity
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                  289708
Seq. No.
                  305652_1.R1011
Contig ID
5'-most EST
                  zuv700355814.h1
                  BLASTX
Method
NCBI GI
                  g1304599
BLAST score
                  169
                  7.0e-12
E value
Match length
                  75
% identity
                  41
```

NCBI Description (U41315) ZNF127-Xp [Homo sapiens]

 Seq. No.
 289709

 Contig ID
 305981_1.R1011

 5'-most EST
 zuv700356542.h1

 Method
 BLASTX

 NCBI GI
 g3297810

 BLAST score
 314

NCBI GI g3297810
BLAST score 314
E value 5.0e-29
Match length 112
% identity 56
NCBI Description (AL03103

NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 289710
Contig ID 306175_1.R1011
5'-most EST zuv700357193.h1
Method BLASTX
NCRI GT 21946329

NCBI GI g1946329
BLAST score 333
E value 5.0e-31
Match length 104
% identity 62

NCBI Description (U69154) prohibitin [Nicotiana tabacum]

Seq. No. 289711

Contig ID 306211_1.R1011 5'-most EST zuv700357456.h1

Seq. No. 289712

Contig ID 306214_1.R1011 5'-most EST nbm700466229.h1

Seq. No. 289713

Contig ID 306230_1.R1011



```
5'-most EST
                  nbm700464507.h1
Method
                  BLASTX
NCBI GI
                  g4586105
BLAST score
                  228
                   6.0e-19
E value
Match length
                  120
% identity
                  36
NCBI Description
                  (AL049638) putative protein [Arabidopsis thaliana]
                  289714
Seq. No.
                  306278_1.R1011
Contig ID
5'-most EST
                  nbm700471141.h1
Method
                  BLASTN
NCBI GI
                  g168649
BLAST score
                  64
                  1.0e-27
E value
Match length
                  136
% identity
                  87
NCBI Description
                  Zea mays transposon MuDR mudrA and mudrB genes, complete
                  289715
Seq. No.
Contig ID
                  306282 1.R1011
5'-most EST
                  nbm700464753.h1
Seq. No.
                  289716
Contig ID
                  306285 1.R1011
5'-most EST
                  nbm700464790.h1
Method
                  BLASTX
NCBI GI
                  q4510403
BLAST score
                  167
                  3.0e-12
E value
Match length
                  66
% identity
                  55
NCBI Description
                  (AC006587) putative DNA repair protein [Arabidopsis
                  thaliana]
Seq. No.
                   289717
Contig ID
                  306315 1.R1011
5'-most EST
                  hbs701182212.h1
Seq. No.
                  289718
Contig ID
                  306331 1.R1011
5'-most EST
                  uer700\overline{5}84114.h1
Method
                  BLASTX
                  g1706910
NCBI GI
BLAST score
                  415
                  5.0e-41
E value
Match length
                  101
% identity
                  80
NCBI Description
                  FERRITIN LIGHT CHAIN 2 (FERRITIN SUBUNIT LG) >gi 193275
```

Seq. No. 289719

Contig ID 306338 1.R1011 5'-most EST fdz701163192.h1

(M73706) ferritin light chain [Mus musculus]



```
289720
Seq. No.
Contig ID
                   306348 1.R1011
5'-most EST
                   nbm700468567.h1
                   BLASTX
Method
                   g2129803
NCBI GI
                   177
BLAST score
E value
                   2.0e-13
Match length
                   35
% identity
                   94
                   probable serine/threonine-specific protein kinase (EC
NCBI Description
                   2.7.1.-) BSK2 - rape >gi_289374 (L12394) serine/threonine
                   protein kinase [Brassica napus] >gi_1097354_prf__2113401B
                   protein kinase [Brassica napus]
                   289721
Seq. No.
Contig ID
                   306405 1.R1011
                   nbm700\overline{4}64850.h1
5'-most EST
Seq. No.
                   289722
                   306424 1.R1011
Contig ID
5'-most EST
                   nbm700\overline{4}70404.h1
                   BLASTX
Method
NCBI GI
                   g1332579
BLAST score
                   239
E value
                   9.0e-33
Match length
                   78
% identity
                   (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
Seq. No.
                   289723
                   306428 1.R1011
Contig ID
                   nbm700\overline{4}64895.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q111625
                   286
BLAST score
                   8.0e-26
E value
Match length
                   59
% identity
                   86
                   ferritin heavy chain - rat (fragment) >gi_204128 (M18053)
NCBI Description
                   ferritin heavy chain [Rattus norvegicus]
Seq. No.
                   289724
Contig ID
                   306449 1.R1011
5'-most EST
                   nbm700\overline{4}64933.h1
Seq. No.
                   289725
Contig ID
                   306451 1.R1011
5'-most EST
                   nbm700\overline{4}77538.h1
Seq. No.
                   289726
Contig ID
                   306569 1.R1011
```

5'-most EST nbm700465120.h1

Method BLASTX NCBI GI g4335735 BLAST score 240 E value 2.0e-20 Match length 101



% identity 47
NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No. 289727 Contig ID 306572

Contig ID 306572_1.R1011 5'-most EST nbm700465131.h1 Method BLASTX

NCBI GI g1184075 BLAST score 206 E value 2.0e-16 Match length 101 % identity 3

NCBI Description (U42444) Cf-2.1 [Lycopersicon pimpinellifolium] >gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon

esculentum]

Seq. No. 289728

Contig ID 306669_1.R1011 5'-most EST nbm700465270.h1

Seq. No. 289729

Contig ID 306703_1.R1011 5'-most EST nbm700465752.h1

Seq. No. 289730

Contig ID 306728_1.R1011 5'-most EST nbm700465811.h1

Seq. No. 289731

Contig ID 306746_1.R1011 5'-most EST nbm700465862.h1

Seq. No. 289732

Contig ID 306826_1.R1011 5'-most EST nbm700465703.h1

Seq. No. 289733

Contig ID 306923_1.R1011 5'-most EST nbm700466005.h1

Seq. No. 289734

Contig ID 306990_1.R1011 5'-most EST nbm700466137.h1

Method BLASTX
NCBI GI g2191184
BLAST score 179
E value 2.0e-13
Match length 53
% identity 60

NCBI Description (AF007271) Similar to sodium/hydrogen exchanger; coded for

by A. thaliana cDNA T75860 [Arabidopsis thaliana]

Seq. No. 289735

Contig ID 307018_1.R1011 5'-most EST nbm700467782.h1

Seq. No. 289736

Contig ID 5'-most EST	307021_1.R1011 nbm700466287.h1
Seq. No. Contig ID 5'-most EST	289737 307049_1.R1011 nbm700467848.h1
Seq. No. Contig ID 5'-most EST	289738 307056_1.R1011 tfd700573139.h1
Seq. No. Contig ID 5'-most EST Method NCBI GI BLAST score E value Match length % identity NCBI Description	289739 307188_1.R1011 nbm700467204.h1 BLASTN g22245 215 1.0e-117 254 96 Zea mays DNA for cin4 element (showing homology to reverse transcriptase)
Seq. No. Contig ID 5'-most EST	289740 307317_1.R1011 nbm700473725.h1
Seq. No. Contig ID 5'-most EST	289741 307342_1.R1011 nbm700472404.h1
Seq. No. Contig ID 5'-most EST	289742 307408_1.R1011 nbm700475705.h1
Seq. No. Contig ID 5'-most EST	289743 307558_1.R1011 nbm700478016.h1
Seq. No. Contig ID 5'-most EST	289744 307621_1.R1011 nbm700467376.h1
Seq. No. Contig ID 5'-most EST	289745 307639_1.R1011 nbm700467446.h1
Seq. No. Contig ID	289746 307691 1.R1011

Contig ID 307691_1.R1011 5'-most EST nbm700468428.h1

Method BLASTX
NCBI GI 94584356
BLAST score 303
E value 6.0e-28
Match length 96
% identity 56

NCBI Description (AC006420) putative replication protein A [Arabidopsis



thaliana]

Seq. No. 289747 Contig ID 307747 1.R1011 5'-most EST nbm700467776.h1 Method BLASTX q2924777 NCBI GI BLAST score 345 8.0e-33 E value Match length 87 % identity 74

NCBI Description (AC002334) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No.
Contig ID
5'-most EST

289748 307809 1.R1011 nbm700468778.h1

Seq. No.
Contig ID
5'-most EST

289749 307841_1.R1011 nbm700467940.h1

Seq. No.
Contig ID
5'-most EST

289750 307989_1.R1011 nbm700468210.h1

Seq. No.
Contig ID
5'-most EST

289751 308025_1.R1011 nwy700445059.h1

Seq. No.
Contig ID
5'-most EST

289752 308098 1.R1011 fdz701164651.h1

Seq. No. Contig ID 5'-most EST 289753 308151_1.R1011 nbm700469271.h1

Seq. No.
Contig ID
5'-most EST

289754 308301_1.R1011 nbm700469048.h1

Seq. No. Contig ID 5'-most EST 289755 308318 1.R1011 fdz701158933.h2

Seq. No. Contig ID 5'-most EST 289756 308367_1.R1011 nbm700468845.h1

Seq. No.
Contig ID
5'-most EST

289757 308397_1.R1011 nbm700468906.h1

Seq. No. 289 Contig ID 308 5'-most EST nbm

289758 308405_1.R1011 nbm700469005.h1



Seq. No. Contig ID 5'-most EST	289759 308600_1.R1011 nbm700469263.h1
Seq. No. Contig ID 5'-most EST	289760 308644_1.R1011 nbm700469354.h1
Seq. No. Contig ID 5'-most EST Method	289761 308660_1.R1011 nbm700469393.h1

Method g1346158 NCBI GI BLAST score 286 E value 2.0e-25 Match length 120

% identity 48

ANTIGEN GOR >gi_218572_dbj_BAA00906_ (D10017) prot GOR [Pan NCBI Description

troglodytes]

289762 Seq. No. 308707 1.R1011 Contig ID $nbm700\overline{4}69519.h1$ 5'-most EST

Seq. No. 289763 308753 1.R1011 Contig ID 5'-most EST nbm700469620.h1

289764 Seq. No. 308808 1.R1011 Contig ID nbm700469751.h1 5'-most EST BLASTX Method g2652938 NCBI GI BLAST score 585

1.0e-60 E value 162 Match length 74 % identity

(Z47554) orf [Zea mays] NCBI Description

289765 Seq. No. 308833 1.R1011 Contig ID 5'-most EST uer700581989.hl

289766 Seq. No. Contig ID 308838_1.R1011 5'-most EST $uer700\overline{5}81995.h1$

Seq. No. 289767 308903_1.R1011 Contig ID 5'-most EST nbm700469968.h1

289768 Seq. No. Contig ID 308992 1.R1011 5'-most EST ceu700428954.h1

Seq. No. 289769



```
Contig ID
                   308996 1.R1011
5'-most EST
                   nbm700470475.hl
                   BLASTX
Method
                   g2827699
NCBI GI
BLAST score
                   181
E value
                   1.0e-13
                   77
Match length
                   49
% identity
NCBI Description
                   (AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.
                   289770
Contig ID
                   309042 1.R1011
                   nbm700470494.h1
5'-most EST
                   289771
Seq. No.
Contig ID
                   309045 1.R1011
5'-most EST
                   tfd700569208.h2
                   289772
Seq. No.
Contig ID
                   309070 1.R1011
5'-most EST
                   uer700578740.hl
                   289773
Seq. No.
Contig ID
                   309086 1.R1011
5'-most EST
                   gct701180437.h1
                   BLASTX
Method
NCBI GI
                   g3046711
BLAST score
                   312
E value
                   8.0e-50
Match length
                   113
% identity
                   (AJ005334) replication factor C/activator 1 subunit [Cicer
NCBI Description
                   arietinum]
Seq. No.
                   289774
                   309088 1.R1011
Contig ID
5'-most EST
                   uer700\overline{5}82990.h1
                   BLASTN
Method
                   q4039154
NCBI GI
BLAST score
                   77
                   2.0e-35
E value
Match length
                   161
% identity
                   87
                   Festuca rubra putative copper-inducible 35.6 kDa protein
NCBI Description
                   (Pmc733) mRNA, complete cds
Seq. No.
                   289775
                   309111 1.R1011
Contig ID
5'-most EST
                   nbm700470934.h1
Method
                   BLASTN
NCBI GI
                   g22245
BLAST score
                   95
E value
                   4.0e-46
```

Match length 185 92 % identity

Zea mays DNA for cin4 element (showing homology to reverse NCBI Description

transcriptase)



Seq. No. 289776 Contig ID 309123_1.R1011 5'-most EST uer700578848.h1

Method BLASTN
NCBI GI g3893859
BLAST score 263
E value 1.0e-146
Match length 274
% identity 99

NCBI Description Zea mays RNA polymerase sigma factor 1 (sig1) mRNA, nuclear

mRNA encoding chloroplast protein, partial cds

Seq. No. 289777

Contig ID 309145_1.R1011 5'-most EST nbm700470482.h1

Seq. No. 289778

Contig ID 309173_1.R1011 5'-most EST uer700583558.h1

Seq. No. 289779

Contig ID 309198_1.R1011 5'-most EST nbm700470562.h1

Seq. No. 289780

Contig ID 309359_1.R1011 5'-most EST nbm700470902.h1

Method BLASTX
NCBI GI g2065531
BLAST score 218
E value 4.0e-37
Match length 144
% identity 62

NCBI Description (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No. 289781

Contig ID 309385_1.R1011 5'-most EST nbm700470942.h1

Seq. No. 289782

Contig ID 309389_1.R1011 5'-most EST nbm700470948.h1

Method BLASTX
NCBI GI g4585988
BLAST score 299
E value 2.0e-27
Match length 97
% identity 57

NCBI Description (AC005287) Similar to phosphoprotein phosphatase 2A

regulatory subunit [Arabidopsis thaliana]

Seq. No. 289783

Contig ID 309489_1.R1011 5'-most EST nbm700471135.h1

Seq. No. 289784



```
309560 1.R1011
Contig ID
                   nbm700471304.hl
5'-most EST
                   289785
Seq. No.
Contig ID
                   309565 1.R1011
5'-most EST
                   nbm700471420.h1
                   289786
Seq. No.
                   309576 1.R1011
Contig ID
                   hvj700623641.h1
5'-most EST
Method
                   BLASTX
                   g4325342
NCBI GI
BLAST score
                   468
                   6.0e-47
E value
                   140
Match length
% identity
                   64
                   (AF128393) No definition line found [Arabidopsis thaliana]
NCBI Description
                   289787
Seq. No.
                   309580 1.R1011
Contig ID
5'-most EST
                   nbm700\overline{4}75627.h1
                   289788
Seq. No.
                   309595 1.R1011
Contig ID
                   nbm700\overline{4}71366.h1
5'-most EST
```

Seq. No. 289789 309631 1.R1011 Contig ID

5'-most EST tfd700576288.h1 Method BLASTN g3483681 NCBI GI BLAST score 171 E value 1.0e-91 Match length 187

98 % identity

Homo sapiens full length insert cDNA clone ZD55G12 NCBI Description

Seq. No. 309655 1.R1011 Contig ID nbm700471442.hl 5'-most EST Method BLASTX q2828293 NCBI GI BLAST score 429 2.0e-42 E value 116 Match length % identity 67

289790

(AL021687) putative protein [Arabidopsis thaliana] NCBI Description

289791 Seq. No. 309662 1.R1011 Contig ID 5'-most EST nbm700471450.h1

289792 Seq. No. 309678_1.R1011 Contig ID 5'-most EST $nbm700\overline{4}71536.h1$

Seq. No. 289793



Contig ID 309690_1.R1011 5'-most EST nbm700471488.h1

Seq. No. 289794

Contig ID 309777_1.R1011 5'-most EST nbm700476026.h1

Method BLASTX
NCBI GI g3876960
BLAST score 216
E value 2.0e-17
Match length 131
% identity 36

NCBI Description (270753) similar to glycosyl hydrolase; cDNA EST

EMBL:D34682 comes from this gene; cDNA EST EMBL:T00845 comes from this gene; cDNA EST CEESP30F comes from this gene; cDNA EST EMBL:D32882 comes from this gene; cDNA EST

EMBL:D332

Seq. No. 289795

Contig ID 309821_1.R1011 5'-most EST nbm700471724.h1

Seq. No. 289796

Contig ID 309857_1.R1011 5'-most EST nbm700473295.h1

Method BLASTX
NCBI GI g4204695
BLAST score 212
E value 9.0e-22
Match length 73
% identity 70

NCBI Description (AF117062) putative inositol polyphosphate 5-phosphatase

At5P1 [Arabidopsis thaliana]

Seq. No. 289797

Contig ID 309866_1.R1011 5'-most EST nbm700471917.h1

Seq. No. 289798

Contig ID 309884_1.R1011 5'-most EST nbm700473242.h1

Seq. No. 289799

Contig ID 309964 1.R1011 5'-most EST fdz701160703.h1

Method BLASTX
NCBI GI g3250695
BLAST score 189
E value 4.0e-14
Match length 70
% identity 51

NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 289800

Contig ID 309964_2.R1011 5'-most EST hbs701185620.h1



```
Seq. No.
Contig ID
                   310031 1.R1011
5'-most EST
                   nbm700\overline{4}72149.h1
                   BLASTN
Method
NCBI GI
                   g4140643
BLAST score
                   146
                   2.0e-76
E value
                   404
Match length
                   97
% identity
                   Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                   complete sequence
                   289802
Seq. No.
                   310075 1.R1011
Contig ID
                   nbm700472239.h1
5'-most EST
Seq. No.
                   289803
Contig ID
                   310100 1.R1011
                   nbm700472288.h1
5'-most EST
                   289804
Seq. No.
Contig ID
                   310194 1.R1011
5'-most EST
                   nbm700472502.h1
                   BLASTX
Method
                   g2257524
NCBI GI
BLAST score
                   172
E value
                   2.0e-12
Match length
                   81
% identity
                   48
                   (ABO04537) HYPOTHETICAL 47.4KD PROTEIN IN SHP1-SEC17
NCBI Description
                   INTERGENIC REGION [Schizosaccharomyces pombe]
Seq. No.
                   289805
Contig ID
                   310284 1.R1011
                   nbm700\overline{4}72649.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4220511
BLAST score
                   245
                   4.0e-27
E value
Match length
                   142
% identity
                   48
NCBI Description
                   (AL035356) DNA polymerase III like protein [Arabidopsis
                   thaliana]
                   289806
Seq. No.
                   310328 1.R1011
Contig ID
5'-most EST
                   nbm700\overline{4}72724.h1
```

Method BLASTN g507770 NCBI GI BLAST score 45 E value 3.0e-16 Match length 202 % identity 86

Zea mays D3L H(+)-transporting ATPase (Mha1) gene, complete NCBI Description

Seq. No. 289807



nbm700473131.h1

Contig ID	310361_1.R1011
5'-most EST	fdz701161180.h1
Seq. No.	289808
Contig ID	310524_1.R1011

 Seq. No.
 289809

 Contig ID
 310641_1.R1011

 5'-most EST
 nbm700473333.h1

 Method
 BLASTN

 NCBI GI
 g4416300

NCBI GI g441630 BLAST score 140 E value 9.0e-73 Match length 413 % identity 84

5'-most EST

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

 Seq. No.
 289810

 Contig ID
 310667_1.R1011

 5'-most EST
 nbm700473394.h1

Seq. No. 289813 Contig ID 310901_1.R1011 5'-most EST nbm700473904.h1

 Seq. No.
 289814

 Contig ID
 310939_1.R1011

 5'-most EST
 nbm700473955.h1

 Seq. No.
 289816

 Contig ID
 311089_1.R1011

 5'-most EST
 nbm700477231.h1

 Method
 BLASTX

NCBI GI g3367574
BLAST score 144
E value 3.0e-09
Match length 93
% identity 41

NCBI Description (AL031135) hypothetical protein [Arabidopsis thaliana]



Seq. No.	
Contig II)
5'-most 1	EST

289818

311222_1.R1011 nbm700474671.h1

Seq. No.
Contig ID
5'-most EST

289819

311340_1.R1011 nbm700474990.h1

Method NCBI GI BLAST score E value BLASTX g2829887 263

Match length 87 % identity 54

3.0e-23 87

NCBI Description

(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.
Contig ID
5'-most EST

289820

311382_1.R1011 nbm700475085.h1

Seq. No.
Contig ID
5'-most EST

289821

311399 1.R1011 nbm700475126.h1

Seq. No.
Contig ID
5'-most EST

289822

311415 1.R1011 nbm700475157.h1

Seq. No.
Contig ID
5'-most EST

289823

311439_1.R1011 nbm700475244.h1

Seq. No.
Contig ID
5'-most EST

289824

311455_1.R1011 nbm700475265.h1

Seq. No.
Contig ID
5'-most EST

289825

311476_1.R1011 nbm700475296.h1

Seq. No.
Contig ID
5'-most EST

289826

311563_1.R1011 nbm700475395.h1

Seq. No.
Contig ID
5'-most EST

289827

311607 1.R1011 gwl700613694.h1

Seq. No.
Contig ID
5'-most EST

289828

311672_1.R1011 nbm700475610.h1

Seq. No. Contig ID 5'-most EST 289829

311734_1.R1011 nbm700475719.h1

Seq. No.



Contig ID 311737_1.R1011 5'-most EST nbm700475722.h1

Seq. No. 289831

Contig ID 311841_1.R1011 5'-most EST nbm700475895.h1 Method BLASTX

NCBI GI g3600048
BLAST score 452
E value 6.0e-45
Match length 180
% identity 49

NCBI Description (AF080120) similar to hypothetical proteins in

Schizosaccharomyces pombe (GB:Z98533) and C. elegans

(GB:Z48334 and Z78419) [Arabidopsis thaliana]

Seq. No. 289832

Contig ID 311945_1.R1011 5'-most EST nbm700476107.h1

Seq. No. 289833

Contig ID 312037_1.R1011 5'-most EST nbm700476278.h1

Method BLASTX
NCBI GI g4557491
BLAST score 279
E value 1.0e-24
Match length 129
% identity 44

NCBI Description cleavage stimulation factor subunit 1

>gi_461848_sp_Q05048_CST1_HUMAN CLEAVAGE STIMULATION
FACTOR, 50 KD SUBUNIT (CSTF 50 KD SUBUNIT) (CF-1 50 KD
SUBUNIT) >gi_345801_pir_A45142 cleavage stimulation factor
50K chain - human >gi_180599 (L02547) cleavage stimulation

factor [Homo sapiens]

Seq. No. 289834

Contig ID 312136_1.R1011 5'-most EST nbm700476495.h1

Method BLASTX
NCBI GI g3024689
BLAST score 169
E value 3.0e-12
Match length 96
% identity 44

NCBI Description TRANSCRIPTION INITIATION FACTOR TFIID 100 KD SUBUNIT

(TAFII-100) (TAFII100) >gi_1491718_emb_CAA64777_ (X95525)

hTAFII100 [Homo sapiens]

Seq. No. 289835

Contig ID 312180_1.R1011 5'-most EST nbm700476809.h1

Seq. No. 289836

Contig ID 312204_1.R1011 5'-most EST nbm700476666.h1



Seq.	No.	
Conti	.g]	[D
5 '-mc	st	EST

289837

312356 1.R1011 $nbm700\overline{4}76990.h1$

Seq. No. Contig ID 5'-most EST 289838 312447 1.R1011

Seq. No. Contig ID nbm700477233.h1 289839

5'-most EST

312573 1.R1011 $nbm700\overline{4}77568.h1$

Seq. No. Contig ID 5'-most EST 289840 312581 1.R1011 $nbm700\overline{4}77584.h1$

Seq. No. Contig ID 5'-most EST Method

289841 312659 1.R1011 $nbm700\overline{4}77660.h1$

NCBI GI BLAST score E value Match length % identity

g4519673 334 1.0e-31 86 62

BLASTX

(AB017694) WREBP-2 [Nicotiana tabacum] NCBI Description

Seq. No. Contig ID 5'-most EST

289842 312670 1.R1011 $nbm700\overline{4}77650.h1$

Seq. No. Contig ID 5'-most EST 289843 312709 1.R1011 pwf700321640.hl

289844

Seq. No. Contig ID 5'-most EST

312716 1.R1011 nbm700477731.h1

Seq. No. Contig ID 5'-most EST

289845 312758 1.R1011 nbm700477802.h1

Seq. No. Contig ID 5'-most EST 289846 312775 1.R1011 uer700577230.hl

Seq. No. Contig ID 5'-most EST 289847 312818 1.R1011 rv1700454985.h1

Seq. No. Contig ID 5'-most EST Method NCBI GI BLAST score 289848 312849 1.R1011 uer700582887.h1 BLASTX

q2494266



```
2.0e-29
E value
Match length
                  91
% identity
                  GTP-BINDING PROTEIN LEPA >gi 1653961_dbj_BAA18871_ (D90917)
NCBI Description
                  LepA [Synechocystis sp.]
```

289849 Seq. No.

312869 1.R1011 Contig ID 5'-most EST nbm700477995.h1

Seq. No. 289850

312921 1.R1011 Contig ID gct701179987.h1 5'-most EST

BLASTX Method q2088657 NCBI GI BLAST score 257 2.0e-22 E value 102 Match length 45 % identity

NCBI Description (AF002109) unknown protein [Arabidopsis thaliana]

289851 Seq. No.

312928 1.R1011 Contig ID rv1700455859.h1 5'-most EST

289852 Seq. No.

313078 1.R1011 Contig ID mwy700438108.hl 5'-most EST

BLASTX Method NCBI GI g3063695 BLAST score 218 5.0e-18 E value Match length 48 79 % identity

(AL022537) hypothetical protein [Arabidopsis thaliana] NCBI Description

289853 Seq. No.

Contig ID 313084 1.R1011 5'-most EST mwy700438118.hl

Seq. No. 289854

Contig ID 313141 1.R1011 5'-most EST mwy700438191.hl

289855 Seq. No.

313200 1.R1011 Contig ID mwy700440966.h1 5'-most EST

289856 Seq. No.

313304 1.R1011 Contig ID pwr700452895.h1 5'-most EST

Seq. No. 289857

Contig ID 313331 1.R1011 5'-most EST $mwy700\overline{4}38541.h1$

289858 Seq. No.



Contig ID 313370_1.R1011 5'-most EST mwy700438624.h1 Method BLASTN NCBI GI g2997740

NCBI GI g2997740
BLAST score 150
E value 4.0e-79
Match length 178
% identity 96

NCBI Description Homo sapiens tetraspan TM4SF (TSPAN-1) mRNA, complete cds

Seq. No. 289859

Contig ID 313385_1.R1011 5'-most EST mwy700440071.h1

Seq. No. 289860

Contig ID 313395_1.R1011 5'-most EST ceu700432456.h1

Seq. No. 289861

Contig ID 313402_1.R1011 5'-most EST mwy700441628.h1

Seq. No. 289862

Contig ID 313423_1.R1011 5'-most EST mwy700438718.h1

Method BLASTX
NCBI GI g3297823
BLAST score 224
E value 1.0e-18
Match length 70
% identity 54

NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 289863

Contig ID 313522_1.R1011 5'-most EST mwy700438948.h1

Seq. No. 289864

Contig ID 313660_1.R1011 5'-most EST mwy700439218.h1

Seq. No. 289865

Contig ID 313676_1.R1011 5'-most EST mwy700439222.h1

Seq. No. 289866

Contig ID 313775 1.R1011 5'-most EST mwy700439388.h1

Seq. No. 289867

Contig ID 313776_1.R1011 5'-most EST pwr700451508.h1

Seq. No. 289868

Contig ID 313786_1.R1011 5'-most EST pwr700451683.h1



```
289869
Seq. No.
                  313838 1.R1011
Contig ID
5'-most EST
                  mwy700439603.hl
                  BLASTX
Method
NCBI GI
                  g4580951
BLAST score
                  297
                   3.0e-27
E value
                  83
Match length
% identity
                   (AF117733) glycerol kinase-like protein 1 [Mus musculus]
NCBI Description
                   289870
Seq. No.
                   313866 1.R1011
Contig ID
                  mwy700439692.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q2264315
BLAST score
                   37
                   2.0e-11
E value
                   73
Match length
                   88
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MRN17, complete sequence [Arabidopsis thaliana]
                   289871
Seq. No.
                   313987 1.R1011
Contig ID
                   mwy700439886.hl
5'-most EST
                   289872
Seq. No.
                   314005 1.R1011
Contig ID
5'-most EST
                   mwy700439922.hl
                   289873
Seq. No.
Contig ID
                   314086 1.R1011
5'-most EST
                   hbs701182610.h1
Method
                   BLASTX
NCBI GI
                   g2194125
BLAST score
                   497
                   2.0e-50
E value
                   122
Match length
% identity
                   76
                   (AC002062) ESTs gb_R30459,gb_N38441 come from this gene.
NCBI Description
                   [Arabidopsis thaliana]
                   289874
Seq. No.
                   314108 1.R1011
Contig ID
                   mwy700440081.hl
5'-most EST
Seq. No.
                   289875
                   314112 1.R1011
Contig ID
                   mwy700440090.hl
5'-most EST
                   289876
Seq. No.
```

Contig ID 314128 1.R1011 mwy700440232.h1 5'-most EST

289877 Seq. No.

314308 1.R1011 Contig ID



```
5'-most EST
```

mwy700441015.hl

Seq. No.

289878

Contig ID 5'-most EST

314344_1.R1011 mwy700440913.h1

Seq. No.

289879

Contig ID 5'-most EST

314399 1.R1011 mwy700440905.h1

Seq. No.

289880

Contig ID 5'-most EST

314433 1.R1011 mwy700442587.h1

Seq. No.

289881

Contig ID 5'-most EST

314489 1.R1011 $mwy700\overline{4}42867.h1$

Seq. No.

289882

Contig ID 5'-most EST

314569 1.R1011 mwy700441038.hl

Seq. No.

289883

Contig ID 5'-most EST 314600 1.R1011 hvj700622742.hl

Seq. No.

289884

Contig ID 5'-most EST 314623 1.R1011 mwy700441136.hl

BLASTX Method g2244971 NCBI GI 276 BLAST score 2.0e-35 E value Match length 103

% identity

(Z97340) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

Contig ID 5'-most EST 314655 1.R1011 $pwr700\overline{4}51449.h1$

Method NCBI GI BLAST score BLASTX g3386607 282

E value Match length % identity

4.0e-25 146

289885

NCBI Description

(AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No.

289886

Contig ID 5'-most EST

314992 1.R1011 mwy700441837.hl

Seq. No.

289887

Contig ID 5'-most EST 315000 1.R1011 mwy700441851.hl

Seq. No.



```
315023 1.R1011
Contig ID
                  mwy700441908.h1
5'-most EST
                   289889
Seq. No.
Contig ID
                   315210 1.R1011
                  mwy700442382.h1
5'-most EST
                   289890 ~
Seq. No.
                   315236 1.R1011
Contig ID
5'-most EST
                   ceu700434609.hl
                   289891
Seq. No.
                   315346 1.R1011
Contig ID
                   uer700577475.hl
5'-most EST
Seq. No.
                   289892
                   315350 1.R1011
Contig ID
5'-most EST
                   ckd700461252.hl
                   289893
Seq. No.
                   315442 1.R1011
Contig ID
5'-most EST
                   mwy700442841.hl
                   289894
Seq. No.
                   315624 1.R1011
Contig ID
                   vfk700404820.h1
5'-most EST
                   BLASTX
Method
                   g3219269
NCBI GI
                   373
BLAST score
                   4.0e-36
E value
                   97
Match length
% identity
                   71
                   (AB015314) MAP kinase kinase 3 [Arabidopsis thaliana]
NCBI Description
                   289895
Seq. No.
                   315727 1.R1011
Contig ID
5'-most EST
                   nwy700\overline{4}47787.h1
                   289896
Seq. No.
                   315733 1.R1011
Contig ID
5'-most EST
                   hvj700620478.hl
Seq. No.
                   289897
                   315796 1.R1011
Contig ID
                   nwy700444264.h1
5'-most EST
                   289898
Seq. No.
                   315812 1.R1011
Contig ID
                   pwr700449472.h1
5'-most EST
                    BLASTX
Method
```

BLAST score E value Match length % identity NCBI Description

NCBI GI

g4502895 523 3.0e-53 112

colipase, pancreatic >gi_116900_sp_P04118_COL_HUMAN COLIPASE PRECURSOR >gi_1070631_pir__XLHU colipase precursor



- human >gi_180886 (J02883) colipase precursor [Homo sapiens] >gi_1483624 (M95529) colipase [Homo sapiens] >gi 227923 prf 1713433A colipase [Homo sapiens]

Seq. No. 289899

Contig ID 315858_1.R1011 5'-most EST nwy700448063.h1

Seq. No. 289900

Contig ID 315878_1.R1011 5'-most EST nwy700443907.h1

Seq. No. 289901

Contig ID 315932_1.R1011 5'-most EST nwy700447505.h1

Seq. No. 289902

Contig ID 315975_1.R1011 5'-most EST nwy700443867.h1

Seq. No. 289903

Contig ID 315993_1.R1011 5'-most EST nwy700447604.h1

Seq. No. 289904

Contig ID 316154_1.R1011 5'-most EST nwy700444165.h1

Seq. No. 289905

Contig ID 316177_1.R1011 5'-most EST nwy700444513.h1

Seq. No. 289906

Contig ID 316252 1.R1011 5'-most EST gct701176169.h1

Seq. No. 289907

Contig ID 316282_1.R1011 5'-most EST gwl700613088.h1

Method BLASTN
NCBI GI g3925238
BLAST score 34
E value 1.0e-09
Match length 50
% identity 92

NCBI Description Zea mays 6-phosphogluconate dehydrogenase isoenzyme A gene,

partial cds

Seq. No. 289908

Contig ID 316298_1.R1011 5'-most EST nwy700444510.h1

Method BLASTN
NCBI GI g187408
BLAST score 380
E value 0.0e+00
Match length 400
% identity 99



NCBI Description Human myelin basic protein (MBP) mRNA, complete cds

Seq. No. 289909

Contig ID 316329_1.R1011 5'-most EST nwy700444430.h1

Seq. No. 289910

Contig ID 316403_1.R1011 5'-most EST nwy700444542.h1

Seq. No. 289911

Contig ID 316455_1.R1011 5'-most EST nwy700445815.h1

Seq. No. 289912

Contig ID 316523_1.R1011 5'-most EST nwy700444836.h1

Method BLASTX
NCBI GI g4406773
BLAST score 364
E value 5.0e-35
Match length 101
% identity 75

NCBI Description (AC006836) putative cell division control protein 48

[Arabidopsis thaliana]

Seq. No. 289913

Contig ID 316564_1.R1011 5'-most EST nwy700446008.h1

Method BLASTN
NCBI GI g1490418
BLAST score 131
E value 9.0e-68
Match length 131
% identity 100

NCBI Description Human ubiquitin gene, complete cds

Seq. No. 289914

Contig ID 316636_1.R1011 5'-most EST nwy700444921.h1

Method BLASTX
NCBI GI g2252847
BLAST score 220
E value 3.0e-18
Match length 49
% identity 82

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 289915

Contig ID 316689_1.R1011 5'-most EST nwy700445864.h1

Seq. No. 289916

Contig ID 316888 1.R1011 5'-most EST nwy700445449.h1

Seq. No. 289917



Contig	ID
5'-most	EST

316897_1.R1011 fdz701159725.h2

Seq. No. Contig ID

289918

Contig ID 5'-most EST

317151_1.R1011 fdz701158408.h1

Seq. No.
Contig ID
5'-most EST

289919 317196_1.R1011 nwy700445870.h1

Seq. No.
Contig ID
5'-most EST

289920

Seq. No. Contig ID 5'-most EST 317259_1.R1011 ceu700433692.h1

317279_1.R1011 nwy700446895.h

289921

289923

Seq. No. Contig ID nwy700446895.hl 289922

Contig ID 31741: 5'-most EST nwy700

317411_1.R1011 nwy700448175.h1

Seq. No.
Contig ID
5'-most EST

317566_1.R1011 nwy700447207.h1

Seq. No.
Contig ID
5'-most EST

289924 317740_1.R1011 nwy700446923.h1

Seq. No.
Contig ID
5'-most EST

289925 317760_1.R1011 nwy700446971.h1

Seq. No.
Contig ID
5'-most EST

289926

317838_1.R1011 nwy700447070.h1

Seq. No.
Contig ID
5'-most EST

289927

318045_1.R1011 gct701167242.h1

Method NCBI GI BLAST score E value Match length BLASTX g1055130 238

Match length 93 % identity 51

3.0e-20 93

NCBI Description

(U39998) coded for by C. elegans cDNA yk92b11.3; coded for by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA

yk78c2.3

Seq. No.
Contig ID
5'-most EST

289928

318096_1.R1011 gct701176862.h1



Method BLASTN
NCBI GI g347852
BLAST score 40
E value 3.0e-13
Match length 128
% identity 83

NCBI Description Saccharum hybrid cultivar H65-7052 glucose transporter

mRNA, partial cds

Seq. No. 289929

Contig ID 318190_1.R1011 5'-most EST nwy700447671.h1

Seq. No. 289930

Contig ID 318363_1.R1011 5'-most EST nwy700448072.h1

Seq. No. 289931

Contig ID 318429_1.R1011 5'-most EST pwr700451982.h1

Seq. No. 289932

Contig ID 318667_1.R1011 5'-most EST wev700405069.h1

Method BLASTX
NCBI GI g2576361
BLAST score 155
E value 2.0e-10
Match length 38
% identity 68

NCBI Description (U39782) lysine and histidine specific transporter

[Arabidopsis thaliana]

Seq. No. 289933

Contig ID 318671 1.R1011 5'-most EST wev700405071.h1

Seq. No. 289934

Contig ID 318692_1.R1011 5'-most EST pwr700448507.h1

Method BLASTX
NCBI GI g4503135
BLAST score 668
E value 2.0e-70
Match length 133
% identity 95

NCBI Description chymotrypsinogen B1 >gi_117617_sp_P17538_CTRB_HUMAN CHYMOTRYPSINOGEN B PRECURSOR >gi_105619_pir__A31299 chymotrypsin (EC 3.4.21.1) precursor - human >gi_181190

(M24400) preprochymotrypsinogen (EC 3.4.21.1) [Homo

sapiens]

Seq. No. 289935

Contig ID 318784_1.R1011 5'-most EST pwr700448667.h1

Seq. No. 289936

4.



```
318854 1.R1011
Contig ID
5'-most EST
                  pwr700450286.h1
                  289937
Seq. No.
Contig ID
                  318942 1.R1011
5'-most EST
                  pwr700451409.h1
                  BLASTX
Method
                  q3878262
NCBI GI
BLAST score
                  357
                   3.0e-34
E value
Match length
                  91
% identity
                  (Z75712) similar to AAA ATPase; cDNA EST yk353e8.5 comes
NCBI Description
                  from this gene [Caenorhabditis elegans]
                   289938
Seq. No.
                   319189 1.R1011
Contig ID
5'-most EST
                  pwr700449476.h1
                   289939
Seq. No.
                   319215 1.R1011
Contig ID
5'-most EST
                  pwr700452437.h1
Method
                  BLASTX
                   g1839467
NCBI GI
                   233
BLAST score
                   9.0e-20
E value
Match length
                   42
% identity
                  (S82198) caldecrin=serum calcium-decreasing factor [human,
NCBI Description
                   pancreas, Peptide, 268 aa] [Homo sapiens]
                   289940
Seq. No.
Contig ID
                   319281 1.R1011
5'-most EST
                   pwr700449630.hl
Method
                   BLASTX
NCBI GI
                   g1086900
BLAST score
                   173
E value
                   2.0e-12
Match length
                   89
% identity
                   37
                   (U41278) contains similarity to G beta repeats
NCBI Description
                   (PROSITE: PS00670) of the beta-transducin family
                   [Caenorhabditis elegans]
                   289941
Seq. No.
                   319311 1.R1011
Contig ID
                   tfd700570869.h1
5'-most EST
Method
                   BLASTN
                   g2996648
NCBI GI
BLAST score
                   261
                   1.0e-145
E value
                   329
Match length
% identity
                   95
                   Homo sapiens chromosome 16, cosmid clone 373C8 (LANL),
NCBI Description
                   complete sequence [Homo sapiens]
```

Seq. No.

289942



```
319320 1.R1011
Contig ID
5'-most EST
                   pwr700453496.h1
Method
                   BLASTX
NCBI GI
                   q3281852
BLAST score
                   170
E value
                   1.0e-12
                   62
Match length
                   50
% identity
                   (AL031004) peroxidase - like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   289943
Contig ID
                   319322 1.R1011
5'-most EST
                   pwr700449703.h2
                   BLASTX
Method
                   g2190547
NCBI GI
BLAST score
                   289
                   3.0e-26
E value
Match length
                   72
                   71
% identity
                    (AC001229) ESTs
NCBI Description
                   gb_T43256,gb_46316,gb_N64930,gb_AA395255,gb AA404382 come
                   from this gene. [Arabidopsis thaliana]
                   289944
Seq. No.
                   319408 1.R1011
Contig ID
                   pwr700449846.h2
5'-most EST
Seq. No.
                    289945
                    320160 1.R1011
Contig ID
5'-most EST
                   pwr700451188.h1
                    289946
Seq. No.
Contig ID
                    320417 1.R1011
5'-most EST
                    act701169026.hl
Method
                    BLASTX
NCBI GI
                    g3165570
BLAST score
                    308
E value
                    5.0e-28
Match length
                    174
% identity
                    (AF067946) similar to Drosophila ring canal protein (kelch)
NCBI Description
                    (SW:Q04652) [Caenorhabditis elegans]
Seq. No.
                    289947
Contig ID
                    320456 1.R1011
5'-most EST
                   pwr700451561.h1
Seq. No.
                    289948
 Contig ID
                    320657 1.R1011
                    sem700\overline{9}30247.h1
 5'-most EST
Method
                    BLASTX
                    g2832696
NCBI GI
```

Method BLASTX
NCBI GI g2832696
BLAST score 315
E value 6.0e-29
Match length 126
% identity 54

NCBI Description (AL021713) putative protein [Arabidopsis thaliana]



```
289949
Seq. No.
                   320781 1.R1011
Contig ID
5'-most EST
                   pwr700453180.hl
                   289950
Seq. No.
Contig ID
                   320936 1.R1011
                   pwr700452451.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4455340
BLAST score
                   170
E value
                   2.0e-12
Match length
                   58
% identity
                   53
NCBI Description (AL035522) putative protein [Arabidopsis thaliana]
Seq. No.
                   289951
                   320957 1.R1011
Contig ID
5'-most EST
                   pwr700452481.hl
Seq. No.
                   289952
                   321208 1.R1011
Contig ID
5'-most EST
                   pwr700453008.h1
Seq. No.
                   289953
                   321268 1.R1011
Contig ID
                   rv1700456314.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4506681
BLAST score
                   345
E value
                   7.0e-33
Match length
                   66
                   98
% identity
                   ribosomal protein S11 >gi_133723_sp_P04643_RS11_HUMAN 40S RIBOSOMAL PROTEIN S11 >gi_71004_pir__R3HU11 ribosomal
NCBI Description
                   protein S11 - human >gi 71005 pir R3RT11 ribosomal protein
                   S11 - rat >gi 36144 emb CAA29834 (X06617) ribosomal
                   protein S11 (AA 1 - 158) [Homo sapiens] >gi 206739 (K03250)
                   ribosomal protein S11 [Rattus norvegicus] >gi 1938406
                   (U93864) ribosomal protein S11 [Mus musculus]
                   289954
Seq. No.
Contig ID
                   321281 1.R1011
5'-most EST
                   pwr700453253.h1
Seq. No.
                   289955
                   321383 1.R1011
Contig ID
```

5'-most EST pwr700453303.h1

BLASTX NCBI GI g4586038 BLAST score 571 E value 7.0e-59 Match length 150 % identity

Method

NCBI Description (AC007109) putative heat shock protein [Arabidopsis

thaliana]



Seq. No. 289956

Contig ID 321391_1.R1011 5'-most EST pwr700453313.h1

Seq. No. 289957

Contig ID 321492_1.R1011 5'-most EST pwr700453646.h1

Method BLASTX
NCBI GI g4572676
BLAST score 209
E value 1.0e-16
Match length 129
% identity 36

NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]

Seq. No. 289958

Contig ID 321541_1.R1011 5'-most EST pwr700453655.h1

Method BLASTX
NCBI GI g3913437
BLAST score 595
E value 7.0e-62
Match length 136

% identity 82

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE >gi_1402875_emb_CAA66825_ (X98130) RNA helicase
[Arabidopsis thaliana] >gi_1495271_emb_CAA66613_ (X97970)

RNA helicase [Arabidopsis thaliana]

Seq. No. 289959

Contig ID 321684_1.R1011 5'-most EST gwl700613714.h1

Seq. No. 289960

Contig ID 321699_1.R1011 5'-most EST rv1700453711.h1

Seq. No. 289961

Contig ID 321722 1.R1011 5'-most EST rv1700453739.h1

Seq. No. 289962

Contig ID 321735_1.R1011 5'-most EST rv1700453759.h1

Seq. No. 289963

Contig ID 321764 1.R1011 5'-most EST rv1700453805.h1

Seq. No. 289964

Contig ID 321812_1.R1011 5'-most EST rv1700453884.h1

Seq. No. 289965

Contig ID 321845_1.R1011 5'-most EST rv1700455543.h1



Seq. No. 28996

Contig ID 321872_1.R1011 5'-most EST rv1700454040.h1

Method BLASTX
NCBI GI g4567311
BLAST score 232
E value 2.0e-19
Match length 60
% identity 67

NCBI Description (AC005956) putative protein kinase [Arabidopsis thaliana]

Seq. No. 289967

Contig ID 321908_1.R1011 5'-most EST rv1700454125.h1

Seq. No. 289968

Contig ID 322019 1.R1011 5'-most EST rv1700454320.h1

Seq. No. 289969

Contig ID 322096_1.R1011 5'-most EST rv1700454443.h1

Seq. No. 289970

Contig ID 322119_1.R1011 5'-most EST rv1700454474.h1

Method BLASTN
NCBI GI g3204107
BLAST score 33

BLAST score 33 E value 4.0e-09 Match length 41 % identity 95

NCBI Description Cicer arietinum mRNA for putative cytidine or

deoxycytidylate deaminase, partial

Seq. No. 289971

Contig ID 322182_1.R1011 5'-most EST rv1700454609.h1

Method BLASTX
NCBI GI g3461815
BLAST score 182
E value 8.0e-22
Match length 79
% identity 71

NCBI Description (AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No. 289972

Contig ID 322259_1.R1011 5'-most EST rv1700457149.h1

Seq. No. 289973

Contig ID 322324_1.R1011 5'-most EST fdz701160619.h1

Method BLASTX
NCBI GI g4584255
BLAST score 328
E value 2.0e-31



Match length 85 % identity 70

NCBI Description (Y18471) SINAlp [Vitis vinifera]

Seq. No. 289974

Contig ID 322410_1.R1011 5'-most EST rv1700455224.h1

Method BLASTX
NCBI GI g2660670
BLAST score 319
E value 6.0e-30
Match length 84
% identity 75

NCBI Description (AC002342) putative Cu2+-transporting ATPase [Arabidopsis

thaliana]

Seq. No. 289975

Contig ID 322459_1.R1011 5'-most EST rv1700458424.h1

Seq. No. 289976

Contig ID 322548_1.R1011 5'-most EST rv1700457240.h1

Method BLASTX
NCBI GI g2980760
BLAST score 218
E value 8.0e-18
Match length 77

% identity

NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 289977

Contig ID 322770_1.R1011 5'-most EST rv1700457312.h1

Seq. No. 289978

Contig ID 322926_1.R1011 5'-most EST rv1700457744.h1

Seq. No. 289979

Contig ID 322965_1.R1011 5'-most EST rv1700456028.h1

Seq. No. 289980

Contig ID 323010_1.R1011 5'-most EST rv1700456092.h1

Method BLASTX
NCBI GI g3834317
BLAST score 264
E value 5.0e-23
Match length 101
% identity 55

NCBI Description (AC005679) Similar to CDC16 protein gb_U18291 (CDC16Hs)

from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 289981

Contig ID 323173 1.R1011



```
5'-most EST rv1700456461.h1
Method BLASTX
NCBI GI q2244865
```

BLAST score 142 E value 4.0e-09 Match length 88 % identity 38

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 289982

Contig ID 323189 1.R1011 5'-most EST rv1700456418.h1

Seq. No. 289983

Contig ID 323215 1.R1011 5'-most EST rv1700456724.h1

Seq. No. 289984

Contig ID 323527 1.R1011 5'-most EST rv1700457063.h1

Seq. No. 289985

Contig ID 323529 1.R1011 5'-most EST fdz701166734.h1

Method BLASTX
NCBI GI g541849
BLAST score 316
E value 2.0e-29
Match length 81
% identity 72

NCBI Description anthranilate synthase (EC 4.1.3.27) beta chain - Arabidopsis thaliana >gi 403434 (L22585) anthranilate

ambhasa baba suburit [7-abidansis thelicas]

...

synthase beta subunit [Arabidopsis thaliana]

Seq. No. 289986

Contig ID 323662_1.R1011 5'-most EST gct701180456.h1 Method BLASTX

NCBI GI g3860258 BLAST score 234 E value 2.0e-19 Match length 103 % identity 48

NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 289987

Contig ID 323665_1.R1011 5'-most EST rv1700457214.h1

Seq. No. 289988

Contig ID 323780_1.R1011 5'-most EST rv1700457396.h1

Seq. No. 289989

Contig ID 323802_1.R1011 5'-most EST rv1700457434.h1



```
289990
Seq. No.
                  323853 1.R1011
Contig ID
5'-most EST
                  rv1700457533.h1
Seq. No.
                  289991
                  323926 1.R1011
Contig ID
                  rv1700457668.h1
5'-most EST
Method
                  BLASTX
                  q1707642
NCBI ĞI
BLAST score
                   375
E value
                   2.0e-36
Match length
                   80
% identity
NCBI Description (Y07748) TMK [Oryza sativa]
Seq. No.
                   289992
Contig ID
                   323953 1.R1011
5'-most EST
                   rv1700458029.h1
                   BLASTX
Method
NCBI GI
                   q3582333
BLAST score
                   262
E value
                   7.0e-24
                   79
Match length
                   67
% identity
NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   289993
                   323981 1.R1011
Contig ID
5'-most EST
                   rv1700457787.h1
Method
                   BLASTX
NCBI GI
                   q1778376
BLAST score
                   307
E value
                   2.0e-28
Match length
                   78
% identity
                   72
                  (U81288) PsRT17-1 [Pisum sativum]
NCBI Description
                   289994
Seq. No.
                   324542 1.R1011
Contig ID
                   ceu700428317.h1
5'-most EST
Method
                   BLASTX
                   g4567281
NCBI GI
BLAST score
                   142
                   8.0e-09
E value
                   59
Match length
                   39
% identity
                   (AC006841) unknown protein [Arabidopsis thaliana]
NCBI Description
                   289995
Seq. No.
                   324598 1.R1011
Contig ID
                   yd1700405405.h1
5'-most EST
Method
                   BLASTX
                   g3334133
NCBI GI
BLAST score
                   356
                   6.0e - 34
E value
```

40325

100

69

Match length % identity

. خچ.



NCBI Description CYTOCHROME P450 89A2 (CYPLXXXIX) (ATH 6-1) >gi_1432145 (U61231) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 289996

Contig ID 324622_1.R1011 5'-most EST yd1700405436.h1

Method BLASTX
NCBI GI g4093153
BLAST score 194
E value 5.0e-15
Match length 47
% identity 79

NCBI Description (AF088280) phytochrome-associated protein 3 [Arabidopsis

thaliana]

Seq. No. 289997

Contig ID 324705_1.R1011 5'-most EST tfd700569162.h1

Seq. No. 289998

Contig ID 324746_1.R1011 5'-most EST gct701177467.h1

Seq. No. 289999

Contig ID 324789_1.R1011 5'-most EST ypc700803283.h1

Seq. No. 290000

Contig ID 324814_1.R1011 5'-most EST ceu700433802.h1

Method BLASTX
NCBI GI g2244816
BLAST score 347
E value 5.0e-33
Match length 94
% identity 65

NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 290001

Contig ID 324924 1.R1011 5'-most EST tfd700575533.h1

Seq. No. 290002

Contig ID 324932_1.R1011 5'-most EST tfd700569573.h1

Seq. No. 290003

Contig ID 325004 1.R1011 5'-most EST tfd700569707.h1

Method BLASTX
NCBI GI g4567281
BLAST score 206
E value 2.0e-16
Match length 113
% identity 42

NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]



Seq. No. 290004

Contig ID 325015_1.R1011 5'-most EST ypc700805212.h1

Method BLASTX
NCBI GI g3859659
BLAST score 489
E value 2.0e-49
Match length 155
% identity 66

NCBI Description (AL031394) putative potassium transporter AtKT5p (AtKT5)

[Arabidopsis thaliana]

Seq. No. 290005

Contig ID 325115_1.R1011 5'-most EST tfd700574173.h1

Seq. No. 290006

Contig ID 325117_1.R1011 5'-most EST tfd700569927.h1

Seq. No. 290007 Contig ID 325187_1.R1011

Contig ID 32518/_1.RIUI1 5'-most EST tfd700570034.h1

Seq. No. 290008

Contig ID 325240_1.R1011 5'-most EST tfd700570105.h1

Seq. No. 290009 Contiq ID 325318 1.1

Contig ID 325318_1.R1011 5'-most EST tfd700570217.h1

Seq. No. 290010

Contig ID 325353_1.R1011 5'-most EST tfd700572413.h1

Seq. No. 290011

Contig ID 325432_1.R1011 5'-most EST tfd700570505.h1

Seq. No. 290012

Contig ID 325446_1.R1011 5'-most EST gct701170766.h1

Seq. No. 290013

Contig ID 325457_1.R1011 5'-most EST uer700583259.h1

Seq. No. 290014

Contig ID 325594_1.R1011 5'-most EST ceu700428785.h1

Seq. No. 290015

Contig ID 325692_1.R1011 5'-most EST tfd700576620.h1

Seq. No. 290016

% identity

NCBI Description

97



```
325757 1.R1011
 Contig ID
 5'-most EST
                     hvj700622279.hl
                     290017
 Seq. No.
                     325886 1.R1011
 Contig ID
 5'-most EST
                     tfd700571251.h1
 Seq. No.
                     290018
                     325919 1.R1011
 Contig ID
                     tfd700571294.hl
್ರ5'-most EST
                     290019
 Seq. No.
                     325937 1.R1011
 Contig ID
                     tfd700\overline{5}71322.h1
 5'-most EST
                     290020
 Seq. No.
                     325947 1.R1011
 Contig ID
                     tfd700\overline{5}71335.h1
 5'-most EST
 Method
                     BLASTX
 NCBI GI
                     g3395439
 BLAST score
                     198
 E value
                     3.0e-15
 Match length
                     74
                     50
 % identity
 NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]
                     290021
 Seq. No.
                     326007 1.R1011
 Contig ID
                     gw1700\overline{6}13410.h1
 5'-most EST
                     290022
 Seq. No.
                     326048 1.R1011
 Contig ID
 5'-most EST
                     tfd700\overline{5}71467.h1
                     290023
 Seq. No.
                     326095 1.R1011
 Contig ID
 5'-most EST
                     tfd700571544.h1
 Seq. No.
                     290024
                     326147 1.R1011
 Contig ID
 5'-most EST
                     gw1700617064.h1
                     290025
 Seq. No.
 Contig ID
                     326171 1.R1011
 5'-most EST
                     gw1700617030.h1
 Seq. No.
                     290026
                     326392 1.R1011
 Contig ID
                     tfd700572033.h1
 5'-most EST
 Method
                     BLASTN
 NCBI GI
                     g4544336
 BLAST score
                     140
                     6.0e-73
 E value
 Match length
                     168
```

Mus musculus GABA-Bla receptor mRNA, complete cds



```
Seq. No.
                  290027
Contig ID
                  326458 1.R1011
5'-most EST
                  tfd700572141.h1
                                                      58
Method
                  BLASTX
NCBI GI
                  q407940
BLAST score
                  142
E value
                  7.0e-09
Match length
                  104
% identity
NCBI Description
                  (U02495) epoxide hydrolase [Solanum tuberosum]
                  290028
Seq. No.
Contig ID
                  326546 1.R1011
5'-most EST
                  tfd700572279.h1
Method
                  BLASTX
NCBI GI
                  q434759
BLAST score
                  485
E value
                  4.0e-49
Match length
                  110
% identity
                  80
                  (D21163) similar to human elongation factor 2 mRNA (HSEF2).
NCBI Description
                  [Homo sapiens]
                  290029
Seq. No.
Contig ID
                  326549 1.R1011
5'-most EST
                  hbs701185177.h1
Method
                  BLASTX
NCBI GI
                  g4589966
BLAST score
                  350
                  6.0e-33
E value
Match length
                  136
% identity
                  49
NCBI Description
                  (AC007169) unknown protein [Arabidopsis thaliana]
                  290030
Seq. No.
Contig ID
                  326563 1.R1011
5'-most EST
                  tfd700572308.h1
Method
                  BLASTX
NCBI GI
                  g2293272
BLAST score
                  198
E value
                  2.0e-15
Match length
                  111
% identity
                  42
                  (AF008220) DNA-polymerase I [Bacillus subtilis]
NCBI Description
                  >gi 2635374 emb CAB14869 (Z99118) DNA polymerase I
                  [Bacillus subtilis]
                  290031
Seq. No.
                  326636_1.R1011
Contig ID
                  uer700577215.h1
```

5'-most EST

Seq. No. 290032

Contig ID 326701 1.R1011 5'-most EST gct701175420.h1 Method

BLASTX NCBI GI g1296955 BLAST score 146



E value 1.0e-09
Match length 65
% identity 43
NCBI Description (X95402) duplicated domain structure protein [Oryza sativa]

Seq. No. 290033
Contig ID 326975_1.R1011
5'-most EST tfd700572850.h2

 Seq. No.
 290034

 Contig ID
 326982_1.R1011

 5'-most EST
 tfd700572858.h2

 Method
 BLASTX

 NCBI GI
 g99957

BLAST score 167
E value 4.0e-21
Match length 60
% identity 93

NCBI Description trypsin inhibitor B (Kunitz) precursor - soybean

>gi_18772_emb_CAA45778_ (X64448) trypsin inhibitor subtype

. . . .

B [Glycine max]

Seq. No. 290035

Contig ID 327072_1.R1011 5'-most EST tfd700572968.h1

Seq. No. 290036

Contig ID 327116_1.R1011 5'-most EST tfd700573025.h1

Seq. No. 290037

Contig ID 327127_1.R1011 5'-most EST tfd700573038.h1

Seq. No. 290038

Contig ID 327303_1.R1011 5'-most EST tfd700573658.h1

Method BLASTX
NCBI GI g3218544
BLAST score 460
E value 5.0e-46
Match length 94
% identity 93

NCBI Description (AB004813) alternative oxidase [Oryza sativa]

>gi_3218546_dbj_BAA28773_ (AB004864) alternative oxidase

[Oryza sativa]

Seq. No. 290039

Contig ID 327584_1.R1011 5'-most EST hvj700620394.h1

Seq. No. 290040

Contig ID 327639_1.R1011 5'-most EST tfd700574049.h1

Method BLASTX NCBI GI g3746071 BLAST score 360



2.0e-34 E value Match length 82 88 % identity

NCBI Description

(AC005311) putative GTP-binding protein [Arabidopsis

thaliana]

Seq. No. Contig ID 5'-most EST 290041 327799 1.R1011 tfd700576595.h1

Seq. No. Contig ID 290042 327874 1.R1011

5'-most EST

tfd700574408.h1

BLASTX Method NCBI GI q322750 436 BLAST score 2.0e-43 E value 94 Match length 95

% identity NCBI Description

ubiquitin / ribosomal protein CEP52 - wood tobacco

>gi 170217 (M74100) ubiquitin fusion protein [Nicotiana

sylvestris]

Seq. No.

290043

Contig ID 5'-most EST 327889 1.R1011 tfd700574426.hl

BLASTX Method q731675 NCBI GI 287 BLAST score 1.0e-25 E value Match length 82 62 % identity

NCBI Description

HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION >gi_626631_pir__S46811 hypothetical protein YHR074w - yeast

(Saccharomyces cerevisiae) >gi_500832 (U10556) Yhr074wp

[Saccharomyces cerevisiae]

290044 Seq. No.

Contig ID 5'-most EST 327910 1.R1011 gw1700618521.h1

290045 Seq. No.

Contig ID 5'-most EST 327915 1.R1011 $ceu700\overline{4}24045.h1$

Seq. No. 290046

Contig ID 5'-most EST 327935 1.R1011 ceu700433980.h2

290047 Seq. No.

327979 1.R1011 Contig ID tfd700576175.h1 5'-most EST

290048 Seq. No.

328022 1.R1011 Contig ID $gw1700\overline{6}13809.h1$ 5'-most EST



Seq. No. Contig ID 5'-most EST

290049

328091_1.R1011 tfd700575990.h1

Seq. No.
Contig ID
5'-most EST

290050 328123_1.R1011 gwl700612507.h1

Seq. No. Contig ID 5'-most EST 290051 328435_1.R1011 ypc700803230.h1

Seq. No.
Contig ID
5'-most EST

290052 328469 1.R1011 tfd700576120.h1

Seq. No.
Contig ID
5'-most EST

290053 328472 1.R1011 tfd700575705.h1

Method BLASTX
NCBI GI g1708421
BLAST score 382
E value 2.0e-50
Match length 104
% identity 86

NCBI Description

ription ISOFLAVONE REDUCTASE HOMOLOG IRL >gi_1205986 (U33318)

sulfur starvation induced isoflavone reductase-like IRL

[Zea mays]

Seq. No.
Contig ID
5'-most EST

290054 328502 1.R1011 tfd700575583.h1

Seq. No.
Contig ID
5'-most EST

290055 328825_1.R1011 gct701174895.h1

Method BLASTX
NCBI GI g4191775
BLAST score 518
E value 1.0e-54
Match length 151

Match length 15: % identity 68

NCBI Description (AC005917) putative acyl-CoA cholesterol acyltransferase

[Arabidopsis thaliana]

Seq. No.
Contig ID
5'-most EST

290056 328844 1.R1011 uer700583265.h1

Seq. No.
Contig ID
5'-most EST

290057 328855 1.R1011 tfd700576245.h1

Seq. No.
Contig ID
5'-most EST

328886_1.R1011 tfd700576318.h1

. 290058



```
290059
Seq. No.
                   328927 1.R1011
Contig ID
                   ceu700422918.hl
5'-most EST
Method
                   BLASTX
                   g1174853
NCBI GI
BLAST score
                   264
                   2.0e-23
E value
                   59
Match length
% identity
                   78
                   UBIQUITIN-CONJUGATING ENZYME E2-18 KD (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42)
                   >gi 481811_pir__S39483 ubiquitin-conjugating enzyme UBC2-1
                   - Arabidopsis thaliana >gi_22658_emb_CAA48378 (X68306)
                   ubiquitin-conjugating enzyme [Arabidopsis thaliana]
                   290060
Seq. No.
                   328929 1.R1011
Contig ID
                   tfd700576617.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2108252
                   293
BLAST score
                   8.0e-27
E value
Match length
                   87
                   33
%.identity
                   (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]
NCBI Description
                   >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2
[Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_
                    (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
                    290061
Seq. No.
                    329031 1.R1011
Contig ID
                   tfd700576507.h1
5'-most EST
                    290062
Seq. No.
                    329061 1.R1011
Contig ID
                    tfd700576539.hl
5'-most EST
                   BLASTN
Method
                    q3603472
NCBI GI
BLAST score
                    54
                    2.0e-21
E value
                    74
Match length
                    93
% identity
                    Oryza sativa elicitor-responsive gene-3 (ERG3) mRNA,
NCBI Description
                    complete cds
Seq. No.
                    290063
                    329133 1.R1011
Contig ID
                    tfd700576651.hl
5'-most EST
                    BLASTX
Method
NCBI GI
                    q3341679
BLAST score
                    392
```

4.0e-38 E value 101 Match length 69 % identity

(AC003672) dynamin-like protein phragmoplastin 12 NCBI Description

[Arabidopsis thaliana]



290064 Seq. No. 329343 1.R1011 Contig ID 5'-most EST qw1700617082.h1 290065 Seq. No. 329411 1.R1011 Contig ID 5'-most EST $uer700\overline{5}81348.h1$

290066 Seq. No. 329462 1.R1011 Contig ID 5'-most EST ceu700431894.h1 Method BLASTX NCBI GI q2829916 216 BLAST score 1.0e-17 E value Match length 45

89

% identity

(AC002291) Unknown protein [Arabidopsis thaliana] NCBI Description

290067 Seq. No. Contig ID 329584 1.R1011 uer700577035.h1 5'-most EST BLASTX Method g2194125 NCBI GI 704

BLAST score E value 1.0e-74 Match length 156 77 % identity

(AC002062) ESTs gb R30459, gb N38441 come from this gene. NCBI Description

[Arabidopsis thaliana]

290068 Seq. No.

329606 1.R1011 Contig ID 5'-most EST $uer700\overline{5}80666.h1$

290069 Seq. No.

329624 1.R1011 Contig ID 5'-most EST uer700578019.h1

Seq. No. 290070

329647 1.R1011 Contig ID $uer700\overline{5}77140.h1$ 5'-most EST

Seq. No. 290071

329651 1.R1011 Contig ID $uer700\overline{5}79580.h1$ 5'-most EST

Seq. No. 290072

329831 1.R1011 Contig ID 5'-most EST uer700581563.hl

290073 Seq. No.

329886 1.R1011 Contig ID 5'-most EST tbg700930426.h1

Method BLASTX NCBI GI g4335771 BLAST score 426



5.0e-42 E value Match length 135

% identity 62 (AC006284) unknown protein [Arabidopsis thaliana]

NCBI Description

290074

Contig ID 5'-most EST

329909 1.R1011 $uer700\overline{5}80534.h1$

Seq. No. Contig ID

Seq. No.

290075 330010 1.R1011 uer700580318.h1

Seq. No.

290076

Contig ID 5'-most EST

5'-most EST

330112 1.R1011 hvj700624341.hl BLASTX

Method NCBI GI BLAST score E value

q3212851 367 3.0e-35

Match length % identity

97 70

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.

Contig ID 5'-most EST 290077

330125 1.R1011 $uer700\overline{5}78754.h1$

Seq. No.

Contig ID 5'-most EST 290078

330163 1.R1011 uer700577977.h1

BLASTX Method q3355480 NCBI GI BLAST score 222 3.0e-18 E value Match length 80 % identity

(AC004218) Medicago nodulin N21-like protein [Arabidopsis NCBI Description

thaliana]

Seq. No. Contig ID 290079

330313 1.R1011 5'-most EST uer700578221.h1

Seq. No.

290080

Contig ID 5'-most EST

330367 1.R1011 uer700578416.hl

Seq. No.

290081

Contig ID 5'-most EST

330370 1.R1011 uer700578420.h1

Seq. No.

290082

Contig ID 5'-most EST

330378 1.R1011 uer700578430.h1

BLASTX Method NCBI GI g1169241



BLAST score 242 E value 9.0e-21 Match length 93 % identity 53

NCBI Description MALONYL-COA DECARBOXYLASE PRECURSOR >gi_283854_pir__S27113

malonyl-CoA decarboxylase (EC 4.1.1.9) - goose

Seq. No. 290084

Contig ID 330412_1.R1011 5'-most EST uer700578477.h1

Seq. No. 290085

Contig ID 330423_1.R1011 5'-most EST uer700578386.h1

Seq. No. 290086

Contig ID 330676 1.R1011 5'-most EST gwl700616117.h1

Seq. No. 290087

Contig ID 330677_1.R1011 5'-most EST uer700578782.h1

Seq. No. 290088

Contig ID 330861_1.R1011 5'-most EST gwl700618040.h1

Seq. No. 290089

Contig ID 330937 1.R1011 5'-most EST uer700582502.h1

Seq. No. 290090

Contig ID 330956_1.R1011 5'-most EST uer700579270.h1

Seq. No. 290091

Contig ID 330979_1.R1011 5'-most EST ceu700421788.h1

Seq. No. 290092

Contig ID 331104 1.R1011 5'-most EST ceu700424003.h1

Seq. No. 290093

Contig ID 331196 1.R1011 5'-most EST uer700579735.h1

Seq. No. 290094

Contig ID 331389_1.R1011 5'-most EST ceu700429565.h1

Seq. No. 290095

Contig ID 331393 1.R1011



5'-most EST uer700580054.h1

Seq. No. 290096

Contig ID 331417_1.R1011 5'-most EST uer700580109.h1

Seq. No. 290097

Contig ID 331419 1.R1011 5'-most EST uer700581711.h1

Seq. No. 290098

Contig ID 331678_1.R1011 5'-most EST hbs701184271.h1

Method BLASTN
NCBI GI g2832242
BLAST score 55
E value 3.0e-22
Match length 209
% identity 88

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 290099

Contig ID 331693_1.R1011 5'-most EST uer700580642.h1

Method BLASTX
NCBI GI g4056506
BLAST score 261
E value 5.0e-23
Match length 82
% identity 62

NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 290100

Contig ID 331715_1.R1011 5'-most EST uer700580671.h1

Seq. No. 290101

Contig ID 331718_1.R1011 5'-most EST ceu700425489.h1

Method BLASTN
NCBI GI g4140643
BLAST score 62
E value 3.0e-26
Match length 110
% identity 89

NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

complete sequence

Seq. No. 290102

Contig ID 331828_1.R1011 5'-most EST uer700580904.h1

Seq. No. 290103

Contig ID 331871_1.R1011 5'-most EST fdz701166431.h1

Seq. No. 290104



Contig ID 331933 1.R1011 5'-most EST uer700581120.h1

Seq. No. 290105

Contig ID 332087_1.R1011 5'-most EST hbs701183371.h1

Seq. No. 290106

Contig ID 332132_1.R1011 5'-most EST uer700581530.h1 Method BLASTX

Method BLASTX
NCBI GI g4127346
BLAST score 245
E value 9.0e-21
Match length 135
% identity 43

NCBI Description (AJ010448) glutathione transferase [Alopecurus myosuroides]

Seq. No. 290107

Contig ID 332212_1.R1011 5'-most EST ceu700425449.h1

Method BLASTX
NCBI GI g1346883
BLAST score 485
E value 4.0e-49
Match length 94
% identity 99

NCBI Description PHYTOENE SYNTHASE PRECURSOR >gi_2130144_pir__S68307

phytoene synthase - maize $>gi_1\overline{0}98665$ ($\overline{U}326\overline{36}$) phytoene

synthase [Zea mays]

Seq. No. 290108

Contig ID 332250_1.R1011 5'-most EST ypc700802523.h1

Seq. No. 290109

Contig ID 332319_1.R1011 5'-most EST uer700581825.h1

Seq. No. 290110

Contig ID 332521_1.R1011 5'-most EST gwl700616231.h1

Method BLASTX
NCBI GI g2827709
BLAST score 147
E value 2.0e-22
Match length 87
% identity 74

NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]

Seq. No. 290111

Contig ID 332563_1.R1011 5'-most EST uer700582289.h1

Seq. No. 290112

Contig ID 332655 1.R1011 5'-most EST gct701172314.h1



 Seq. No.
 290113

 Contig ID
 332904 1.R1011

 5'-most EST
 uer700582853.h1

Seq. No. 290114

Contig ID 333184 1.R1011 5'-most EST uer700583650.h1

Seq. No. 290115

Contig ID 333336_1.R1011 5'-most EST uer700583943.h1

Seq. No. 290116

Contig ID 333470_1.R1011 5'-most EST ckd700461201.h1

Method BLASTX
NCBI GI g4579744
BLAST score 282
E value 2.0e-25
Match length 97
% identity 54

NCBI Description (AB017104) DNA helicase Q1 [Mus musculus]

Seq. No. 290117

Contig ID 333473_1.R1011 5'-most EST ckd700461106.h1

Seq. No. 290118

Contig ID 333490_1.R1011 5'-most EST ckd700461128.h1

Method BLASTX
NCBI GI g461498
BLAST score 226
E value 3.0e-19
Match length 83
% identity 59

NCBI Description ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC

TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)

(ALAAT-2) >gi_320619_pir__ S28429 alanine transaminase (EC 2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421)

alanine aminotransferase [Panicum miliaceum]

Seq. No. 290119

Contig ID 333506_1.R1011 5'-most EST ckd700461149.h1

Seq. No. 290120

Contig ID 333511_1.R1011 5'-most EST ckd700461154.h1

Seq. No. 290121

Contig ID 333519_1.R1011 5'-most EST fdz701164157.h1

Seq. No. 290122

Contig ID 333532 1.R1011



5'-most EST ckd700461181.h1

Seq. No. 290123

Contig ID 333535_1.R1011 5'-most EST ckd700461185.h1

Method BLASTN NCBI GI g2393774 BLAST score 190

E value 1.0e-103

Match length 230 % identity 96

NCBI Description Zea mays endosperm-specific prolamin box binding factor

(PBF) mRNA, complete cds

``. ĕ,`

Seq. No. 290124

Contig ID 333537_1.R1011 5'-most EST ckd700461189.h1

Seq. No. 290125

Contig ID 333642_1.R1011 5'-most EST gwl700612377.h1

Method BLASTX
NCBI GI g4406821
BLAST score 296
E value 5.0e-27
Match length 85
% identity 68

NCBI Description (AC006201) hypothetical protein [Arabidopsis thaliana]

Seq. No. 290126

Contig ID 333669 1.R1011 5'-most EST gwl700612436.h1

Seq. No. 290127

Contig ID 333959 1.R1011 5'-most EST gwl700615366.h1

Seq. No. 290128

Contig ID 333975 1.R1011 5'-most EST fdz701161145.h1

Seq. No. 290129

Contig ID 334039_1.R1011 5'-most EST gwl700613041.h1

Seq. No. 290130

Contig ID 334261_1.R1011 5'-most EST gwl700613439.h1

Seq. No. 290131

Contig ID 334845 1.R1011 5'-most EST gwl700614956.h1

Seq. No. 290132

Contig ID 334912 1.R1011 5'-most EST hbs701185756.h1



82

% identity

NCBI Description

```
Seq. No.
Contig ID
                   335332 1.R1011
                   gw1700617690.hl
5'-most EST
                   290134
Seq. No.
                   335440 1.R1011
Contig ID
5'-most EST
                   ceu700\overline{4}24669.h1
                   290135
Seq. No.
                   335459 1.R1011
Contig ID
5'-most EST
                   gwl700617459.hl
Seq. No.
                   290136
Contig ID
                   335609 1.R1011
                   qw1700615867.h1
5'-most EST
Method
                   BLASTX
                   g1838961
NCBI GI
BLAST score
                   184
                   6.0e-14
E value
                   75
Match length
                   55
% identity
                  (Y10994) acyl carrier protein [Casuarina glauca]
NCBI Description
                   290137
Seq. No.
                   335761 1.R1011
Contig ID
                   qw1700616207.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1946373
BLAST score
                   432
                   8.0e-43
E value
                   125
Match length
% identity
                   62
                   (U93215) leader peptidase I isolog [Arabidopsis thaliana]
NCBI Description
                   290138
Seq. No.
Contig ID
                   335907 1.R1011
5'-most EST
                   gw1700616459.h1
Method
                   BLASTX
NCBI GI
                   q2832664
BLAST score
                   298
                   4.0e-27
E value
Match length
                   105
% identity
                   48
                   (AL021710) pollen-specific protein - like [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   290139
                   335957 1.R1011
Contig ID
5'-most EST
                   gw1700616651.h1
Method
                   BLASTX
                   q4587572
NCBI GI
                   271
BLAST score
                   2.0e-24
E value
                   56
Match length
```

(AC006550) Similar to gb U70015 lysosomal trafficking

regulator from Mus musculus and contains 2 PF_00400 WD40,



G-beta repeats. ESTs gb T43386 and gb AA395236 come from this gene. [Arabidopsis thaliana]

290140 Seq. No. 336114 1.R1011 Contig ID

5'-most EST $qw1700\overline{6}16933.h1$

Seq. No. 290141

336140 1.R1011 Contig ID 5'-most EST qw1700616977.h1

Seq. No. 290142

Contig ID 336142 1.R1011 fdz701165460.h1 5'-most EST

Method BLASTX a4584110 NCBI GI 285 BLAST score E value 1.0e-25 98 Match length 56 % identity

NCBI Description (AJ133639) SAH7 protein [Arabidopsis thaliana]

290143 Seq. No.

Contig ID 336147 1.R1011 hbs701180993.h1 5'-most EST

290144 Seq. No.

336161 1.R1011 Contig ID 5'-most EST ceu700430939.h1

BLASTX Method g2494075 NCBI GI BLAST score 330 E value 7.0e-31 Match length 68 96

% identity

NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE NCBI Description

(NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE

DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE

(NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE)

>qi 1084478 pir S43833 glyceraldehyde-3-phosphate

dehydrogenase (NADP+) (EC 1.2.1.9) - maize

>gi 474408 emb CAA53075_ (X75326)

glyceraldehyde-3-phosphate dehydrogenase (GAPN) [Zea mays]

290145 Seq. No.

336166 1.R1011 Contig ID 5'-most EST gw1700617026.h1

290146 Seq. No.

336271 1.R1011 Contig ID 5'-most EST qw1700617267.h1

290147 Seq. No.

336773 1.R1011 Contig ID 5'-most EST gwl700618507.hl

Seq. No. 290148



336927 1.R1011 Contig ID hvj700618807.h1 5'-most EST BLASTN Method g3249127 NCBI GI 154 BLAST score 2.0e-81 E value Match length 225 47 % identity Homo sapiens chromosome 17, clone hRPC.117_B_12, complete NCBI Description sequence [Homo sapiens] 290149 Seq. No.

Seq. No. 290149 Contig ID 336977_1.R1011 5'-most EST hbs701185106.h1

 Seq. No.
 290150

 Contig ID
 337090_1.R1011

 5'-most EST
 hvj700619069.h1

 Seq. No.
 290151

 Contig ID
 337562_1.R1011

 5'-most EST
 hvj700623502.h1

 Seq. No.
 290152

 Contig ID
 337634_1.R1011

 5'-most EST
 hvj700620724.h1

 Seq. No.
 290153

 Contig ID
 337795_1.R1011

 5'-most EST
 hvj700620224.h1

 Method
 BLASTX

 NCBI GI
 q4587556

NCBI GI g4587556
BLAST score 303
E value 1.0e-27
Match length 97
% identity 63

NCBI Description (AC006577) Similar to gi_1653162 (p)ppGpp

3-pyrophosphohydrolase from Synechocystis sp genome gb_D90911. EST gb_W43807 comes from this gene.

[Arabidopsis thaliana]

 Seq. No.
 290154

 Contig ID
 337809_1.R1011

 5'-most EST
 hvj700620250.h1

Seq. No. 290155 Contig ID 337863_1.R1011 5'-most EST hvj700620611.h1

Seq. No. 290156 Contig ID 337868_1.R1011 5'-most EST hvj700620351.h1

 Seq. No.
 290157

 Contig ID
 337883 1.R1011

 5'-most EST
 hvj700620616.h1



Seq. No. 290158 Contig ID 337967_1.R1011 5'-most EST hvj700620525.h1

Seq. No. 290159

Contig ID 337977 1.R1011 5'-most EST hvj700620849.h1

Method BLASTX
NCBI GI g4378663
BLAST score 221
E value 6.0e-31
Match length 94
% identity 63

NCBI Description (AF107765) cytochrome P450 [Prunus dulcis]

Seq. No. 290160

Contig ID 338054_1.R1011 5'-most EST hvj700620719.h1

Seq. No. 290161

Contig ID 338080_1.R1011 5'-most EST hvj700620758.h1

Seq. No. 290162

Contig ID 338148_1.R1011 5'-most EST hvj700620862.h1

Seq. No. 290163

Contig ID 338224_1.R1011 5'-most EST 1tv700479631.h1

Method BLASTX
NCBI GI g3935168
BLAST score 278
E value 1.0e-24
Match length 98
% identity 57

NCBI Description (AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No. 290164

Contig ID 338304_1.R1011 5'-most EST hvj700621157.h1

Seq. No. 290165

Contig ID 338378_1.R1011 5'-most EST ceu700430758.h1

Seq. No. 290166

Contig ID 338585_1.R1011 5'-most EST hvj700623903.h1

Seq. No. 290167

Contig ID 338664_1.R1011 5'-most EST hvj700621816.h1

Seq. No. 290168

Contig ID 338675_1.R1011 5'-most EST jfc700968632.h1

Seq. No.

290181



Seq. No. Contig ID 5'-most EST	290169 338721_1.R1011 hvj700621931.h1
Seq. No. Contig ID 5'-most EST	290170 338788_1.R1011 ceu700425012.h1
BLAST score E value Match length % identity	290171 339148_1.R1011 hvj700622636.h1 BLASTX g4314355 261 8.0e-23 94 51 (AC006340) unknown protein [Arabidopsis thaliana]
Seq. No. Contig ID 5'-most EST	290172 339375_1.R1011 gct701168526.h1
Seq. No. Contig ID 5'-most EST	290173 339426_1.R1011 gct701179310.h1
Seq. No. Contig ID 5'-most EST	290174 339482_1.R1011 hvj700623307.h1
Seq. No. Contig ID 5'-most EST	290175 339491_1.R1011 hvj700623690.h1
Seq. No. Contig ID 5'-most EST	290176 339506_1.R1011 hvj700623346.h1
Seq. No. Contig ID 5'-most EST	290177 339733_1.R1011 hvj700623761.h1
Seq. No. Contig ID 5'-most EST	290178 339799_1.R1011 hvj700623884.h1
Seq. No. Contig ID 5'-most EST	290179 339810_1.R1011 hvj700623908.h1
Seq. No. Contig ID 5'-most EST	290180 339821_1.R1011 ceu700433362.h1

Contig ID 5'-most EST	339926_1.R1011 hvj700624092.h1
Seq. No. Contig ID 5'-most EST	290182 339978_1.R1011 hvj700624275.h1
Seq. No. Contig ID 5'-most EST	290183 340118_1.R1011 hvj700624439.h1
BLAST score E value Match length % identity	,
Seq. No.	290185

Seq. No.	290185
Contig ID	340174_1.R1011
5'-most EST	hvj700624542.h1
•	

Seq. No.	290186
Contig ID	340386_1.R1011
5'-most EST	$hbs701\overline{1}85659.h1$

Seq. No.	290187
Contig ID	340462 1.R1011
5'-most EST	ypc700806285.h1

Seq. No.	290188
Contig ID	340468 1.R1011
5'-most EST	ypc700798795.h1

Seq. No.	290189
Contig ID	340536 1.R1011
5'-most EST	ypc700799015.h1

Seq. No.	290190
Contig ID	340598 1.R1011
5'-most EST	ypc700806246.h1

Seq. No.	290191
Contig ID	340601 1.R1011
5'-most EST	$ypc700\overline{8}04274.h1$

Seq. No.	290192
Contig ID	340610 1.R1011
5'-most EST	$ypc700\overline{8}04245.h1$

 Seq. No.
 290193

 Contig ID
 340699_1.R1011

 5.'-most EST
 ypc700805313.h1



```
Seq. No.
                  290194
                  340768 1.R1011
Contig ID
                 ypc700799862.hl
5'-most EST
                  290195
Seq. No.
Contig ID
                  340770 1.R1011
                  ypc700799866.h1
5'-most EST
Method
                  BLASTN
NCBI ĞI
                  g168663
BLAST score
                  129
E value
                  2.0e-66
Match length
                  203
% identity
                  97
NCBI Description Maize sulfur-rich zein protein of Mr 15,000, complete cds
                  290196
Seq. No.
Contig ID
                  340792 1.R1011
                  ypc700800292.hl
5'-most EST
Method
                  BLASTX
                  g127243
NCBI GI
BLAST score
                  285
E value
                  8.0e-26
Match length
                  87
% identity
                  60
                 AUTONOMOUS TRANSPOSABLE ELEMENT EN-1 MOSAIC PROTEIN
NCBI Description
                  (SUPPRESSOR-MUTATOR SYSTEM PROTEIN) (SPM)
                 290197
Seq. No.
                  340868 1.R1011
Contig ID
5'-most EST
                  ypc700800344.h1
                  BLASTN
Method
NCBI GI
                  g168654
BLAST score
                  266
E value
                  1.0e-148
Match length
                  274
% identity
                  99
                  Zea mays ADP glucose pyrophosphorylase (shrunken-2) gene,
NCBI Description
                  complete cds
                  290198
Seq. No.
                  340956 1.R1011
Contig ID
5'-most EST
                  ypc700802270.h1
Method
                  BLASTX
NCBI GI
                  g2281780
BLAST score
                  253
E value
                  4.0e-22
                  77
Match length
                  64
% identity
                  (AB003041) O-acetylserine (thiol) lyase [Arabidopsis
```

thaliana] 290199

NCBI Description

Seq. No.

340959 1.R1011 Contig ID



```
5'-most EST ypc700800649.h1

Seq. No. 290200
Contig ID 341122_1.R1011
5'-most EST ypc700801452.h1
Method BLASTX
```

NCBI GI 94063760
BLAST score 187
E value 2.0e-14
Match length 77
% identity 45

NCBI Description (AC005561) putative POL3 protein [Arabidopsis thaliana]

 Seq. No.
 290201

 Contig ID
 341188_1.R1011

 5'-most EST
 ypc700803736.h1

 Seq. No.
 290202

 Contig ID
 341250_1.R1011

 5'-most EST
 ypc700806560.h1

 Seq. No.
 290203

 Contig ID
 341385_1.R1011

 5'-most EST
 ypc700802172.h1

 Seq. No.
 290204

 Contig ID
 341409_1.R1011

 5'-most EST
 ypc700802255.h1

 Seq. No.
 290205

 Contig ID
 341495_1.R1011

 5'-most EST
 ypc700806556.h1

 Method
 BLASTX

 NCBI GI
 g2245099

NCBI GI g2245099
BLAST score 317
E value 2.0e-29
Match length 76
% identity 75

NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

 Seq. No.
 290206

 Contig ID
 341552_1.R1011

 5'-most EST
 ypc700802890.h1

 Seq. No.
 290207

Contig ID 341656_1.R1011 5'-most EST ypc700803275.h1

Seq. No. 290208 Contig ID 341700_1.R1011 5'-most EST ypc700803436.h1

 Seq. No.
 290209

 Contig ID
 341867_1.R1011

 5'-most EST
 ypc700803964.h1

Seq. No. 290210

Contig ID 5'-most EST	342055_1.R1011 ypc700804635.h1
Seq. No. Contig ID 5'-most EST	290211 342460_1.R1011 ypc700805954.h1
Seq. No. Contig ID 5'-most EST	290212 342533_1.R1011 ypc700806227.h1
Seq. No. Contig ID 5'-most EST	290213 342591_1.R1011 ypc700806386.h1
Seq. No. Contig ID 5'-most EST Method NCBI GI BLAST score E value Match length	290214 342898_1.R1011 ceu700421532.h1 BLASTX g4580391 229 6.0e-19

% identity (ACOO7171) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 290215 Contig ID 342967 1.R1011 $ceu700\overline{4}21656.h1$ 5'-most EST

290216 Seq. No. Contig ID 343051 1.R1011 $ceu700\overline{4}21790.h1$ 5'-most EST

Seq. No. 290217 343063 1.R1011 Contig ID $ceu700\overline{4}23892.h1$ 5'-most EST Method BLASTX g3738299 NCBI GI BLAST score Ī83

7.0e-14E value Match length 61 % identity 56

NCBI Description (AC005309) putative glutaredoxin [Arabidopsis thaliana] >gi_4249395 (AC006072) putative glutaredoxin [Arabidopsis

thaliana]

290218 Seq. No. Contig ID

343091 1.R1011 5'-most EST $ceu700\overline{4}21869.h1$

Seq. No. 290219

343099 1.R1011 Contig ID 5'-most EST ceu700421882.hl Method BLASTX

NCBI GI g4559380 BLAST score 262



E value 1.0e-40 Match length 133 % identity 58

NCBI Description (AC006526) putative auxin-responsive GH3 protein

[Arabidopsis thaliana]

Seq. No. 290220

Contig ID 343154_1.R1011 5'-most EST ceu700421987.h1

Seq. No. 290221

Contig ID 343155_1.R1011 5'-most EST ceu700421989.h1

Method BLASTX
NCBI GI g3724366
BLAST score 193
E value 3.0e-15
Match length 53
% identity 64

NCBI Description (AB018379) unknown ORF [Thermus thermophilus]

Seq. No. 290222

Contig ID 343169_1.R1011 5'-most EST ceu700422024.h1

Seq. No. 290223

Contig ID 343177 1.R1011 5'-most EST gct701180013.h1

Seq. No. 290224

Contig ID 343180_1.R1011 5'-most EST ceu700422043.h1

Seq. No. 290225

Contig ID 343186 1.R1011 5'-most EST ceu700422054.h1

Seq. No. 290226

Contig ID 343203_1.R1011 5'-most EST ceu700422081.h1

Seq. No. 290227

Contig ID 343211_1.R1011 5'-most EST fxb700397586.h1

Seq. No. 290228

Contig ID 343220 1.R1011 5'-most EST ceu700424128.h1

Seq. No. 290229

Contig ID 343231_1.R1011 5'-most EST ceu700427532.h1

Seq. No. 290230

Contig ID 343239_1.R1011 5'-most EST ceu700424367.h1



```
290231
Seq. No.
                   343260 1.R1011
Contig ID
                   ceu700422164.hl
5'-most EST
                   290232
Seq. No.
                   343282 1.R1011
Contig ID
                   ceu700\overline{4}22196.h1
5'-most EST
                   290233
Seq. No.
                   343321 1.R1011
Contig ID
                   ceu700\overline{4}33023.h1
5'-most EST
                   290234
Seq. No.
                   343358 1.R1011
Contig ID
                   ceu700422418.h1
5'-most EST
                   290235
Seq. No.
                   343364 1.R1011
Contig ID
                   ceu700431151.h1
5'-most EST
                   290236
Seq. No.
                   343407_1.R1011
Contig ID
                   ceu700426111.hl
5'-most EST
                   BLASTX
Method
                   g2144902
NCBI GI
                   461
BLAST score
                   2.0e-46
E value
                   91
Match length
                   98
% identity
                   semenogelin I precursor - human >gi_487420 (M81650) SEMGI
NCBI Description
                   [Homo sapiens] >gi_1147569_emb_CAA87636_ (Z47556)
                   semenogelin I [Homo sapiens]
                   290237
Seq. No.
                   343410 1.R1011
Contig ID
5'-most EST
                   ceu700422487.h1
                   BLASTX
Method
                   q4468812
NCBI GI
                   163
BLAST score
                   1.0e-16
E value
                   67
Match length
                   61
% identity
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]
Seq. No.
                   290238
                    343475 1.R1011
Contig ID
5'-most EST
                   ceu700422596.hl
                    290239
Seq. No.
                    343492 1.R1011
 Contig ID
                    gct701177179.h1
 5'-most EST
                   BLASTN
Method
```

40351

g1044939

2.0e-97 244

181

94

NCBI GI

BLAST score E value

Match length

% identity



NCBI Description Z.mays mRNA for ubiquitin/ribosomal protein S27a fusion protein

Seq. No. 290240

Contig ID 343526_1.R1011 5'-most EST ceu700425069.h1

Seq. No. 290241

Contig ID 343544 1.R1011 5'-most EST ceu700422707.h1

Method BLASTX
NCBI GI g2984278
BLAST score 189
E value 1.0e-14
Match length 72
% identity 57

NCBI Description (AE000770) DNA helicase [Aquifex aeolicus]

Seq. No. 290242

Contig ID 343547 1.R1011 5'-most EST ceu700422711.h1

Method BLASTN
NCBI GI g3360404
BLAST score 162
E value 4.0e-86
Match length 258
% identity 94

NCBI Description Homo sapiens clone 23765 mRNA sequence

Seq. No. 290243

Contig ID 343621_1.R1011 5'-most EST ceu700428372.h1

Method BLASTX
NCBI GI g2827536
BLAST score 405
E value 1.0e-39
Match length 106
% identity 63

NCBI Description (AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No. 290244

Contig ID 343624_1.R1011 5'-most EST ceu700425463.h1

Seq. No. 290245

Contig ID 343654_1.R1011 5'-most EST ceu700425421.h1

Seq. No. 290246

Contig ID 343704 1.R1011 5'-most EST ceu700425132.h1

Method BLASTX
NCBI GI g3540195
BLAST score 401
E value 4.0e-39
Match length 97
% identity 35



NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No. 290247

Contig ID 343730_1.R1011 5'-most EST ceu700422987.h1

Seq. No. 290248

Contig ID 343763_1.R1011 5'-most EST ceu700423037.h1

Seq. No. 290249

Contig ID 343770_1.R1011 5'-most EST ceu700424180.h1

Seq. No. 290250

Contig ID 343835_1.R1011 5'-most EST ceu700428340.h1

Seq. No. 290251

Contig ID 343851_1.R1011 5'-most EST ceu700423183.h1

Seq. No. 290252

Contig ID 343984_1.R1011 5'-most EST ceu700423490.h1

Seq. No. 290253

Contig ID 344002_1.R1011 5'-most EST ceu700433484.h1

Seq. No. 290254

Contig ID 344114_1.R1011 5'-most EST ceu700426702.h1

Seq. No. 290255

Contig ID 344215_1.R1011 5'-most EST ceu700423895.h1

Method BLASTX
NCBI GI g2062168
BLAST score 152
E value 3.0e-10
Match length 39
% identity 72

NCBI Description (AC001645) hypothetical protein [Arabidopsis thaliana]

Seq. No. 290256

Contig ID 344325_1.R1011 5'-most EST ceu700433628.h1

Seq. No. 290257

Contig ID 344371 1.R1011 5'-most EST ceu700431757.h1

Seq. No. 290258

Contig ID 344709_1.R1011 5'-most EST ceu700425283.h1



```
290259
Seq. No.
                  344918 1.R1011
Contig ID
                  ceu700425433.h1
5'-most EST
                  BLASTX
Method
                  g3522946
NCBI GI
                  241
BLAST score
                  1.0e-20
E value
                  76
Match length
                  62
% identity
NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
                  290260
Seq. No.
                  344938 1.R1011
Contig ID
5'-most EST
                  ceu700425434.h1
                  290261
Seq. No.
                  344942 1.R1011
Contig ID
                  ceu700425440.hl
5'-most EST
                  290262
Seq. No.
                   344949 1.R1011
Contig ID
                   ceu700\overline{4}25451.h1
5'-most EST
                  BLASTX
Method
                   g2131161
NCBI GI
BLAST score
                   170
                   2.0e-12
E value
                   78
Match length
                   49
% identity
                   4-nitrophenylphosphatase (EC 3.1.3.41) - yeast
NCBI Description
                   (Saccharomyces cerevisiae) >gi_1431400_emb_CAA98816_
                   (Z74284) ORF YDL236w [Saccharomyces cerevisiae]
                   290263
Seq. No.
                   344970 1.R1011
Contig ID
                   ceu700425486.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3386600
                   272
BLAST score
E value
                   5.0e-24
Match length
                   103
% identity
                   59
NCBI Description (AC004665) putative glycoprotein [Arabidopsis thaliana]
                   290264
Seq. No.
                   344985 1.R1011
Contig ID
                   ceu700431339.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q533775
BLAST score
                   186
E value
                   3.0e-14
Match length
                   50
                   76
 % identity
NCBI Description (U09989) H(+)-transporting ATPase [Zea mays]
```

Seq. No. 290265

Contig ID 345033_1.R1011 5'-most EST ceu700426129.h1

```
Method
                   g2982453
NCBI GI
                    213
BLAST score
                    2.0e-17
E value
                    68
Match length
                    60
% identity
                    (AL022223) fructose-bisphosphate aldolase-like protein
NCBI Description
                    [Arabidopsis thaliana]
                    290266
Seq. No.
                    345062_1.R1011
Contig ID
                    ceu700\overline{4}34186.h1
5'-most EST
                    BLASTX
Method
NCBI GI
                    g3894197
                    415
BLAST score
                    6.0e-41
E value
                    106
Match length
                    67
% identity
                   (AC005662) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    290267
Seq. No.
                    345063 1.R1011
Contig ID
                    ceu700\overline{4}26126.h1
5'-most EST
Seq. No.
                    290268
                    345147_1.R1011
Contig ID
                    ceu700\overline{4}26185.h1
5'-most EST
                    290269
Seq. No.
                    345237 1.R1011
Contig ID
                    ceu700432746.hl
5'-most EST
                    BLASTX
Method
                    g2347195
NCBI GI
BLAST score
                    246
                    3.0e-21
E value
Match length
                    84
                    56
% identity
                    (AC002338) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    290270
                    345251 1.R1011
Contig ID
                    ceu700\overline{4}30919.h1
5'-most EST
                    290271
Seq. No.
                    345252 1.R1011
Contig ID
                    gct701177724.h1
 5'-most EST
                    290272
Seq. No.
                    345259 1.R1011
Contig ID
                    ceu700\overline{4}30901.h1
 5'-most EST
                    BLASTX
Method
                    q3033398
NCBI GI
```

293 BLAST score 2.0e-27 E value 90 Match length 73 % identity

NCBI Description (AC004238) putative phosphoribosylaminoimidazolecarboxamide



formyltransferase [Arabidopsis thaliana]

 Seq. No.
 290273

 Contig ID
 345264_1.R1011

 5'-most EST
 ceu700426411.h1

Seq. No. 290274

Contig ID 345317_1.R1011 5'-most EST ceu700426587.h1

Seq. No. 290275

Contig ID 345346_1.R1011 5'-most EST ceu700426653.h1

Seq. No. 290276

Contig ID 345352_1.R1011 5'-most EST ceu700426672.h1

Seq. No. 290277

Contig ID 345381 1.R1011 5'-most EST ceu700430384.h1

Seq. No. 290278

Contig ID 345417_1.R1011 5'-most EST ceu700429592.h1

Seq. No. 290279

Contig ID 345422_1.R1011 5'-most EST ceu700426813.h1

Method BLASTX
NCBI GI g1465735
BLAST score 190
E value 6.0e-15
Match length 46
% identity 78

NCBI Description (U44133) violaxanthin de-epoxidase precursor [Arabidopsis

thaliana] >gi_3063441 (AC003981) F22013.3 [Arabidopsis

thaliana]

Seq. No. 290280

Contig ID 345436_1.R1011 5'-most EST gct701173723.h1

Seq. No. 290281

Contig ID 345476_1.R1011 5'-most EST fdz701161737.h1 Method BLASTN

Method BLASTN
NCBI GI g2463510
BLAST score 185
E value 1.0e-100
Match length 252
% identity 44

NCBI Description Z.mays small nuclear RNA genes snoR1.1, snoR2.2, snoR3.2,

U14.1a, U14.1b, U14.1c and U14.1d

Seq. No. 290282

Contig ID 345498_1.R1011



```
ceu700427023.hl
5'-most EST
                   290283
Seq. No.
                   345542 1.R1011
Contig ID
                   ceu700430335.hl
5'-most EST
                   290284
Seq. No.
                   345561 1.R1011
Contig ID
                   ceu700\overline{4}27170.h1
5'-most EST
                   290285
Seq. No.
                   345601_1.R1011
Contig ID
5'-most EST
                   ceu700431128.hl
                   290286
Seq. No.
                   345618 1.R1011
Contig ID
5'-most EST
                   ceu700427274.h1
                   290287
Seq. No.
                   345640 1.R1011
Contig ID
5'-most EST
                   ceu700\overline{4}27322.h1
                   290288
Seq. No.
Contig ID
                   345644 1.R1011
5'-most EST
                   ceu700427326.h1
Method
                   BLASTX
                   g2493493
NCBI GI
                   169
BLAST score
                   3.0e-12
E value
Match length
                   39
                   74
% identity
                   SERINE CARBOXYPEPTIDASE II-1 PRECURSOR (CP-MII.1)
NCBI Description
                   >gi 619352_bbs 153538 CP-MII.1=serine carboxypeptidase
                   [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 324
                   aa]
Seq. No.
                   290289
                   345675 1.R1011
Contig ID
5'-most EST
                   ceu700433733.hl
Method
                   BLASTX
NCBI GI
                   q3023742
BLAST score
                   200
E value
                   8.0e-16
Match length
                   48
% identity
                   71
                   FERREDOXIN 2 PRECURSOR >gi 1931646 (U95973) ferredoxin
NCBI Description
                   precusor isolog [Arabidopsis thaliana]
```

Seq. No.

290290

Contig ID 34576 5'-most EST ceu70

345763_1.R1011 ceu700429210.h1

Seq. No.
Contig ID
5'-most EST

290291

345794_1.R1011 ceu700427692.h1

Seq. No.



```
345795 1.R1011
Contig ID
                   ceu700\overline{4}27694.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1922938
                   303
BLAST score
                   6.0e-28
E value
Match length
                   89
                   64
% identity
                   (AC000106) Similar to Caenorhabditis hypothetical protein
NCBI Description
                   CO7A9.11 (gb Z29094). [Arabidopsis thaliana]
Seq. No.
                   290293
                   345796 1.R1011
Contig ID
5'-most EST
                   ceu700429305.hl
                   290294
Seq. No.
                   345829 1.R1011
Contig ID
5'-most EST
                   ceu700427783.h1
                   BLASTX
Method
                   g3785977
NCBI GI
BLAST score
                   427
                   2.0e-42
E value
Match length
                   93
% identity
                   78
                   (AC005560) putative growth regulator protein [Arabidopsis
NCBI Description
                   thaliana]
                   290295
Seq. No.
Contig ID
                   345883 1.R1011
5'-most EST
                   ceu700427920.h1
                   290296
Seq. No.
                   345887 1.R1011
Contig ID
                   fdz701160868.hl
5'-most EST
                   290297
Seq. No.
                   345890 1.R1011
Contig ID
                   ceu700427928.h1
5'-most EST
Method
                   BLASTX
                   g4455272
NCBI GI
                   190
BLAST score
                   2.0e-14
E value
                   73
Match length
% identity
                   62
                   (AL035527) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
                   290298
Seq. No.
                   345920 1.R1011
Contig ID
                   ceu700430108.h1
5'-most EST
                   290299
Seq. No.
```

345932 1.R1011 Contig ID 5'-most EST $ceu700\overline{4}28016.h1$

290300 Seq. No.

345941 1.R1011 Contig ID ceu700428031.hl 5'-most EST



Seq. No. Contig ID 5'-most EST	290301 345949_1.R1011 ceu700428046.h1
Seq. No. Contig ID 5'-most EST	290302 345960_1.R1011 ceu700428067.h1
Seq. No. Contig ID 5'-most EST	290303 346105_1.R1011 ceu700428334.h1
Seq. No. Contig ID 5'-most EST	290304 346121_1.R1011 ceu700428364.h1
Seq. No. Contig ID 5'-most EST	290305 346170_1.R1011 ceu700431684.h1
Seq. No. Contig ID 5'-most EST Method NCBI GI BLAST score E value Match length % identity NCBI Description	290306 346209_1.R1011 ceu700428606.h1 BLASTX g2244996 227 5.0e-19 89 51 (Z97341) similarity to a membrane-associated salt-inducible protein [Arabidopsis thaliana]
Seq. No. Contig ID 5'-most EST Method NCBI GI BLAST score E value Match length % identity NCBI Description	290307 346261_1.R1011 ceu700428701.h1 BLASTN g4156151 239 1.0e-132 275 97 Homo sapiens clone GS051M12, complete sequence [Homo sapiens]
Seq. No. Contig ID 5'-most EST	290308 346269_1.R1011 ceu700428718.h1
Sea No	290309

290309

Seq. No. Contig ID 5'-most EST 346291 1.R1011 $ceu700\overline{4}28909.h1$

Seq. No. 290310

Contig ID 5'-most EST 346298_1.R1011 sem700930275.h1



Seq. No.	290311
Contig ID	346361 1.R1011
5'-most EST	ceu700428915.h1

Seq. No.	290312	
Contig ID	346652	1.R1

Contig ID 346652_1.R1011 5'-most EST ceu700429528.h1

Seq. No. 290313

Contig ID 346653_1.R1011 5'-most EST ceu700434101.h1

Seq. No. 290314

Contig ID 346705_1.R1011 5'-most EST ceu700429822.h1

Seq. No. 290315

Contig ID 346787_1.R1011 5'-most EST ceu700429760.h1

Seq. No. 290316

Contig ID 346799_1.R1011 5'-most EST ceu700434386.h1

Seq. No. 290317

Contig ID 346876_1.R1011 5'-most EST ceu700430119.h1

Method BLASTX
NCBI GI g2262136
BLAST score 150
E value 2.0e-12
Match length 49
% identity 84

NCBI Description (AC002330) predicted protein of unknown function

[Arabidopsis thaliana] >gi_4263520_gb_AAD15346_ (AC004044)

predicted protein of unknown function [Arabidopsis

thaliana]

Seq. No. 290318

Contig ID 346877_1.R1011 5'-most EST ceu700430431.h1

Seq. No. 290319

Contig ID 347045_1.R1011 5'-most EST ceu700430449.h1

Seq. No. 290320

Contig ID 347103_1.R1011 5'-most EST ceu700430421.h1

Seq. No. 290321

Contig ID 347145_1.R1011 5'-most EST ceu700430383.h1

Seq. No. 290322

Contig ID 347284 1.R1011 5'-most EST ceu700430711.h1



```
290323
Seq. No.
                   347314 1.R1011
Contig ID
                   ceu700430771.hl
5'-most EST
                   BLASTX
Method
                   q3641836
NCBI GI
BLAST score
                   193
                   5.0e-15
E value
                   94
Match length
                   48
% identity
                   (AL023094) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   290324
Seq. No.
                   347633 1.R1011
Contig ID
5'-most EST
                   ceu700431393.hl
Seq. No.
                   290325
                   347695 1.R1011
Contig ID
                   ceu700\overline{4}31525.h1
5'-most EST
                   290326
Seq. No.
Contig ID
                   347757 1.R1011
5'-most EST
                   ceu700431702.hl
                   290327
Seq. No.
                   347824 1.R1011
Contig ID
                   ceu700\overline{4}31696.h1
5'-most EST
                   290328
Seq. No.
                   347825 1.R1011
Contig ID
                   ceu700\overline{4}31701.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q2618746
BLAST score
                   57
                   2.0e-23
E value
Match length
                    93
                    90
% identity
                   Fugu rubripes zinc finger protein, isotocin, fatty acid
NCBI Description
                   binding protein, sepiapterin reductase and vasotocin genes,
                   complete cds
                   290329
Seq. No.
                   347902 1.R1011
Contig ID
5'-most EST
                   ceu700\overline{4}31838.h1
Seq. No.
                    290330
                   347997 1.R1011
Contig ID
                   gct701180004.h1
5'-most EST
```

Seq. No. 290331

Contig ID 348107 1.R1011 5'-most EST gct701176540.h1

Seq. No. 290332

Contig ID 348150_1.R1011 5'-most EST ceu700432991.h1



Seq. No. 290333

Contig ID 348171_1.R1011 5'-most EST ceu700432462.h1

Method BLASTX
NCBI GI g3386607
BLAST score 222
E value 1.0e-18
Match length 57
% identity 72

NCBI Description (AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No. 290334

Contig ID 348201_1.R1011 5'-most EST ceu700432491.h1

Seq. No. 290335

Contig ID 348444_1.R1011 5'-most EST gct701172910.h2

Seq. No. 290336

Contig ID 348476_1.R1011 5'-most EST ceu700433234.h1

Seq. No. 290337

Contig ID 348484_1.R1011 5'-most EST ceu700433150.h1

Seq. No. 290338

Contig ID 348498_1.R1011 5'-most EST gct701177579.h1

Seq. No. 290339

Contig ID 348519_1.R1011 5'-most EST ceu700433211.h1

Seq. No. 290340

Contig ID 348533_1.R1011 5'-most EST ceu700433249.h1

Seq. No. 290341

Contig ID 348549_1.R1011 5'-most EST gct701180632.h1

Seq. No. 290342

Contig ID 348622_1.R1011 5'-most EST gct701175031.h1

Seq. No. 290343

Contig ID 348639_1.R1011 5'-most EST gct701180051.h1

Seq. No. 290344

Contig ID 348640_1.R1011 5'-most EST ceu700433516.h1

Seq. No. 290345



Contig ID 5'-most EST	348691_1.R1011 ceu700433608.h1
Seq. No. Contig ID 5'-most EST	290346 348717_1.R1011 ceu700433681.h1
Seq. No. Contig ID. 5'-most EST	290347 349156_1.R1011 ceu700434547.h1
Seq. No. Contig ID 5'-most EST	290348 349207_1.R1011 gct701175911.h1
Seq. No. Contig ID 5'-most EST	290349 349247_1.R1011 gct701176427.h1
Seq. No. Contig ID 5'-most EST Method NCBI GI BLAST score E value Match length % identity NCBI Description	290350 349335_1.R1011 fdz701161192.h1 BLASTX g2431771 212 3.0e-17 64 66 (U62753) acidic ribosomal protein P2b [Zea mays]
Seq. No. Contig ID 5'-most EST Method NCBI GI BLAST score E value Match length % identity NCBI Description	290351 349338_1.R1011 fdz701161118.h1 BLASTX g1710546 358 3.0e-34 83 84 60S RIBOSOMAL PROTEIN L36 >gi_1276967 (U47095) putative ribosomal protein [Daucus carota]
Seq. No. Contig ID 5'-most EST	290352 349342_1.R1011 fdz701161174.h1
Seq. No.	290353 349344 1.R1011

349344_1.R1011 Contig ID 5'-most EST fdz701158329.h1

Seq. No. Contig ID 5'-most EST

290354

349354 1.R1011 fdz701158347.h1

Seq. No. Contig ID 5'-most EST 290355

349401_1.R1011 fdz701159093.hl



```
290356
Seq. No.
                  349437 1.R1011
Contig ID
                  hbs701181470.h1
5'-most EST
                  290357
Seq. No.
                  349442 1.R1011
Contig ID
                  fdz701158505.hl
5!-most EST
                  BLASTX
Method
                  g3608481
NCBI GI
                  246
BLAST score
                  5.0e-33
E value
                  83
Match length
% identity
                  86
                  (AF088913) ribosomal protein L27a [Petunia x hybrida]
NCBI Description
                  290358
Seq. No.
                   349445 1.R1011
Contig ID
                  fdz701158510.h1
5'-most EST
                  BLASTX
Method
                   g2618699
NCBI GI
                   153
BLAST score
                   2.0e-10
E value
                   66
Match length
                   42
% identity
                  (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
                   290359
Seq. No.
                   349453 1.R1011
Contig ID
                   fdz701158527.h1
5'-most EST
                   BLASTX
Method
                   g3176668
NCBI GI
                   384
BLAST score
                   2.0e-37
E value
                   82
Match length
                   89
% identity
                   (AC004393) Similar to ribosomal protein L17 gb_X62724 from
NCBI Description
                   Hordeum vulgare. ESTs gb Z34728, gb F19974, gb_T75677 and
                   gb Z33937 come from this gene. [Arabidopsis thaliana]
                   290360
Seq. No.
                   349518 1.R1011
Contig ID
                   fdz701161442.h1
5'-most EST
                   290361
Seq. No.
                   349540 1.R1011
Contig ID
                   fdz701158676.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3287696
BLAST score
                   309
                   9.0e-29
E value
Match length
                   79
                   75
 % identity
                   (AC003979) Strong similarity to phosphoribosylanthranilate
NCBI Description
```

[Arabidopsis thaliana]

transferase gb D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region.



 Seq. No.
 290362

 Contig ID
 349545_1.R1011

 5'-most EST
 fdz701164821.h1

Seq. No. 290363

Contig ID 349582 1.R1011 5'-most EST fdz701163156.h1

Seq. No. 290364

Contig ID 349633_1.R1011 5'-most EST fdz701159061.h1

Seq. No. 290365

Contig ID 349648_1.R1011 5'-most EST fdz701158888.h1

Seq. No. 290366

Contig ID 349707_1.R1011 5'-most EST fdz701167004.h1

Seq. No. 290367

Contig ID 349728_1.R1011 5'-most EST fdz701159049.h1

Seq. No. 290368

Contig ID 349739_1.R1011 5'-most EST fdz701161873.h1

Method BLASTN
NCBI GI g2078526
BLAST score 193
E value 1.0e-104
Match length 265
% identity 93

NCBI Description Human chromosome X clone Qc15B1, complete sequence [Homo

sapiens]

Seq. No. 290369

Contig ID 349777_1.R1011 5'-most EST fdz701159547.h1

Method BLASTX
NCBI GI g3402751
BLAST score 158
E value 7.0e-11
Match length 97
% identity 38

NCBI Description (AL031187) putative protein [Arabidopsis thaliana]

Seq. No. 290370

Contig ID 349959_1.R1011 5'-most EST fdz701160303.h1

Method BLASTN
NCBI GI g3478633
BLAST score 169
E value 3.0e-90
Match length 277
% identity 90



Homo sapiens 12p13.3 PAC RPCI5-977L1 (Roswell Park Cancer NCBI Description

Institute Human PAC library) complete sequence [Homo

sapiens]

290371 Seq. No. Contig ID

349973 1.R1011 fdz701160320.hl

Seq. No.

5'-most EST

290372 350064 1.R1011

Contig ID 5'-most EST Method

fdz701160479.h1 BLASTX

NCBI GI BLAST score E value

205 2.0e-16 87

g2465923

Match length % identity

48

NCBI Description

(AF024648) receptor-like serine/threonine kinase

[Arabidopsis thaliana]

Seq. No. Contig ID 5'-most EST 290373 350078 1.R1011 fdz701160484.h1

Seq. No. Contig ID 290374

5'-most EST

350085 1.R1011 fdz701160493.h1

BLASTN Method g4507204 NCBI GI BLAST score 143 8.0e-75 E value 243 Match length % identity

NCBI Description

Homo sapiens serum response factor (c-fos serum response

element-binding transcription factor) (SRF) mRNA

>gi_338479_gb_J03161_HUMSRF Human serum response factor

(SRF) mRNA, complete cds

Seq. No. Contig ID 290375

350105 1.R1011 fdz701160523.h1 5'-most EST

Seq. No.

290376

350107 1.R1011 Contig ID hbs701184139.hl 5'-most EST

Seq. No.

290377

Contig ID 5'-most EST 350137 1.R1011 fdz701160576.hl

Seq. No. Contig ID 290378

350227 1.R1011 fdz701165927.hl 5'-most EST

Seq. No. Contig ID 5'-most EST 290379

350248 1.R1011 fdz701163160.hl



 Seq. No.
 290380

 Contig ID
 350262 1.R1011

 5'-most EST
 fdz701160803.h1

 Method
 BLASTX

NCBI GI g3114615 BLAST score 277 E value 6.0e-25 Match length 63 % identity 86

NCBI Description (AF052483) 40S ribosomal protein S12 [Erysiphe graminis f.

sp. hordei]

Seq. No. 290381

Contig ID 350317 1.R1011 5'-most EST fdz701164509.h1

Seq. No. 290382

Contig ID 350327_1.R1011 5'-most EST hbs701185551.h1

Seq. No. 290383

Contig ID 350367_1.R1011 5'-most EST fdz701161193.h1

Seq. No. 290384

Contig ID 350392 1.R1011 5'-most EST fdz701161015.h1

Seq. No. 290385

Contig ID 350420 1.R1011 5'-most EST fdz701164143.h1

Seq. No. 290386

Contig ID 350479 1.R1011 5'-most EST hbs701185516.h1

Seq. No. 290387

Contig ID 350531 1.R1011 5'-most EST fdz701161220.h1

Seq. No. 290388

Contig ID 350582 1.R1011 5'-most EST fdz701161304.h1

Seq. No. 290389

Contig ID 350625 1.R1011 5'-most EST fdz701163760.h1

Seq. No. 290390

Contig ID 350643_1.R1011 5'-most EST fdz701161390.h1

Seq. No. 290391

Contig ID 350710 1.R1011 5'-most EST fdz701161519.h1



Seq. No.	290392
Contig ID	350758

Contig ID 350758_1.R1011 5'-most EST fdz701165604.h1

Seq. No. 290393

Contig ID 350823_1.R1011 5'-most EST fdz701161721.h1

Seq. No. 290394

Contig ID 350886_1.R1011 5'-most EST fdz701161825.h1

Seq. No. 290395

Contig ID 350916_1.R1011 5'-most EST fdz701167061.h1

Seq. No. 290396

Contig ID 351021_1.R1011 5'-most EST fdz701162852.h1

Seq. No. 290397

Contig ID 351027_1.R1011 5'-most EST fdz701165259.h1

Seq. No. 290398

Contig ID 351042 1.R1011 5'-most EST fdz701162878.h1

Seq. No. 290399

Contig ID 351071 1.R1011 5'-most EST hbs701180874.h1

Seq. No. 290400

Contig ID 351079_1.R1011 5'-most EST fdz701165310.h1

Method BLASTX
NCBI GI g3142291
BLAST score 257
E value 2.0e-22
Match length 87
% identity 57

NCBI Description (AC002411) Contains similarity to adenylate cyclase

gb_AF012921 from Magnaporthe grisae. EST gb_Z24512 comes

from this gene. [Arabidopsis thaliana]

. . .

Seq. No. 290401

Contig ID 351123_1.R1011 5'-most EST fdz701165883.h1

Seq. No. 290402

Contig ID 351187 1.R1011 5'-most EST fdz701163130.h1

Seq. No. 290403

Contig ID 351264_1.R1011 5'-most EST jfc700968530.h1



Seq. No.	290404
Contig ID	351298_1.R1011
5'-most EST	fdz701166546.h1
Seq. No.	290405
Contig ID	351336_1.R1011
5'-most EST	fdz701164390.h1
Seq. No.	290406
Contig ID	351357_1.R1011
5'-most EST	fdz701163428.h1
Seq. No.	290407
Contig ID	351573 <u>1.R1011</u>
5'-most EST	fdz701163791.h1
Seq. No.	290408
Contig ID	351582_1.R1011
5'-most EST	fdz701163789.h1
Seq. No.	290409
Contig ID	351794_1.R1011
5'-most EST	fdz701165863.h1
Seq. No.	290410
Contig ID	351830_1.R1011
5'-most EST	hbs701186042.h1
Seq. No.	290411
Contig ID	351849_1.R1011
5'-most EST	fdz701164290.h1
Seq. No.	290412
Contig ID	351866_1.R1011
5'-most EST	fdz701164323.h1
Seq. No.	290413
Contig ID	352010_1.R1011
5'-most EST	fdz701164631.h1
Seq. No.	290414
Contig ID	352057_1.R1011
5'-most EST	hbs701181829.h1
Seq. No.	290415
Contig ID	352148_1.R1011
5'-most EST	fdz701164985.h1
Seq. No.	290416
Contig ID	352157_1.R1011
5'-most EST	fdz701164968.h1
Seq. No. Contig ID 5'-most EST Method NCBI GI	290417 352190_1.R1011 gct701175484.h1 BLASTX g4376815



BLAST score 173 E value 2.0e-12 Match length 110 % identity 37

NCBI Description (AE001637) GutQ/KpsF Family Sugar-P Isomerase [Chlamydia

pneumoniae]

Seq. No. 290418

Contig ID 352425_1.R1011 5'-most EST gct701173957.h1

Seq. No. 290419

Contig ID 352534_1.R1011 5'-most EST fdz701165643.h1

Seq. No. 290420

Contig ID 352743_1.R1011 5'-most EST fdz701165967.h1

Seq. No. 290421

Contig ID 352796_1.R1011 5'-most EST fdz701166071.h1

Method BLASTN
NCBI GI g507844
BLAST score 36
E value 5.0e-11
Match length 72
% identity 88

NCBI Description Zea mays A188 retrotransposon gag gene, complete cds

Seq. No. 290422

Contig ID 352823_1.R1011 5'-most EST fdz701166116.h1

Seq. No. 290423

Contig ID 352878_1.R1011 5'-most EST hbs701185213.h1

Seq. No. 290424

Contig ID 352924 1.R1011 5'-most EST gct701172925.h2

Seq. No. 290425

Contig ID 353180_1.R1011 5'-most EST fdz701167066.h1

Seq. No. 290426

Contig ID 353198_1.R1011 5'-most EST hbs701181433.h1

Seq. No. 290427

Contig ID 353219 1.R1011 5'-most EST fdz701167034.h1

Seq. No. 290428

Contig ID 353255_1.R1011 5'-most EST fdz701167083.h1



Seq.	No.	
Conti	g I	D _
5'-mo	st	EST

290429

353256 1.R1011 fdz701167081.h1

Seq. No. Contig ID 5'-most EST 290430 353326 1.R1011 hbs701182643.hl

Seq. No. Contig ID 5'-most EST

290431 353374 1.R1011 hbs701182916.h1

Seq. No. Contig ID 5'-most EST 290432 353427 1.R1011 gct701167426.h1

Seq. No. Contig ID 5'-most EST 290433 353461 1.R1011 gct701167188.h1

Seq. No. Contig ID 5'-most EST

290434 353468_1.R1011 gct701167407.h1

BLASTX Method q3540 NCBI GI 252 BLAST score 5.0e-22 E value Match length 85 54

% identity

NCBI Description (X61275) cif1 [Saccharomyces cerevisiae]

Seq. No. Contig ID 5'-most EST 290435 353483 1.R1011 hbs701181735.h1

Seq. No. Contig ID 5'-most EST 290436 353495 1.R1011 gct701167365.h1

Seq. No. Contig ID 5'-most EST

290437 353590 1.R1011 gct701167531.h1

Seq. No. Contig ID 5'-most EST

290438 353670 1.R1011 hbs701181460.h1

Seq. No. Contig ID 5'-most EST

290439 353673 1.R1011 gct701180521.h1

Seq. No. Contig ID 5'-most EST

290440 353679 1.R1011 gct701167916.hl

Seq. No.

290441



353803 1.R1011 Contig ID 5'-most EST gct701168218.hl Method BLASTX g1805654 NCBI GI 270 BLAST score 7.0e-24 E value 118 Match length % identity 53 (X99972) calmodulin-stimulated calcium-ATPase [Brassica NCBI Description oleracea] 290442 Seq. No. Contig ID 353848 1.R1011 gct701178560.h1 5'-most EST 290443 Seq. No. 353865 1.R1011 Contig ID 5'-most EST gct701178890.hl Method BLASTX g4455276 NCBI GI BLAST score 272 4.0e-24 E value 101 Match length % identity 53 (AL035527) peptide transporter-like protein [Arabidopsis NCBI Description thaliana] 290444 Seq. No. Contig ID 354007 1.R1011 qct701168947.hl 5'-most EST 290445 Seq. No. 354012 1.R1011 Contig ID 5'-most EST gct701168945.hl Seq. No. 290446 354060 1.R1011 Contig ID 5'-most EST gct701169112.hl Seq. No. 290447 354076 1.R1011 Contig ID 5'-most EST gct701169134.h1 Seq. No. 290448 354129 1.R1011 Contig ID 5'-most EST gct701169290.h1 290449 Seq. No. 354187 1.R1011 Contig ID gct701176975.hl 5'-most EST 290450 Seq. No. 354236 1.R1011 Contig ID

5'-most EST gct701175303.h1
Method BLASTX

NCBI GI g1173198 BLAST score 296



E value 4.0e-27

Match length 79
% identity 72

NCBI Description 40S RIBOSOMAL PROTEIN S13 >gi_480095_pir__S36423 ribosomal protein S13.e - garden pea >gi_396639_emb_CAA80974_
(Z25509) ribosomal protein S13 [Pisum sativum]

Seq. No. 290451 Contig ID 354251_1.R1011

5'-most EST gct701171003.h1

Seq. No. 290452

Contig ID 354329_1.R1011 5'-most EST gct701170906.h1 Method BLASTX

Method BLASTX
NCBI GI g464706
BLAST score 202
E value 4.0e-16
Match length 86
% identity 48

NCBI Description 40S RIBOSOMAL PROTEIN S15 (S12) >gi_1078669_pir__A53793

ribosomal protein S12, cytosolic - Podospora anserina >gi_401841_emb_CAA80805_ (Z23267) cytoplasmic ribosomal

protein S12 [Podospora anserina]

Seq. No. 290453

Contig ID 354378_1.R1011 5'-most EST gct701173013.h2

Seq. No. 290454

Contig ID 354384_1.R1011 5'-most EST gct701171025.h1

Method BLASTX
NCBI GI g4539657
BLAST score 266
E value 2.0e-23
Match length 87
% identity 54

NCBI Description (AF061282) serine-type carboxypeptidase [Sorghum bicolor]

Seq. No. 290455

Contig ID 354402_1.R1011 5'-most EST gct701178852.h1

Method BLASTX
NCBI GI g2245137
BLAST score 235
E value 6.0e-20
Match length 53
% identity 77

NCBI Description (Z97344) MYB transcription factor homolog [Arabidopsis

thaliana]

Seq. No. 290456

Contig ID 354467_1.R1011 5'-most EST gct701177274.h1

Method BLASTX NCBI GI g2911358



BLAST score E value 2.0e-53 Match length 114 90 % identity

NCBI Description (AF041043) NADPH HC toxin reductase [Zea mays]

Seq. No. 290457

354562 1.R1011 Contig ID 5'-most EST gct701172630.h1

Seq. No. 290458

Contig ID 354595_1.R1011 5'-most EST gct701173024.h2

290459 Seq. No.

354596 1.R1011 Contig ID 5'-most EST gct701173467.h2

Seq. No. 290460

Contig ID 354611 1.R1011 5'-most EST gct701172757.h2

290461 Seq. No.

Contig ID 354628 1.R1011 5'-most EST gct701172990.h2

Seq. No. 290462

354630 1.R1011 Contig ID 5'-most EST gct701172803.h2

290463 Seq. No.

Contig ID 354655 1.R1011 5'-most EST gct701180680.hl

Method BLASTX NCBI GI q122094 BLAST score 204 E value 2.0e-16 Match length 42 % identity 100

NCBI Description

HISTONE H4.2 >gi_101786_pir__S11940 histone H4.2 - Emericella nidulans >gi_296339_emb_CAA39156_ (X55550) histone H4.2 [Emericella nidulans] >gi_529957 (U12631) histone H4.2 [Emericella nidulans] >gi_227598 prf__1707275D

histone H4.2 [Emericella nidulans]

Seq. No. 290464

354675 1.R1011 Contig ID gct701173015.h2 5'-most EST

290465 Seq. No.

354724_1.R1011 Contig ID gct701173025.h2 5'-most EST

290466 Seq. No.

354830 1.R1011 Contig ID 5'-most EST gct701173283.h2



Seq. No. 290467 Contig ID 354865 1.R1011 5'-most EST gct701173387.h2 290468 Seq. No. Contig ID 355051 1.R1011 5'-most EST gct701175005.hl 290469 Seq. No. 355057 1.R1011 Contig ID 5'-most EST gct701173913.h1 Seq. No. 290470 355064 1.R1011 Contig ID 5'-most EST gct701173965.hl Method BLASTX g2832698 NCBI GI BLAST score 255 3.0e-22 E value Match length 81 62 % identity (AL021713) starch synthase-like protein [Arabidopsis NCBI Description thaliana] Seq. No. 290471 355077_1.R1011 Contig ID 5'-most EST gct701180351.h1 BLASTX Method g3548810 NCBI GI BLAST score 155 E value 1.0e-10 Match length 85 % identity 47 NCBI Description (AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana] Seq. No. 290472 Contig ID 355156 1.R1011 5'-most EST gct701174291.h1 290473 Seq. No. Contig ID 355258 1.R1011 5'-most EST gct701174763.h1 Seq. No. 290474 Contig ID 355305 1.R1011 5'-most EST gct701174784.h1 Method BLASTX

NCBI GI q1208496 BLAST score 148 7.0e-10 E value Match length 28 % identity 93

(D38124) EREBP-3 [Nicotiana tabacum] NCBI Description

290475 Seq. No.

355311 1.R1011 Contig ID

BLAST score

% identity

E value Match length 57 2.0e-23

131 54

NCBI Description Z.mays GapC2 gene



```
5'-most EST
                  qct701177833.h1
                  290476
Seq. No.
                  355317 1.R1011
Contig ID
                  qct701174819.h1
5'-most EST
Seq. No.
                  290477
                  355334 1.R1011
Contig ID
5'-most EST
                  gct701177211.h1
                  BLASTX
Method
NCBI GI
                  g134607
BLAST score
                   232
E value
                   1.0e-19
                   70
Match length
                   60
% identity
                  SUPEROXIDE DISMUTASE (CU-ZN) >gi_85253_pir__S03606
NCBI Description
                   superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - fruit fly
                   (Drosophila virilis) >gi_9205_emb_CAA32060_ (X13831) sod
                   protein [Drosophila virilis]
                   290478
Seq. No.
                   355339 1.R1011
Contig ID
5'-most EST
                   gct701174885.hl
Method
                   BLASTX
NCBI GI
                   q3056591
                   271
BLAST score
                   3.0e-24
E value
                   75
Match length
                   69
% identity
                  (AC004255) T1F9.12 [Arabidopsis thaliana]
NCBI Description
                   290479
Seq. No.
                   355354 1.R1011
Contig ID
5'-most EST
                   gct701174931.h1
Seq. No.
                   290480
                   355422 1.R1011
Contig ID
                   gct701176235.h1
5'-most EST
Seq. No.
                   290481
                   355446 1.R1011
Contig ID
5'-most EST
                   gct701175383.hl
Seq. No.
                   290482
                   355482 1.R1011
Contig ID
                   gct701175416.h1
5'-most EST
Seq. No.
                   290483
                   355485 1.R1011
Contig ID
5'-most EST
                   gct701175282.hl
Method
                   BLASTN
NCBI GI
                   g312178
```



290484 Seq. No. 355501 1.R1011 Contig ID gct701176507.hl 5'-most EST 290485 Seq. No. 355514 1.R1011 Contig ID gct701175358.hl 5'-most EST BLASTX Method g4262228 NCBI GI 450 BLAST score 8.0e-45 E value 142 Match length % identity 63 (AC006200) putative receptor protein kinase [Arabidopsis NCBI Description thaliana] 290486 Seq. No. 355543 1.R1011 Contig ID gct701175413.h1 5'-most EST 290487 Seq. No. 355571_1.R1011 Contig ID 5'-most EST gct701175474.h1 290488 Seq. No. 355585 1.R1011 Contig ID gct701175507.h1 5'-most EST BLASTX Method q4455338 NCBI GI 261 BLAST score 4.0e-23 E value 86 Match length 62 % identity (AL035525) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 290489 355693 1.R1011 Contig ID 5'-most EST gct701175955.h1 290490 Seq. No. 355713 1.R1011 Contig ID 5'-most EST gct701176001.hl Seq. No. 290491 355742 1.R1011 Contig ID 5'-most EST gct701176055.h1

Seq. No. 290492

Contig ID 355744_1.R1011 5'-most EST gct701176236.h1

Seq. No. 290493

Contig ID 355755 1.R1011 5'-most EST gct701176092.h1

Seq. No. 290494



Contig ID 355773 1.R1011 5'-most EST gct701176126.h1

Seq. No. 290495

Contig ID 355796_1.R1011 5'-most EST gct701176186.h1

Method BLASTX
NCBI GI g126899
BLAST score 330
E value 4.0e-31
Match length 84
% identity 75

NCBI Description MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR

>gi_319829_pir__DERTMM malate dehydrogenase (EC 1.1.1.37)
precursor, mitochondrial - rat >gi_56643_emb_CAA27812_
(X04240) pro-malate dehydrogenase (aa -24 to 314) [Rattus

norvegicus]

Seq. No. 290496

Contig ID 355800_1.R1011 5'-most EST gct701176455.h1

Method BLASTX
NCBI GI g133892
BLAST score 369
E value 1.0e-35
Match length 71
% identity 99

NCBI Description 40S RIBOSOMAL PROTEIN S26E (CRP5) (13.6 KD RIBOSOMAL

PROTEIN) >gi_71055_pir__R4NC26 ribosomal protein S26.e - Neurospora crassa >gi_3076_emb_CAA39162_ (X55637) ribosomal

protein [Neurospora crassa]

Seq. No. 290497

Contig ID 355812_1.R1011 5'-most EST gct701176216.h1

Method BLASTX
NCBI GI g3415009
BLAST score 189
E value 1.0e-14
Match length 84
% identity 44

NCBI Description (AF080245) sesquiterpene synthase [Elaeis oleifera]

Seq. No. 290498

Contig ID 355847_1.R1011 5'-most EST gct701177865.h1

Seq. No. 290499

Contig ID 355973_1.R1011 5'-most EST gct701176584.h1

Seq. No. 290500

Contig ID 356087_1.R1011 5'-most EST gct701176908.h1

Method BLASTX NCBI GI g4455367 BLAST score 144



```
E value
                  3.0e-09
                  73
Match length
% identity
                  49
                  (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                  290501
Seq. No.
Contig ID
                  356105 1.R1011
5'-most EST
                  gct701176955.h1
Seq. No.
                  290502
Contig ID
                  356192 1.R1011
5'-most EST
                  gct701177180.h1
Method
                  BLASTX
NCBI GI
                  q3128243
BLAST score
                  166
E value
                  9.0e-12
Match length
                  50
% identity
                  58
                  (AF004672) ribosomal protein L41 [Xanthophyllomyces
NCBI Description
                  dendrorhous]
                  290503
Seq. No.
Contig ID
                  356213 1.R1011
5'-most EST
                  gct701177236.h1
                  BLASTX
Method
                  q2739387
NCBI GI
                  220
BLAST score
                  3.0e-18
E value
Match length
                  87
                  53
% identity
                  (AC002505) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  290504
Seq. No.
Contig ID
                  356231 1.R1011
5'-most EST
                  gct701177270.h1
Method
                  BLASTX
NCBI GI
                  g2642153°
BLAST score
                  285
E value
                  7.0e-26
Match length
                  85
% identity
                  64
                   (AC003000) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 2795810 (AC003674) unknown protein [Arabidopsis
                  thaliana]
                  290505
Seq. No.
                  356272 1.R1011
Contig ID
5'-most EST
                  gct701177551.h1
                  290506
Seq. No.
```

356289 1.R1011 Contig ID gct701179501.h1 5'-most EST

BLASTX Method g1351083 NCBI GI BLAST score 203 4.0e-16 E value Match length 46



% identity

SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_1066118 (U39843) NCBI Description

manganese superoxide dismutase [Cayla porcellus]

290507 Seq. No.

356356 1.R1011 Contig ID 5'-most EST gct701177590.hl

290508 Seq. No.

Contig ID 356378_1.R1011 5'-most EST gct701177657.hl

Seq. No. 290509

Contig ID 356391 1.R1011 5'-most EST gct701177807.h1

BLASTN Method g21893 NCBI GI BLAST score 82 E value 2.0e-38 134 Match length % identity 91

NCBI Description T.aestivum (clone pTAU1.5) U1 snRNA

290510 Seq. No.

Contig ID 356478 1.R1011 5'-most EST gct701180466.h1

290511 Seq. No.

356554_1.R1011 Contig ID gct701178293.h1 5'-most EST

BLASTN Method g21889 NCBI GI 77 BLAST score E value 2.0e-35 Match length 117

% identity 92

NCBI Description T.aestivum (clone pTAU1.1) U1 snRNA

290512 Seq. No.

Contig ID 356577 1.R1011 5'-most EST gct701178241.h1

Seq. No. 290513

Contig ID 356602 1.R1011 5'-most EST gct701178929.h1

290514 Seq. No.

Contig ID 356612 1.R1011 5'-most EST gct701178662.h1

290515 Seq. No.

356618 1.R1011 Contig ID 5'-most EST gct701178347.h1

Seq. No. 290516

356778 1.R1011 Contig ID gct701179611.h1 5'-most EST



290517 Seq. No. 356803 1.R1011 Contig ID gct701178810.h1 5'-most EST Method BLASTX NCBI GI g1351227 BLAST score 277 E value 7.0e-25 Match length 90 56 % identity NCBI Description TRANSCRIPTION ELONGATION FACTOR S-II (TFIIS) >gi_2130486_pir__S63845 transcription elongation factor
TFIIS - fission yeast (Schizosaccharomyces pombe) >qi 924620 (U20526) TFIIS [Schizosaccharomyces pombe]

290518 Seq. No.

Contig ID 356807 1.R1011 5'-most EST gct701178815.hl

290519 Seq. No.

356815 1.R1011 Contig ID 5'-most EST gct701178827.h1

Seq. No. 290520

356821 1.R1011 Contig ID 5'-most EST gct701178842.h1

290521 Seq. No.

Contig ID 356852 1.R1011 5'-most EST qct701178913.h1

290522 Seq. No.

Contig ID 356890 1.R1011 5'-most EST gct701178987.hl

Seq. No. 290523

Contig ID 356912 1.R1011 qct701179047.hl 5'-most EST Method

BLASTX g114141 NCBI GI BLAST score 241 1.0e-20 E value 82 Match length % identity 55

ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT) NCBI Description

>gi_2117765_pir__S61868 acetylornithine transaminase (EC
2.6.1.11) - yeast (Saccharomyces cerevisiae) >gi_171083 (M32795) acetylornithine aminotransferase (ARG8) (EC

2.6.1.11) [Saccharomyces cerevisiae]

>gi 1177625 emb CAA58853 (X84036) ARG8 [Saccharomyces
cerevisiae] >gi 1420036 emb CAA99161 (Z74882) ORF YOL140w

[Saccharomyces cerevisiae]

290524 Seq. No.

356963 1.R1011 Contig ID 5'-most EST gct701179153.h1



 Seq. No.
 290525

 Contig ID
 356964_1.R1011

 5'-most EST
 gct701179479.h1

Seq. No. 290526

Contig ID 357000 1.R1011 5'-most EST gct701179755.h1

Seq. No. 290527

Contig ID 357009_1.R1011 5'-most EST gct701179346.h1

Seq. No. 290528

Contig ID 357031_1.R1011 5'-most EST gct701179334.h1

Method BLASTN
NCBI GI g3293558
BLAST score 80
E value 3.0e-37
Match length 136
% identity 90

NCBI Description Oryza sativa germin-like protein 7 (GER7) mRNA, complete

cds

Seq. No. 290529

Contig ID 357058_1.R1011 5'-most EST gct701179404.h1

Seq. No. 290530

Contig ID 357099_1.R1011 5'-most EST gct701179508.h1

Method BLASTX
NCBI GI g1076287
BLAST score 165
E value 5.0e-12
Match length 48
% identity 60

NCBI Description amine acid permease - Arabidopsis thaliana

>qi 510236 emb CAA50672 (X71787) amine acid permease

4

[Arabidopsis thaliana]

Seq. No. 290531

Contig ID 357146_1.R1011 5'-most EST gct701179624.h1

Seq. No. 290532

Contig ID 357159_1.R1011 5'-most EST gct701180549.h1

Seq. No. 290533

Contig ID 357290_1.R1011 5'-most EST gct701180291.h1

Method BLASTX
NCBI GI g1352666
BLAST score 363
E value 5.0e-35
Match length 75



% identity

NCBI Description SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-BETA, CATALYTIC SUBUNIT >gi_164298 (M20193) protein phosphatase 2A beta subunit [Sus scrofa]

Seq. No. 290534

357291 1.R1011 Contig ID 5'-most EST gct701180292.h1

Seq. No. 290535

Contig ID 357371 1.R1011 5'-most EST gct701180294.h1

Seq. No. 290536

357434 1.R1011 Contig ID 5'-most EST gct701180609.h1

Seq. No. 290537

357466 1.R1011 Contig ID 5'-most EST gct701180511.h1

Seq. No. 290538

Contig ID 357514 1.R1011 5'-most EST gct701180539.h1

Seq. No. 290539

357571 1.R1011 Contig ID 5'-most EST hbs701185771.h1

Seq. No. 290540

357665 1.R1011 Contig ID 5'-most EST $sem700\overline{9}30293.h1$

Seq. No. 290541

357760 1.R1011 Contig ID 5'-most EST tbg700930377.h1

Seq. No. 290542

357889 1.R1011 Contig ID 5'-most EST hbs701181018.h1

Seq. No. 290543

358138 1.R1011 Contig ID 5'-most EST hbs701181689.h1

290544 Seq. No.

358289 1.R1011 Contig ID 5'-most EST hbs701182258.h1

Seq. No. 290545

358385_1.R1011 Contig ID 5'-most EST hbs701182152.h1

Seq. No. 290546

Contig ID 358423 1.R1011 5'-most EST hbs701182735.h1



Seq. No.	290547
Contig ID	358493 1.R1011
5'-most EST	hbs701185666.h
ř	学 类。

 Seq. No.
 290548

 Contig ID
 358501_1.R1011

 5'-most EST
 hbs701182689.h1

 Seq. No.
 290549

 Contig ID
 358507_1.R1011

 5'-most EST
 hbs701182408.h1

 Seq. No.
 290550

 Contig ID
 358569 1.R1011

 5'-most EST
 hbs701182660.h1

 Seq. No.
 290551

 Contig ID
 358615_1.R1011

 5'-most EST
 hbs701182645.h1

 Seq. No.
 290552

 Contig ID
 359041_1.R1011

 5'-most EST
 hbs701183616.h1

 Seq. No.
 290553

 Contig ID
 359048_1.R1011

 5'-most EST
 hbs701183537.h1

Seq. No. 290554 359063 1.R1011 Contig ID 5'-most EST hbs701183557.h1 BLASTX Method g4506635 NCBI GI BLAST score 212 3.0e-17 E value Match length 51 % identity 75

NCBI Description

ribosomal protein L32 >gi_132886_sp_P02433_RL32_HUMAN 60S

RIBOSOMAL PROTEIN L32 >gi_71335_pir__R5HU32_ribosomal

protein L32 - human >gi_71336_pir__R5MS32_ribosomal protein

L32 - mouse >gi_71337_pir__R5RT32_ribosomal protein L32
rat >gi_36132_emb_CAA27048_(X03342)_rpL32_(aa 1-135)_[Homo

sapiens] >gi_57117_emb_CAA29777_(X06483)_ribosomal protein

L32_[Rattus_norvegicus] >gi_200781_(K02060)_ribosomal

protein L32-3A_[Mus_musculus] >gi_226004_prf__1405339A

ribosomal protein L32 [Rattus norvegicus]

 Seq. No.
 290555

 Contig ID
 359089_1.R1011

 5'-most EST
 hbs701183605.h1

 Seq. No.
 290556

 Contig ID
 359118_1.R1011

 5'-most EST
 hbs701185711.h1

 Method
 BLASTX

 NCBI GI
 g4557026

 BLAST score
 150



E value 8.0e-10
Match length 64
% identity 47

NCBI Description hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 >gi_1477565

(U50078) p532 [Homo sapiens]

Seq. No. 290557

Contig ID 359126 1.R1011 5'-most EST hbs701183676.h1

Seq. No. 290558

Contig ID 359147 1.R1011 5'-most EST hbs701183715.h1 Method BLASTX

NCBI GI g1732517 BLAST score 230 E value 2.0e-19 Match length 81

Match length 81 % identity 58

NCBI Description (U62745) putative cytoskeletal protein [Arabidopsis

thaliana]

Seq. No. 290559

Contig ID 359430 1.R1011 5'-most EST hbs701184316.h1

Seq. No. 290560

Contig ID 359473 1.R1011 5'-most EST hbs701184671.h1

Seq. No. 290561

Contig ID 359664 1.R1011 5'-most EST hbs701185553.h1

Seq. No. 290562

Contig ID 359699 1.R1011 5'-most EST hbs701185288.h1

Seq. No. 290563

Contig ID 359729 1.R1011 5'-most EST hbs701185379.h1

Seq. No. 290564

Contig ID 359865 1.R1011 5'-most EST hbs701185591.h1

Seq. No. 290565

Contig ID 359868 1.R1011 5'-most EST hbs701185594.h1

Seq. No. 290566

Contig ID 359958_1.R1011 5'-most EST hbs701185780.h1

Seq. No. 290567

Contig ID 360183 1.R1011

```
5'-most EST
                  hbs701186235.h1
                  290568
Seq. No.
                  LIB143-001-Q1-E1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352469
BLAST score
                  226
                  5.0e-19
E value
Match length
                  66
% identity
                  68
NCBI Description
                  BETA-FRUCTOFURANOSIDASE, CELL WALL ISOZYME PRECURSOR
                   (SUCROSE-6-PHOSPHATE HYDROLASE) (INVERTASE) >gi_736359
                   (U17695) invertase [Zea mays] >gi_1582380_prf__2118364A
                  cell wall invertase [Zea mays]
                  290569
Seq. No.
                  LIB143-002-Q1-E1-B8
Seq. ID
Method
                  ·BLASTX
NCBI GI
                  g4220524
BLAST score
                  213
```

4.0e-17 E value Match length 93 43 % identity

290570

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. LIB143-002-Q1-E1-C12 Seq. ID Method BLASTX NCBI GI q3294467 418 BLAST score 2.0e-41 E value 82 Match length 100 % identity

NCBI Description (U89341) phosphoglucomutase 1 [Zea mays]

Seq. No. 290571 Seq. ID LIB143-002-Q1-E1-G3 Method BLASTX NCBI GI q1562544 BLAST score 251 E value 1.0e-21 Match length 87 % identity 61

NCBI Description (U69129) isocitrate lyase [Zea mays]

Seq. No. 290572

Seq. ID LIB143-002-Q1-E1-G4

Method BLASTX NCBI GI g548770 BLAST score 667 2.0e-70 E value 131 Match length 94 % identity

60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal NCBI Description

protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630) ribosomal protein L3 [Oryza sativa]



```
Seq. No.
Seq. ID
                   LIB143-002-Q1-E1-G9
Method
                   BLASTN
NCBI GI
                    q22334
BLAST score
                    35
                    2.0e-10
E value
Match length
                    43
                    95
% identity
NCBI Description Z.mays mRNA for heat shock protein 17.2
                    290574
Seq. No.
Seq. ID
                    LIB143-002-Q1-E1-H1
Method
                    BLASTX
NCBI GI
                    g2662310
BLAST score
                    218
                    2.0e-30
E value
Match length
                    81
                    86
% identity
                   (AB009307) bpw1 [Hordeum vulgare]
NCBI Description
                    290575
Seq. No.
                    LIB143-003-Q1-E1-A10
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2760606
BLAST score
                    158
E value
                    1.0e-20
                    87
Match length
                    68
% identity
                    (AB001568) phospholipid hydroperoxide glutathione
NCBI Description
                    peroxidase-like protein [Arabidopsis thaliana] >gi_3004869
                    (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis
                    thaliana] >gi_4539451_emb_CAB39931.1_ (AL049500)
                    phospholipid hydroperoxide glutathione peroxidase
                    [Arabidopsis thaliana]
Seq. No.
                    290576
Seq. ID
                    LIB143-003-Q1-E1-C12
Method
                    BLASTX
NCBI GI
                    q113026
BLAST score
                    234
E value
                    1.0e-19
Match length
                    82
% identity
NCBI Description
                    ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
                    >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape
>gi_255220_bbs_112862 isocitrate lyase, threo-D
                    S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482)
                    isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A
                    isocitrate lyase [Brassica napus]
                    290577
Seq. No.
Seq. ID
                    LIB143-003-Q1-E1-G6
Method
                    BLASTX
```

40387

g3402692

3.0e-12

150

NCBI GI

E value

BLAST score



Match length 58 % identity 71

NCBI Description (AC004697) putative

CDP-diacylglycerol--glycerol-3-phosphate

3-phosphatidyltransferase [Arabidopsis thaliana]

Seq. No. 290578

Seq. ID LIB143-003-Q1-E1-G9

Method BLASTX
NCBI GI g3004950
BLAST score 290
E value 3.0e-38
Match length 115
% identity 79

NCBI Description (AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays]

Seq. No. 290579

Seq. ID LIB143-003-Q1-E1-H11

Method BLASTX
NCBI GI g1213073
BLAST score 141
E value 9.0e-09
Match length 84
% identity 39

NCBI Description (X75616) heat shock protein 17.8 [Oryza sativa]

Seq. No. 290580

Seq. ID LIB143-004-Q1-E1-A3

Method BLASTX
NCBI GI g2668750
BLAST score 489
E value 1.0e-49
Match length 92
% identity 100

NCBI Description (AF034949) ribosomal protein L30 [Zea mays]

Seq. No. 290581

Seq. ID LIB143-004-Q1-E1-C5

Method BLASTN
NCBI GI g217973
BLAST score 49
E value 1.0e-18
Match length 65
% identity 94

NCBI Description Zea mays gene for triosephosphate isomerase, complete cds

Seq. No. 290582

Seq. ID LIB143-004-Q1-E1-D1

Method BLASTN
NCBI GI g1124857
BLAST score 217
E value 1.0e-119
Match length 334
% identity 91

NCBI Description Pelargonium hortorum clone pGAC-2G 1-aminocyclopropane

1-carboxylate synthase gene, partial cds



```
Seq. No.
Seq. ID
                   LIB143-004-Q1-E1-D12
Method
                   BLASTX,
NCBI GI
                   g3309243
BLAST score
                   485
E value
                   6.0e-49
Match length
                   103
                   88
% identity
                   (AF073507) aconitase-iron regulated protein 1 [Citrus
NCBI Description
Seq. No.
                   290584
Seq. ID
                   LIB143-004-Q1-E1-E5
Method
                   BLASTX
NCBI GI
                   g4206197
BLAST score
                   168
E value
                   6.0e-12
Match length
                   34
% identity
                   94
NCBI Description
                   (AF071527) putative pre-mRNA splicing factor [Arabidopsis
                   thaliana]
Seq. No.
                   290585
                   LIB143-004-Q1-E1-G12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4234841
BLAST score
                   80
E value
                   5.0e-37
Match length
                   193
                   91
% identity
NCBI Description Zea mays copia-like retrotransposon Sto-1, partial sequence
Seq. No.
                   290586
Seq. ID
                   LIB143-004-Q1-E1-H3
Method
                   BLASTX
NCBI GI
                   g4455323
BLAST score
                   171
                   3.0e-12
E value
Match length
                   97
% identity
                   41
                   (AL035525) aminopeptidase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   290587
Seq. No.
Seq. ID
                   LIB143-005-Q1-E1-A1
Method
                   BLASTX
NCBI GI
                   g2459417
BLAST score
                   190
E value
                   1.0e-14
Match length
                   54
                   74
% identity
                   (AC002332) putative pre-mRNA splicing factor PRP19
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 290588

Seq. ID LIB143-005-Q1-E1-A8

Method BLASTX



```
NCBI GI
                  q1076809
BLAST score
                  362
                  7.0e-35
E value
Match length
                  89
% identity
                  80
NCBI Description
                  H+-transporting ATPase (EC 3.6.1.35) - maize
                  >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase
                   [Zea mays]
Seq. No.
                  290589
Seq. ID
                  LIB143-005-Q1-E1-B1
Method
                  BLASTX
NCBI GI
                  q1370603
BLAST score
                  296
E value
                  4.0e-27
Match length
                  77
                  74
% identity
NCBI Description
                  (X98245) annexin p35 [Zea mays]
Seq. No.
                  290590
Seq. ID
                  LIB143-005-Q1-E1-B2
Method
                  BLASTX
NCBI GI
                  q417154
BLAST score
                  216
E value
                  8.0e-24
Match length
                  85
                  67
% identity
NCBI Description
                  HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
Seq. No.
                  290591
Seq. ID
                  LIB143-005-Q1-E1-B7
Method
                  BLASTX
NCBI GI
                  q2827141
BLAST score
                  275
E value
                  3.0e-24
Match length
                  141
                  45
% identity
                   (AF027173) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  290592
Seq. ID
                  LIB143-005-Q1-E1-C10
Method
                  BLASTN
NCBI GI
                  g304114
BLAST score
                  58
E value
                  4.0e-24
Match length
                  174
                  83
% identity
                  Arabidopsis thaliana thioglucosidase mRNA, complete cds
NCBI Description
```

Seq. No. 290593

Seq. ID LIB143-005-Q1-E1-C9

Method BLASTX NCBI GI g585536



BLAST score 294 E value 6.0e-50 Match length 135 % identity 76

NCBI Description MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE) >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase

[Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194)

thioglucosidase [Arabidopsis thaliana]

Seq. No. 290594

Seq. ID LIB143-005-Q1-E1-D8

Method BLASTX
NCBI GI g533775
BLAST score 142
E value 1.0e-16
Match length 74
% identity 76

NCBI Description (U09989) H(+)-transporting ATPase [Zea mays]

Seq. No. 290595

Seq. ID LIB143-005-Q1-E1-F11

Method BLASTX
NCBI GI g3891593
BLAST score 234
E value 2.0e-19
Match length 47
% identity 98

NCBI Description Structure Of Glutathione S-Transferase Iii In Apo Form

Seq. No. 290596

Seq. ID LIB143-005-Q1-E1-G10

Method BLASTX
NCBI GI g2246621
BLAST score 153
E value 3.0e-10
Match length 64
% identity 52

NCBI Description (AF004393) salt-stress induced tonoplast intrinsic protein

[Arabidopsis thaliana]

Seq. No. 290597

Seq. ID LIB143-005-Q1-E1-G9

Method BLASTX
NCBI GI g3688799
BLAST score 560
E value 9.0e-58
Match length 117
% identity 97

NCBI Description (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis

thaliana]

Seq. No. 290598

Seq. ID LIB143-005-Q1-E1-H11

Method BLASTX NCBI GI g417154 BLAST score 179



```
E value
                  4.0e-13
Match length
                  37
                  95
% identity
                  HEAT SHOCK PROTEIN 82 >gi_100685_pir S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  >gi 20256 emb CAA77978 (Z11920) heat shock protein 82
                  (HSP82) [Oryza sativa]
                  290599
Seq. No.
Seq. ID
                  LIB143-005-Q1-E1-H9
Method
                  BLASTX
NCBI GI
                  q3281848
BLAST score
                  328
                  1.0e-31
E value
                  97
Match length
                  77
% identity
                 (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                  290600
Seq. No.
                  LIB143-006-Q1-E1-A7
Seq. ID
                  BLASTX
Method
                  q1351014
NCBI GI
BLAST score
                  217
E value
                  1.0e-17
                  71
Match length
% identity
                  66
                  40S RIBOSOMAL PROTEIN S8 >qi 968902 dbj BAA07207 (D38010)
NCBI Description
                  ribosomal protein S8 [Oryza sativa]
Seq. No.
                  290601
Seq. ID
                  LIB143-006-Q1-E1-C11
Method
                  BLASTN
NCBI GI
                  g1808687
BLAST score
                  86
E value
                  1.0e-40
Match length
                  286
% identity
                  82
NCBI Description S.stapfianus pSD.13 mRNA
                  290602
Seq. No.
Seq. ID
                  LIB143-006-Q1-E1-C9
Method
                  BLASTX
                  g4309743
NCBI GI
BLAST score
                  301
                  2.0e-27
E value
Match length
                  96
% identity
                  64
                  (AC006439) putative inorganic pyrophosphatase [Arabidopsis
NCBI Description
                  thaliana]
                  290603
Seq. No.
Seq. ID
                  LIB143-006-Q1-E1-D2
```

Method BLASTX

NCBI GI g3128180 BLAST score 350 4.0e-33 E value 92 Match length



154

92

37

3.0e-10

BLAST score

Match length

% identity

E value

```
% identity
                  (AC004521) citrate synthetase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  290604
                  LIB143-006-Q1-E1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1171965
BLAST score
                  297
                  4.0e-27
E value
Match length
                  106
% identity
                  62
                  PHOSPHATIDYLINOSITOL 3-KINASE, ROOT ISOFORM (PI3-KINASE)
NCBI Description
                  (PTDINS-3-KINASE) (PI3K) (SPI3K-5) >gi 736339 (L27265)
                  phosphatidylinositol 3-kinase [Glycine max]
                  290605
Seq. No.
                  LIB143-006-Q1-E1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1408222
BLAST score
                  227
E value
                  8.0e-19
Match length
                  81
% identity
                  (U60764) pathogenesis-related protein [Sorghum bicolor]
NCBI Description
                  290606
Seq. No.
                  LIB143-006-Q1-E1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q282994
BLAST score
                  426
E value
                  6.0e-42
Match length
                  90
% identity
                  88
                  Sip1 protein - barley >gi 167100 (M77475) seed imbibition
NCBI Description
                  protein [Hordeum vulgare]
Seq. No.
                  290607
                  LIB143-006-Q1-E1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q417154
BLAST score
                  333
                  3.0e-31
E value
                  93
Match length
                  70
% identity
                  HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  >gi 20256 emb CAA77978 (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                  290608
Seq. No.
                  LIB143-006-Q1-E1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g944842
```



NCBI Description (X80023) ATP/ADP carrier protein [Triticum turgidum]

Seq. No. 290609 Seq. ID LIB143

Seq. ID LIB143-011-Q1-E1-A2

Method BLASTX
NCBI GI g631978
BLAST score 279
E value 7.0e-25
Match length 118
% identity 47

NCBI Description cytochrome P-450 oxidase - Mentha piperita

>gi_493475_emb_CAA83941_ (Z33875) cytochrome P-450 oxidase

[Mentha x piperita]

Seq. No. 290610

Seq. ID LIB143-011-Q1-E1-B5

Method BLASTX
NCBI GI g4038055
BLAST score 441
E value 7.0e-44
Match length 127
% identity 62

NCBI Description (AC005897) putative cytochrome P450 [Arabidopsis thaliana]

>gi_4557077_gb_AAD22516.1_AC007045_16 (AC007045) putative

cytochrome p450 [Arabidopsis thaliana]

Seq. No. 290611

Seq. ID LIB143-011-Q1-E1-B9

Method BLASTX
NCBI GI g127579
BLAST score 211
E value 4.0e-22
Match length 75

% identity 75

NCBI Description MYB-RELATED PROTEIN HV1 >gi_82423_pir__S04896 transforming

protein (myb) homolog (clone Hv1) - barley
>gi_2130044_pir__S61506 Myb1 protein - barley

>gi_19051_emb_CAA50222 (X70877) MybHv1 [Hordeum vulgare]
>gi_19053_emb_CAA50224 (X70879) MybHv1 [Hordeum vulgare]
>gi_227030_prf_1613412A_myb-related_gene_Hv1 [Hordeum

vulgare var. distichum]

Seq. No. 290612

Seq. ID LIB143-011-Q1-E1-C9

Method BLASTX
NCBI GI g2760325
BLAST score 288
E value 6.0e-26
Match length 113
% identity 61

NCBI Description (AC002130) F1N21.10 [Arabidopsis thaliana]

Seq. No. 290613

Seq. ID LIB143-011-Q1-E1-D6

Method BLASTX NCBI GI g1076758 BLAST score 168



```
E value
Match length
                  66
% identity
                  62
                  heat-shock protein precursor - rye >gi_2130093 pir__S65776
NCBI Description
                  heat-shock protein, 82K, precursor - rye
                  >gi 556673 emb_CAA82945_ (Z30243) heat-shock protein
                   [Secale cereale]
                  290614
Seq. No.
Seq. ID
                  LIB143-011-Q1-E1-G10
Method
                  BLASTN
NCBI GI
                  q1944204
BLAST score
                  52
                  2.0e-20
E value
                  68
Match length
                  94
% identity
NCBI Description Oryza sativa mRNA for RicMT, complete cds
                  290615
Seq. No.
                  LIB143-012-Q1-E1-B8
Seq. ID
Method
                  BLASTX
                  q3396079
NCBI GI
BLAST score
                  184
E value
                  8.0e-14
Match length
                  71
% identity
                  51
                   (AF080173) inositol 1,3,4-trisphosphate 5/6-kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   290616
Seq. ID
                  LIB143-012-Q1-E1-D6
Method
                  BLASTX
NCBI GI
                  g1076758
BLAST score
                   432
E value
                   6.0e-43
Match length
                  107
% identity
                   83
                  heat-shock protein precursor - rye >gi 2130093 pir S65776
NCBI Description
                  heat-shock protein, 82K, precursor - rye
                  >gi_556673_emb_CAA82945_ (Z30243) heat-shock protein
                   [Secale cereale]
                  290617
Seq. No.
Seq. ID
                  LIB143-012-Q1-E1-E9
                  BLASTN
Method
NCBI GI
                   g4218109
BLAST score
                   64
                   1.0e-27
E value
Match length
                  120
                   88
% identity
```

Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16 NCBI Description

(ESSAII project)

Seq. No.

290618 Seq. ID LIB143-012-Q1-E1-F1

Method BLASTX NCBI GI

g1616661



```
BLAST score
                  3.0e-23
E value
Match length
                  83
                  67
% identity
NCBI Description (U49388) adenylosuccinate synthetase [Zea mays]
Seq. No.
                  290619
                  LIB143-012-Q1-E1-F11
Seq. ID
Method '
                  BLASTN
NCBI GI
                  q3294468
BLAST score
                  174
E value
                  4.0e-93
Match length
                  190
                  98
% identity
NCBI Description Zea mays phosphoglucomutase 2 mRNA, complete cds
                  290620
Seq. No.
Seq. ID
                  LIB143-012-Q1-E1-F3
Method
                  BLASTX
                  q4467153
NCBI GI
                  369
BLAST score
                  2.0e-35
E value
Match length
                  102
% identity
                   68
                   (AL035540) putative thaumatin-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  290621
Seq. No.
Seq. ID
                  LIB143-012-Q1-E1-F5
Method
                  BLASTX
NCBI GI
                  g20290
BLAST score
                  296
E value
                   6.0e-27
Match length
                  79
% identity
                  70
NCBI Description (X57563) phytochrome B [Oryza sativa]
                   290622
Seq. No.
Seq. ID
                  LIB143-012-Q1-E1-F6
Method
                  BLASTX
                   g1352461
NCBI GI
BLAST score
                   424
E value
                   6.0e-42
Match length
                  84
                   98
% identity
NCBI Description IN2-2 PROTEIN
                  290623
Seq. No.
Seq. ID
                  LIB143-013-Q1-E1-A7
Method
                  BLASTX
                   q1705678
NCBI GI
                  179
BLAST score
```

Method BLASTX
NCBI GI g1705678
BLAST score 179
E value 4.0e-13
Match length 40
% identity 82

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING

PROTEIN HOMOLOG) (VCP) >gi 862480 (U20213)





valosin-containing protein [Glycine max]

```
Seq. No.
                   290624
                   LIB143-013-Q1-E1-B1
Seq. ID
Method
                   BLASTX
                   q4262142
NCBI GI
BLAST score
                   249
                   3.0e-21
E value
Match length
                   93
                   55
% identity
                   (AC005275) putative alcohol dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
                   290625
Seq. No.
                   LIB143-013-Q1-E1-B8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g575730
BLAST score
                   41
E value
                   8.0e-14
Match length
                   61
                   92
% identity
NCBI Description Z.mays mRNA for transmembrane protein
                   290626
Seq. No.
Seq. ID
                   LIB143-013-Q1-E1-C6
Method
                   BLASTX
                   g2146739
NCBI GI
BLAST score
                   198
                   2.0e-15
E value
Match length
                   103
                   46
% identity
NCBI Description hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521
                   (U28214) hexokinase 1 [Arabidopsis thaliana]
                   290627
Seq. No.
Seq. ID
                   LIB143-013-Q1-E1-F3
Method
                   BLASTX
NCBI GI
                   q1170092
BLAST score
                   410
E value
                   3.0e-40
Match length
                   94
                   84
% identity
                   GLUTATHIONE S-TRANSFERASE IV (GST-IV) (GST-27) (CLASS PHI)
NCBI Description
                   >gi_1076807_pir__S52037 glutathione transferase (EC
                   2.5.1.18) 27K chain - maize >gi_529015 (U12679) glutathione S-transferase IV [Zea mays] >gi_695789_emb_CAA56047_
                    (X79515) glutathione transferase [Zea mays]
                   >gi 1094866 prf 2106424A glutathione
                   S-transferase: ISOTYPE=IV [Zea mays]
                   290628
Seq. No.
                   LIB143-013-Q1-E1-F8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3859536
BLAST score
                   207
                   2.0e-16
E value
```

40397

87

Match length



% identity (AF095453) asparagine synthetase [Arabidopsis thaliana] NCBI Description 290629 Seq. No. LIB143-013-Q1-E1-G8 Seq. ID Method BLASTX NCBI GI g3548802 BLAST score 318 E value 2.0e-29 Match length 148 44 % identity (ACO05313) axi 1-like protein [Arabidopsis thaliana] NCBI Description >gi 4335769_gb_AAD17446_ (AC006284) putative axi1 protein [Nicotiana tabacum] [Arabidopsis thaliana] 290630 Seq. No. LIB143-013-Q1-E1-H5 Seq. ID Method BLASTX g3264596 NCBI GI BLAST score 142 5.0e-09 E value Match length 71 51 % identity (AF057183) putative tonoplast aquaporin [Zea mays] NCBI Description 290631 Seq. No. LIB143-014-Q1-E1-D9 Seq. ID Method BLASTX NCBI GI q1707980 BLAST score 146 E value 8.0e-10 Match length 43 % identity 63 NCBI Description GLUTAREDOXIN >gi_1084458_pir__S41736 glutaredoxin thioltransferase - Rice >gi_485953_emb_CAA54397_ (X77150) glutaredoxin [Oryza sativa] 290632 Seq. No. Seq. ID LIB143-014-Q1-E1-E6 Method BLASTX NCBI GI q3986691 BLAST score 194 E value 3.0e-29 106 Match length % identity NCBI Description (AF101421) heat shock protein [Cichorium intybus] Seq. No. 290633 Seq. ID LIB143-014-Q1-E1-G1 Method BLASTN NCBI GI g311238 136

BLAST score 2.0e-70 E value Match length 312 % identity 74

NCBI Description Z.mays cat1 gene for catalase



Seq. No. 290634 Seq. ID LIB143-015-Q1-E1-B3 Method BLASTX NCBI GI g1345587 BLAST score 329 E value 5.0e-31 Match length 75 89 % identity 14-3-3-LIKE PROTEIN GF14-6 >gi 998430 bbs 164522 (S77133) NCBI Description GF14-6=14-3-3 protein homolog [Zea mays, XL80, Peptide, 261 aa] [Zea mays] Seq. No. 290635 Seq. ID LIB143-015-Q1-E1-D1 Method BLASTX NCBI GI q1814403 BLAST score 190 E value 2.0e-14 Match_length 86 % identity 51 (U84889) methionine synthase [Mesembryanthemum NCBI Description crystallinum] Seq. No. 290636 Seq. ID LIB143-015-Q1-E1-F10 Method BLASTX NCBI GI g2842648 BLAST score 159 1.0e-10 E value Match length 64 % identity 53 U2 SMALL NUCLEAR RIBONUCLEOPROTEIN AUXILIARY FACTOR 35 KD NCBI Description SUBUNIT RELATED-PROTEIN 2 >gi_2137782_pir__A57120 small nuclear ribonucleoprotein auxiliary factor U2 - mouse >gi 927659 dbj BAA08143 (D45205) U2af1-rs2 [Mus musculus] Seq. No. 290637 Seq. ID LIB143-016-Q1-E1-C3 Method BLASTX NCBI GI g1019946 BLAST score 202 E value 5.0e-16 Match length 89 % identity 46 (U37060) ascorbate peroxidase [Gossypium hirsutum] NCBI Description 290638 Seq. No. Seq. ID LIB143-016-Q1-E1-D4

Method BLASTX
NCBI GI 94581108
BLAST score 166
E value 1.0e-11
Match length 80
% identity 55

NCBI Description (AC005825) putative chloroplast outer membrane protein 86,also very similar to GTP-inding protein from pea

(GB:L36857) [Arabidopsis thaliana]

NCBI Description



```
Seq. No.
                  290639
Seq. ID
                  LIB143-016-Q1-E1-E8
Method
                  BLASTX
NCBI GI
                  g2651303
BLAST score
                  194
                   2.0e-15
E value
Match length
                  58
% identity
NCBI Description
                   (AC002336) putative potassium transporter [Arabidopsis
                  thaliana]
Seq. No.
                  290640
Seq. ID
                  LIB143-016-Q1-E1-H1
Method
                  BLASTX
NCBI GI
                  q4581139
BLAST score
                   386
E value
                  2.0e-37
Match length
                   137
% identity
                   50
NCBI Description (AC006919) putative ABC transporter [Arabidopsis thaliana]
Seq. No.
                  290641
Seq. ID
                  LIB143-016-Q1-E1-H4
Method
                  BLASTX
NCBI GI
                  q418854
BLAST score
                   575
E value
                  2.0e-59
Match length
                   117
% identity
                   18
NCBI Description
                  ubiquitin precursor - parsley >gi_288112_emb_CAA45621_
                   (X64344) polyubiquitin [Petroselinum crispum]
                   >gi_288114_emb_CAA45622_ (X64345) polyubiquitin
                   [Petroselinum crispum]
                  290642
Seq. No.
Seq. ID
                  LIB143-017-Q1-E1-C4
Method
                  BLASTX
NCBI GI
                  q532623
BLAST score
                   275
                   2.0e-34
E value
Match length
                  127
% identity
                   62
NCBI Description
                  (L35913) lipase [Zea mays]
                  290643
Seq. No.
Seq. ID
                  LIB143-017-Q1-E1-D12
Method
                  BLASTX
NCBI GI
                  g629641
BLAST score
                   386
                   2.0e-37
E value
Match length
                  91
                  80
% identity
```

(Z32537) PsHSC71.0 [Pisum sativum]

PsHSC71.0 protein - garden pea >gi 1076530 pir S53500

HSC71.0 protein - garden pea >gi 473217 emb CAA83548

NCBI GI

BLAST score

g2435518

176



```
Seq. No.
Seq. ID
                  LIB143-017-Q1-E1-D4
Method
                  BLASTX
NCBI GI
                  g168424
BLAST score
                  369
E value
                  2.0e-35
Match length
                  113
% identity
                  67
                  (M59449) polypeptide chain-binding protein [Zea mays]
NCBI Description
Seq. No.
                  290645
Seq. ID
                  LIB143-017-Q1-E1-G12
Method
                  BLASTN
NCBI GI
                  q4580720
BLAST score
                  50
E value
                  4.0e-19
Match length
                  62
% identity
                  95
NCBI Description
                  Urochloa panicoides phosphoenolpyruvate carboxykinase 4
                  (PCK4) gene, partial cds
Seq. No.
                  290646
Seq. ID
                  LIB143-017-Q1-E1-G2
Method
                  BLASTX
NCBI GI
                  q4371280
BLAST score
                  307
E value
                  4.0e-28
Match length
                  74
% identity
                  81
                  (AC006260) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  290647
Seq. No.
Seq. ID
                  LIB143-017-Q1-E1-G4
Method
                  BLASTX
NCBI GI
                  g1184776
BLAST score
                  471
                  2.0e-47
E value
                  90
Match length
                  98
% identity
                  (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC4 [Zea mays]
                  290648
Seq. No.
Seq. ID
                  LIB143-017-Q1-E1-H8
                  BLASTX
Method
NCBI GI
                  g2213583
BLAST score
                  219
                  8.0e-18
E value
Match length
                  105
                  47
% identity
NCBI Description (AC000348) T7N9.3 [Arabidopsis thaliana]
Seq. No.
                  290649
Seq. ID
                  LIB143-018-Q1-E1-D8
Method
                  BLASTX
```



```
E value
                  1.0e-12
Match length
                  62
                  63
% identity
                   (AF024504) contains similarity to C3HC4-type zinc fingers
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  290650
Seq. ID
                  LIB143-018-Q1-E1-E1
Method
                  BLASTX
NCBI GI
                  q3522956
BLAST score
                  201
E value
                  1.0e-15
Match length
                  55
                  55
% identity
                   (AC004411) putative pectinacetylesterase precursor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  290651
                  LIB143-018-Q1-E1-E11
Seq. ID
Method
                  BLASTX
                  q4582468
NCBI GI
                  269
BLAST score
E value
                  1.0e-23
Match length
                  58
% identity
                  88
                  (AC007071) putative 40S ribosomal protein; contains
NCBI Description
                  C-terminal domain [Arabidopsis thaliana]
Seq. No.
                  290652
Seq. ID
                  LIB143-018-Q1-E1-F6
Method
                  BLASTX
NCBI GI
                   q2583126
BLAST score
                   298
E value
                   2.0e-31
Match length
                   115
% identity
                   60
                   (AC002387) putative DNA repair protein (RAD57) [Arabidopsis
NCBI Description
                   thaliana]
                   290653
Seq. No.
Seq. ID
                   LIB143-018-Q1-E1-H9
Method
                  BLASTN
NCBI GI
                   g3821780
BLAST score
                   35
                   4.0e-10
E value
Match length
                   35
% identity
                   100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   290654
```

LIB143-019-Q1-E1-B4 Seq. ID

BLASTX Method NCBI GI g112994 BLAST score 401 3.0e-39 E value Match length 84 % identity 94



75

68

Match length % identity

```
GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                   ABA-inducible gene protein [Zea mays]
                   >gi_226091_prf__1410284A abscisic acid inducible gene [Zea
                  mays]
                   290655
Seq. No.
                  LIB143-019-Q1-E1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4426617
BLAST score
                   173
E value
                   1.0e-12
Match length
                   57
                   61
% identity
                  (AF099203) cysteine endopeptidase precursor [Oryza sativa]
NCBI Description
                   290656
Seq. No.
                   LIB143-019-Q1-E1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g135398
BLAST score
                   626
E value
                   2.0e-65
Match length
                   116
% identity
                   100
                   TUBULIN ALPHA-1 CHAIN >gi_82731_pir__S15773 tubulin alpha-1
NCBI Description
                   chain - maize >gi_22147_emb_CAA33734_ (X15704)
                   alpha1-tubulin [Zea mays]
                   290657
Seq. No.
                   LIB143-019-Q1-E1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2760349
BLAST score
                   523
                   2.0e-53
E value
Match length
                   123
% identity
                   17
NCBI Description (U84969) ubiquitin [Arabidopsis thaliana]
Seq. No.
                   290658
                   LIB143-019-Q1-E1-F5
Seq. ID
Method
                   BLASTX
                   g2827002
NCBI GI
BLAST score
                   175
                   9.0e-21
E value
Match length
                   114
% identity
                   50
NCBI Description (AF005993) HSP70 [Triticum aestivum]
Seq. No.
                   290659
                   LIB143-020-Q1-E1-B9
Seq. ID
                   BLASTX
Method
                   g112994
NCBI GI
BLAST score
                   247
                   3.0e-21
E value
```



```
GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                   >gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                   ABA-inducible gene protein [Zea mays]
                   >qi 226091 prf 1410284A abscisic acid inducible gene [Zea
                   mays]
Seq. No.
                   290660
Seq. ID
                   LIB143-020-Q1-E1-D11
Method
                   BLASTX
NCBI GI
                   q2191166
BLAST score
                   250
E value
                   2.0e-21
                   73
Match length
                   67
% identity
                   (AF007270) A IG002P16.15 gene product [Arabidopsis
NCBI Description
                   thaliana]
                   290661
Seq. No.
                   LIB143-020-Q1-E1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q120670
BLAST score
                   191
E value
                   4.0e-15
Match length
                   46
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_100879_pir__S06879 glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) C - maize
                   >gi 295853 emb CAA33620 (X15596) GAPDH [Zea mays]
Seq. No.
                   290662
Seq. ID
                   LIB143-020-Q1-E1-F5
Method
                   BLASTX
NCBI GI
                   g1321661
BLAST score
                   267
                   2.0e-23
E value
Match length
                   75
% identity
                   69
                  (D45423) ascorbate peroxidase [Oryza sativa]
NCBI Description
                   290663
Seq. No.
Seq. ID
                   LIB143-020-Q1-E1-G2
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   34
                   2.0e-09
E value
Match length
                   34
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   290664
Seq. No.
Seq. ID
                   LIB143-020-Q1-E1-H11
```

Method BLASTX

NCBI GI g3719211 BLAST score 197 E value 2.0e-22

% identity

NCBI Description

82

translocator (ANT-G1)



```
Match length
                  65
% identity
                  (U97021) UIP2 [Arabidopsis thaliana]
NCBI Description
                  290665
Seq. No.
Seq. ID
                  LIB143-021-Q1-E1-C9
Method
                  BLASTX
NCBI GI
                  g1762130
BLAST score
                  169
E value
                  3.0e-12
Match length
                  88
% identity
                  48
                  (U46136) chaperonin-60 beta subunit [Solanum tuberosum]
NCBI Description
                  290666
Seq. No.
Seq. ID
                  LIB143-021-Q1-E1-E10
Method
                  BLASTN
NCBI GI
                  q296593
BLAST score
                  56
E value
                  1.0e-22
Match length
                  76
                  93
% identity
NCBI Description H. vulgare pZE40 gene
Seq. No.
                  290667
Seq. ID
                  LIB143-021-Q1-E1-E2
Method
                  BLASTN
NCBI GI
                  q1184773
BLAST score
                  94
                  7.0e-46
E value
Match length
                  114
% identity
                  96
NCBI Description
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC3
                   (gpc3) mRNA, complete cds
Seq. No.
                  290668
Seq. ID
                  LIB143-021-Q1-E1-F11
                  BLASTX
Method
NCBI GI
                  q3986289
                  177
BLAST score
                  7.0e-13
E value
Match length
                  58
                  59
% identity
                  (AB017357) L-Galactono-1,4-lactone dehydrogenase [Ipomoea
NCBI Description
                  batatas]
Seq. No.
                  290669
Seq. ID
                  LIB143-021-Q1-E1-F3
Method
                  BLASTN
NCBI GI
                  g22165
BLAST score
                  43
                  5.0e-15
E value
Match length
                  200
```

40405

Maize gene for mitochondrial adenine nucleotide



```
Seq. No.
                  290670
Seq. ID
                  LIB143-021-Q1-E1-G4
Method
                  BLASTN
NCBI GI
                  g259442
BLAST score
                  37
E value
                  2.0e-11
Match length
                  56
% identity
                  91
                  glycine-rich protein {clone atGRP-1} [Arabidopsis thaliana,
NCBI Description
                  C24, mRNA Partial, 740 nt]
Seq. No.
                  290671
Seq. ID
                  LIB143-022-Q1-E1-C5
Method
                  BLASTX
NCBI GI
                  q710626
BLAST score
                  189
E value
                  3.0e-14
Match length
                  72
                  58
% identity
NCBI Description
                  (D30719) ERD15 protein [Arabidopsis thaliana] >gi 3241941
                   (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                  thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis
                  thaliana]
Seq. No.
                  290672
Seq. ID
                  LIB143-022-Q1-E1-E2
Method
                  BLASTX
NCBI GI
                  q22166
BLAST score
                  225
                  1.0e-18
E value
Match length
                  96
% identity
                  50
NCBI Description
                 (X15711) adenine nucleotide translocator [Zea mays]
Seq. No.
                  290673
Seq. ID
                  LIB143-022-Q1-E1-E4
Method
                  BLASTN
NCBI GI
                  q1498596
BLAST score
                  100
                  5.0e-49
E value
                  348
Match length
                  82
% identity
NCBI Description Zea mays phospholipid transfer protein mRNA, complete cds
                  290674
Seq. No.
Seq. ID
                  LIB143-022-Q1-E1-H3
Method
                  BLASTN
NCBI GI
                  g22192
BLAST score
                  43
                  6.0e-15
E value
                  71
Match length
                  90
% identity
NCBI Description Z.mays B-I gene for B transcriptional activator
```

Seq. No. 290675

Seq. ID LIB143-022-Q1-E1-H9

Method BLASTN



```
NCBI GI
                  g1514952
BLAST score
                  40
                  3.0e-13
E value
Match length
                  72
% identity
                  89
NCBI Description Rice seedling mRNA for cysteine proteinase, complete cds
                  290676
Seq. No.
Seq. ID
                  LIB143-023-Q1-E1-C1
Method
                  BLASTX
NCBI GI
                  q3882355
BLAST score
                  452
E value
                  4.0e-45
Match length
                  106
% identity
NCBI Description
                  (U92460) 12-oxophytodienoate reductase OPR1 [Arabidopsis
                  thaliana]
                  290677
Seq. No.
Seq. ID
                  LIB143-023-Q1-E1-E9
Method
                  BLASTX
NCBI GI
                  q3342802
BLAST score
                  141
E value
                  5.0e-09
Match length
                  55
                  58
% identity
NCBI Description
                  (AF061838) putative cytosolic 6-phosphogluconate
                  dehydrogenase [Zea mays]
Seq. No.
                  290678
Seq. ID
                  LIB143-023-Q1-E1-G8
Method
                  BLASTX
NCBI GI
                  g2982320
BLAST score
                  252
E value
                  1.0e-21
Match length
                  98
% identity
                  50
NCBI Description
                  (AF051245) hypothetical protein [Picea mariana]
                  290679
Seq. No.
Seq. ID
                  LIB143-023-Q1-E1-G9
                  BLASTN
Method
NCBI GI
                  g3821780
BLAST score
                  35
E value
                   4.0e-10
Match length
                  35
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  290680
Seq. No.
Seq. ID
                  LIB143-023-Q1-E1-H4
Method
                  BLASTX
NCBI GI
                  g2501790
```

NCBI GI g2501790
BLAST score 206
E value 3.0e-16
Match length 75
% identity 57

NCBI Description

Seq. No.

290686





```
NCBI Description
                   (U86072) omega-6 fatty acid desaturase [Petroselinum
                  crispum]
Seq. No.
                  290681
Seq. ID
                  LIB143-023-Q1-E1-H6
Method
                  BLASTX
NCBI GI
                  q541920
BLAST score
                  222
                  6.0e-19
E value
                  94
Match length
% identity
                  59
NCBI Description Acetoacyl-CoA-thiolase - radish
Seq. No.
                  290682
Seq. ID
                  LIB143-024-Q1-E1-C2
Method
                  BLASTX
NCBI GI
                  g2760323
BLAST score
                  235
E value
                  1.0e-19
Match length
                  64
% identity
                  38
NCBI Description (AC002130) F1N21.8 [Arabidopsis thaliana]
Seq. No.
                  290683
Seq. ID
                  LIB143-024-Q1-E1-D8
Method
                  BLASTX
NCBI GI
                  q1707019
BLAST score
                  219
E value
                   9.0e-18
Match length
                  118
% identity
NCBI Description
                  (U78721) hypothetical protein [Arabidopsis thaliana]
                  290684
Seq. No.
Seq. ID
                  LIB143-024-Q1-E1-E1
Method
                  BLASTX
NCBI GI
                  q3776559
BLAST score
                   487
E value
                  3.0e-49
Match length
                  116
% identity
                  77
                  (AC005388) Strong similarity to gene F14J9.26 gi 3482933
NCBI Description
                   cdc2 protein kinase homolog from A. thaliana BAC
                  gb AC003970. ESTs gb Z35332 and gb F19907 come from this
                  gene. [Arabidopsis thaliana]
                  290685
Seq. No.
Seq. ID
                  LIB143-024-Q1-E1-E10
Method
                  BLASTX
NCBI GI
                  g4567226
BLAST score
                  220
                  7.0e-18
E value
Match length
                  96
                  59
% identity
```

40408

(AC007119) unknown protein [Arabidopsis thaliana]



```
LIB143-024-Q1-E1-F12
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     q1815660
  BLAST score
                     371
                     1.0e-35
  E value
  Match length
                     100
  % identity
                     74
                     (U83669) low molecular mass heat shock protein Oshsp17.3
  NCBI Description
                     [Oryza sativa]
  Seq. No.
                     290687
  Seq. ID
                     LIB143-024-Q1-E1-G4
  Method
                     BLASTX
  NCBI GI
                     q1841355
  BLAST score
                     186
  E value
                     3.0e-16
                     59
  Match length
   % identity
                     71
                     (D85381) cytochrome c oxidase subunit Vb precursor [Oryza
  NCBI Description
                     sativa]
                     290688
  Seq. No.
  Seq. ID
                     LIB143-025-Q1-E1-A3
  Method
                     BLASTX
                     q3935181
  NCBI GI
                     183
  BLAST score
                     1.0e-13
  E value
                     43
  Match length
   % identity
                     79
                     (AC004557) F17L21.24 [Arabidopsis thaliana]
  NCBI Description
                     290689
   Seq. No.
   Seq. ID
                     LIB143-025-Q1-E1-A4
   Method
                     BLASTX
   NCBI GI
                     g232031
   BLAST score
                     298
- E value
                     4.0e-27
  Match length
                     79
   % identity
                     73
                     ELONGATION FACTOR 1 BETA' >gi 322851 pir S29224
   NCBI Description
                     translation elongation factor eEF-1 beta chain - rice
                     >gi 218161 dbj BAA02253 (D12821) elongation factor 1 beta'
                     [Oryza sativa]
                     290690
   Seq. No.
   Seq. ID
                     LIB143-025-Q1-E1-A7
   Method
                     BLASTX
   NCBI GI
                     q584795
   BLAST score
                     188
                     3.0e-30
   E value
                     98
   Match length
                     78
   % identity
                     PLASMA MEMBRANE ATPASE 3 (PROTON PUMP) >gi_170295 (M80490)
   NCBI Description
                     plasma membrane H+ ATPase [Nicotiana plumbaginifolia]
```

Seq. No. 290691

Seq. ID LIB143-025-Q1-E1-B2



```
Method
                  BLASTX
NCBI GI
                  q1928991
BLAST score
                  179
E value
                  4.0e-13
                  64
Match length
                  58
% identity
NCBI Description
                  (U92815) heat shock protein 70 precursor [Citrullus
                  lanatus]
                  290692
Seq. No.
Seq. ID
                  LIB143-025-Q1-E1-F12
Method
                  BLASTX
NCBI GI
                  q3763849
BLAST score
                  415
                  1.0e-40
E value
                  97
Match length
                  89
% identity
NCBI Description
                  (AB018377) early nodulin [Oryza sativa]
                  290693
Seq. No.
Seq. ID
                  LIB143-025-Q1-E1-F9
Method
                  BLASTX
NCBI GI
                  q1922964
BLAST score
                  240
                  1.0e-20
E value
Match length
                  81
% identity
                  60
                  (AC000106) Similar to Schizosaccharomyces CCAAT-binding
NCBI Description
                  factor (gb U88525). EST gb T04310 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                  290694
Seq. ID
                  LIB143-025-Q1-E1-G6
Method
                  BLASTX
NCBI GI
                  g3821793
BLAST score
                  426
E value
                  3.0e-42
Match length
                  80
% identity
                  96
                  (Y11526) casein kinase II alpha subunit [Zea mays]
NCBI Description
                  290695
Seq. No.
Seq. ID
                  LIB143-025-Q1-E1-H1
Method
                  BLASTX
NCBI GI
                  g1362026
BLAST score
                  157
                  2.0e-19
E value
Match length
                  98
                  52
% identity
                  probable serine/threonine-specific protein kinase (EC
NCBI Description
                  2.7.1.-) BSK1 - rape >gi 289372 (L12393) serine/threonine
                  protein kinase [Brassica napus] >gi_1097353_prf__2113401A
                  protein kinase [Brassica napus]
```

od BLASTX

290696

LIB143-026-Q1-E1-A5

Seq. No. Seq. ID

Method



```
NCBI GI
                   q464734
BLAST score
                   233
E value
                   9.0e-20
Match length
                   56
% identity
                   ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                   HYDROLASE) (ADOHCYASE) >gi_481237_pir__S38379
adenosylhomocysteinase (EC 3.3.1.1) - Madagascar periwinkle
                   >gi_407412_emb_CAA81527_ (Z26881) S-adenosyl-L-homocysteine
                   hydrolase [Catharanthus roseus]
Seq. No.
                   290697
Seq. ID
                   LIB143-026-Q1-E1-C3
Method
                   BLASTX
                   q3510259
NCBI GI
                   267
BLAST score
                   2.0e-23
E value
Match length
                   68
% identity
                   74
                   (AC005310) putative inorganic pyrophosphatase [Arabidopsis
NCBI Description
                   thaliana] >gi_3522960 (AC004411) putative inorganic
                   pyrophosphatase [Arabidopsis thaliana]
Seq. No.
                   290698
                   LIB143-026-Q1-E1-D1
Seq. ID
Method
                   BLASTX
                   g730456
NCBI GI
BLAST score
                   244
E value
                   7.0e-21
Match length
                   81
% identity
                   58
NCBI Description 40S RIBOSOMAL PROTEIN S19
Seq. No.
                   290699
Seq. ID
                   LIB143-026-Q1-E1-D11
Method
                   BLASTX
NCBI GI
                   q3004950
BLAST score
                   269
E value
                   6.0e-24
Match length
                   89
% identity
NCBI Description (AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays]
Seq. No.
                   290700
Seq. ID
                   LIB143-026-Q1-E1-E2
Method
                   BLASTX
NCBI GI
                   q4056490
BLAST score
                   168
```

Method BLASTX
NCBI GI g4056490
BLAST score 168
E value 9.0e-12
Match length 93
% identity 49

NCBI Description (AC005896) hypothetical protein [Arabidopsis thaliana]

Seq. No. 290701

Seq. ID LIB143-026-Q1-E1-G10

Method BLASTX NCBI GI g3319372

BLAST score

E value Match length 301 2.0e-27



```
BLAST score
E value
                   4.0e-23
Match length
                   134
% identity
                   42
                   (AF077409) similar to reverse transcriptases (PFam:
NCBI Description
                   rvt.hmm, score: 60.13) [Arabidopsis thaliana]
Seq. No.
                   290702
Seq. ID
                   LIB143-026-Q1-E1-G2
Method
                   BLASTX
NCBI GI
                   q135398
BLAST score
                   149
E value
                   7.0e-10
                   37
Match length
                   78
% identity
                   TUBULIN ALPHA-1 CHAIN >gi_82731_pir__S15773 tubulin alpha-1 chain - maize >gi_22147_emb_CAA33734_ (X15704)
NCBI Description
                   alpha1-tubulin [Zea mays]
                   290703
Seq. No.
                   LIB143-026-Q1-E1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1709970
BLAST score
                   408
                   4.0e-40
E value
Match length
                   113
% identity
                   71
                  60S RIBOSOMAL PROTEIN L10A
NCBI Description
                   290704
Seq. No.
                   LIB143-026-Q1-E1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4512667
BLAST score
                   221
E value
                   3.0e-18
Match length
                   96
% identity
                   47
                   (AC006931) putative MAP kinase [Arabidopsis thaliana]
NCBI Description
                   290705
Seq. No.
                   LIB143-026-Q1-E1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2245001
BLAST score
                   141
                   4.0e-13
E value
Match length
                   64
% identity
                   60
NCBI Description
                    (Z97341) similarity to NADH dehydrogenase (ubiquinone)
                    [Arabidopsis thaliana]
                   290706
Seq. No.
Seq. ID
                   LIB143-026-Q1-E1-H6
Method
                   BLASTX
NCBI GI
                   g3980383
```

Seq. ID



```
% identity
NCBI Description
                  (AC004561) unknown protein [Arabidopsis thaliana]
                  290707
Seq. No.
                  LIB143-027-Q1-E1-C2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2282583
BLAST score
                  66
                  6.0e-29
E value
Match length
                  130
                  88
% identity
NCBI Description
                  Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete
Seq. No.
                  290708
                  LIB143-027-Q1-E1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g602605
                  132
BLAST score
                  2.0e-68
E value
Match length
                  212
                  48
% identity
NCBI Description Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin
                  290709
Seq. No.
                  LIB143-028-Q1-E1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q300082
BLAST score
                  175
E value
                  4.0e-94
Match length
                  179
                  99
% identity
                  hsp82=82 kda heat shock protein [Zea mays, seedling,
NCBI Description
                  leaves, Genomic, 3468 nt]
Seq. No.
                  290710
Seq. ID
                  LIB143-028-Q1-E1-F3
Method
                  BLASTX
NCBI GI
                  g1747294
BLAST score
                  245
E value
                  2.0e-21
Match length
                  50
% identity
                  100
NCBI Description (D45383) vacuolar H+-pyrophosphatase [Oryza sativa]
Seq. No.
                  290711
Seq. ID
                  LIB143-028-Q1-E1-F7
Method
                  BLASTN
NCBI GI
                  g426481
BLAST score
                  141
                  1.0e-73
E value
Match length
                  153
                  98
% identity
NCBI Description Zea mays alpha-amylase mRNA, complete cds
                  290712
Seq. No.
```

40413

LIB143-029-Q1-E1-C2

Seq. ID



```
Method
                  BLASTX
NCBI GI
                  q4191775
BLAST score
                  413
                  7.0e-41
E value
Match length
                  85
                  79
% identity
                  (ACO05917) putative acyl-CoA cholesterol acyltransferase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  290713
Seq. ID
                  LIB143-029-Q1-E1-D7
Method
                  BLASTN
NCBI GI
                  q4416300
BLAST score
                  40
E value
                  2.0e-13
Match length
                  136
                  82
% identity
NCBI Description
                  Zea mays chromosome 4 22 kDa zein-associated intercluster
                  region, complete sequence
Seq. No.
                  290714
Seq. ID
                  LIB143-029-Q1-E1-H1
Method
                  BLASTX
NCBI GI
                  q120670
BLAST score
                  259
E value
                  8.0e-23
Match length
                  73
                  71
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_100879_pir__S06879 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) C - maize
                  >gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]
                  290715
Seq. No.
Seq. ID
                  LIB143-030-Q1-E1-A2
                  BLASTX
Method
NCBI GI
                  q1076761
BLAST score
                  227
                  1.0e-18
E value
Match length
                  90
                  51
% identity
                  AWJL172 protein - wheat >gi 551208 emb_CAA57132_ (X81367)
NCBI Description
                  AWJL172 [Triticum aestivum]
Seq. No.
                  290716
Seq. ID
                  LIB143-030-Q1-E1-A7
Method
                  BLASTX
NCBI GI
                  g4455223
BLAST score
                  401
                  4.0e-39
E value
                  128
Match length
                  62
% identity
NCBI Description
                  (AL035440) putative DNA binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  290717
```

40414

LIB143-030-Q1-E1-B2



Method BLASTX NCBI GI g134228 BLAST score 146 2.0e-09 E value Match length 46 67 % identity GTP-BINDING PROTEIN SAS1 >gi 102241 pir A34716 GTP-binding NCBI Description protein SAS1 - slime mold (Dictyostelium discoideum) >gi 167877 (M34457) GTP-binding protein (SAS2) [Dictyostelium discoideum] Seq. No. 290718 Seq. ID LIB143-030-Q1-E1-B8 Method BLASTN NCBI GI q2274987 BLAST score 47 E value 3.0e-17 Match length 92 87 % identity NCBI Description Hordeum vulgare mRNA for expressed sequence tag 290719 Seq. No. Seq. ID LIB143-030-Q1-E1-C8 Method BLASTX q4263707 NCBI GI 383 BLAST score 5.0e-37 E value 136 Match length % identity 54 (AC006223) putative 70kD heat shock protein [Arabidopsis NCBI Description thaliana] 290720 Seq. No. Seq. ID LIB143-030-Q1-E1-E10 Method BLASTX NCBI GI q113621 BLAST score 205 E value 2.0e-16 Match length 58 % identity 66 FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME NCBI Description >gi 68196 pir ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366 (X12872) fructose bisphosphate aldolase [Zea mays] >gi 225624 prf 1307278A cytoplasmic aldolase [Zea mays] Seq. No. 290721 Seq. ID LIB143-030-Q1-E1-E11 Method BLASTX q1184774 NCBI GI

Method BLASTX
NCBI GI g1184774
BLAST score 193
E value 4.0e-15
Match length 65
% identity 74

NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC3 [Zea mays]



```
Seq. No.
                  290722
                  LIB143-030-Q1-E1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2119187
BLAST score
                  417
E value
                  5.0e-41
Match length
                  86
                  94
% identity
                  transmembrane protein, glucose starvation-induced - maize
NCBI Description
                  >gi 575731 emb CAA57955 (X82633) transmembrane protein
                  [Zea mays]
                  290723
Seq. No.
Seq. ID
                  LIB143-030-Q1-E1-E9
Method
                  BLASTN
                  g1184773
NCBI GI
BLAST score
                  97
                  4.0e-47
E value
Match length
                  157
                  90
% identity
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC3
NCBI Description
                   (gpc3) mRNA, complete cds
Seq. No.
                  290724
Seq. ID
                  LIB143-030-Q1-E1-G6
Method
                  BLASTX
                  g4432837
NCBI GI
BLAST score
                  150
E value
                  1.0e-09
Match length
                  44
% identity
                   68
NCBI Description (AC006283) hypothetical protein [Arabidopsis thaliana]
                  290725
Seq. No.
Seq. ID
                  LIB143-030-Q1-E1-H10
Method
                  BLASTX
NCBI GI
                   q4056502
BLAST score
                   369
E value
                   2.0e-35
Match length
                   100
                   71
% identity
NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
                   290726
Seq. No.
                   LIB143-030-Q1-E1-H11
Seq. ID
Method
                  BLASTX
                   g3450893
NCBI GI
BLAST score
                   169
                   5.0e-12
E value
                   46
Match length
                  72
% identity
                   (AF084005) ras-like small monomeric GTP-binding protein
NCBI Description
                   [Avena fatua]
```

40416

290727

LIB143-030-Q1-E1-H3

Seq. No.

Seq. ID

Seq. ID Method



```
BLASTX
Method
                  q1169534
NCBI GI
                  166
BLAST score
                  4.0e-12
E value
                  64
Match length
                  55
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi 542019 pir S39203
                  phosphopyruvate hydratase (EC 4.2.1.11) - castor bean
                  >gi 433609 emb CAA82232 (Z28386) enolase [Ricinus
                  communis]
                  290728
Seq. No.
Seq. ID
                  LIB143-031-Q1-E1-A3
Method
                  BLASTX
NCBI GI
                  g2286153
BLAST score
                  289
                  3.0e-26
E value
                  75
Match length
% identity
                  83
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
Seq. No.
                  290729
Seq. ID
                  LIB143-031-Q1-E1-C2
Method
                  BLASTX
NCBI GI
                  q3445208
BLAST score
                  225
E value
                  4.0e-31
                  99
Match length
                  69
% identity
                  (AC004786) putative amino-acid acetyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                  290730
Seq. No.
Seq. ID
                  LIB143-031-Q1-E1-D2
                  BLASTX
Method
                  g2160692
NCBI GI
                  155
BLAST score
                  3.0e-19
E value
                  84
Match length
                  58
% identity
                  (U73527) B' regulatory subunit of PP2A [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  290731
Seq. ID
                  LIB143-031-Q1-E1-D4
                  BLASTX
Method
NCBI GI
                  q3135543
BLAST score
                  179
                  1.0e-13
E value
Match length
                  49
% identity
                  76
NCBI Description (AF062393) aquaporin [Oryza sativa]
Seq. No.
                  290732
```

40417

LIB143-031-Q1-E1-F5

BLASTX



```
NCBI GI
                  q554565
                  328
BLAST score
                  1.0e-30
E value
                  82
Match length
% identity
                  76
NCBI Description (M24889) glutathione S-transferase [Artificial gene]
                  290733
Seq. No.
Seq. ID
                  LIB143-031-Q1-E1-G10
Method
                  BLASTN
NCBI GI
                  g22292
BLAST score
                  46
E value
                  3.0e-17
Match length
                  74
                  91
% identity
NCBI Description Z.mays mRNA for glycine-rich protein
Seq. No.
                  290734
Seq. ID
                  LIB143-031-Q1-E1-G6
Method
                  BLASTN
NCBI GI
                  q4140643
BLAST score
                  71
E value
                  1.0e-31
Match length
                  222
                  84
% identity
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
                  complete sequence
                  290735
Seq. No.
Seq. ID
                  LIB143-032-Q1-E1-C6
Method
                  BLASTX
NCBI GI
                  g4097340
BLAST score
                  221
                  5.0e-18
E value
Match length
                  43
% identity
                  93
NCBI Description (U57639) hydrophobic LEA-like protein [Oryza sativa]
                  290736
Seq. No.
Seq. ID
                  LIB143-032-Q1-E1-D4
                  BLASTN
Method
NCBI GI
                  g1944204
BLAST score
                  36
                  7.0e-11
E value
                  52
Match length
                  92
% identity
NCBI Description Oryza sativa mRNA for RicMT, complete cds
                  290737
Seq. No.
Seq. ID
                  LIB143-032-Q1-E1-F11
Method
                  BLASTX
NCBI GI
                  g3334259
BLAST score
                  186
                  5.0e-14
E value
Match length
                  46
% identity
                  72
NCBI Description WD-40 REPEAT PROTEIN MSI4 >gi 2599092 (AF028711) WD-40
```





repeat protein MSI4 [Arabidopsis thaliana]

```
Seq. No.
                   290738
Seq. ID
                   LIB143-032-Q1-E1-F5
Method
                   BLASTX
NCBI GI
                   q3790188
BLAST score
                   299
E value
                   9.0e-43
Match length
                   128
% identity
                   73
NCBI Description
                   (Y14431) NAD-dependent isocitrate dehydrogenase [Nicotiana
                   tabacum]
Seq. No.
                   290739
Seq. ID
                   LIB143-032-Q1-E1-H11
Method
                   BLASTN
NCBI GI
                   q1658314
BLAST score
                   46
E value
                   9.0e-17
Match length
                   62
                   94
% identity
NCBI Description O.sativa osr40g3 gene
Seq. No.
                   290740
Seq. ID
                   LIB143-032-Q1-E1-H2
Method
                  BLASTX
NCBI GI
                   q3309243
BLAST score
                   387
E value
                   2.0e-37
Match length
                   114
% identity
                   67
NCBI Description
                   (AF073507) aconitase-iron regulated protein 1 [Citrus
                   limon]
Seq. No.
                   290741
Seq. ID
                  LIB143-033-Q1-E1-B10
Method
                  BLASTX
NCBI GI
                   g4455338
BLAST score
                   345
E value
                   1.0e-32
Match length
                   117
% identity
                   55
NCBI Description
                  (AL035525) putative protein [Arabidopsis thaliana]
                   290742
Seq. No.
Seq. ID
                  LIB143-033-Q1-E1-D1
Method
                  BLASTN
NCBI GI
                  g4584956
BLAST score
                   65
                   4.0e-28
E value
Match length
                  217
% identity
                  84
NCBI Description
                  Zea mays heat shock protein 101 (HSP101) gene, complete cds
Seq. No.
                  290743
Seq. ID
                  LIB143-033-Q1-E1-D9
Method
                  BLASTX
```



```
NCBI GI
                   q729762
BLAST score
                   302
E value
                   1.0e-27
Match length
                   92
                   72
% identity
NCBI Description
                   17.0 KD CLASS II HEAT SHOCK PROTEIN (HSP 18)
                   >gi_477225_pir_A48425 heat shock protein HSP18 - maize >gi_300079_bbs_130952 (S59777) HSP18=18 kda heat shock
                   protein [Zea mays, Oh43, clone cMHSP18-1, Peptide, 154 aa]
                   [Zea mays]
Seq. No.
                   290744
Seq. ID
                   LIB143-034-Q1-E1-C12
Method
                   BLASTX
NCBI GI
                   q3341685
BLAST score
                   220
E value
                   7.0e-18
Match length
                   80
% identity
                   61
NCBI Description
                   (AC003672) unknown protein [Arabidopsis thaliana]
Seq. No.
                   290745
Seq. ID
                   LIB143-034-Q1-E1-C6
Method
                   BLASTX
NCBI GI
                   g3334222
BLAST score
                   284
                   2.0e-25
E value
Match length
                   87
% identity
                   66
                   4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) (HPD)
NCBI Description
                   >gi 2695710 emb CAA04245 (AJ000693)
                   4-hydroxyphenylpyruvate dioxygenase [Hordeum vulgare]
Seq. No.
                   290746
Seq. ID
                   LIB143-034-Q1-E1-D10
Method
                   BLASTX
NCBI GI
                   q730536
BLAST score
                   257
E value
                   8.0e-23
Match length
                   53
                   94
% identity
                   60S RIBOSOMAL PROTEIN L23 >gi_310933 (L18915) 60S ribosomal
NCBI Description
                   protein subunit L17 [Nicotiana tabacum]
Seq. No.
                   290747
Seq. ID
                   LIB143-034-Q1-E1-D4
Method
                   BLASTX
NCBI GI
                   q417488
```

Method BLASTX
NCBI GI g417488
BLAST score 350
E value 3.0e-33
Match length 97
% identity 72

NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE H) >gi_100452 pir A40995 starch phosphorylase (EC 2.4.1.1)

H - potato >gi_169473 (M69038) alpha-glucan phosphorylase

type H isozyme [Solanum tuberosum]



```
Seq. No.
                   290748
Seq. ID
                   LIB143-034-Q1-E1-F3
Method
                   BLASTX
NCBI GI
                   q1362162
BLAST score
                   413
E value
                   1.0e-42
Match length
                   130
% identity
                   59
NCBI Description beta-glucosidase BGQ60 precursor - barley >gi 804656
                   (L41869) beta-glucosidase [Hordeum vulgare]
Seq. No.
                   290749
Seq. ID
                   LIB143-034-Q1-E1-F4
Method
                   BLASTN
NCBI GI
                   g1944204
                   52
BLAST score
E value
                   2.0e-20
Match length
                   68
% identity
                   94
NCBI Description Oryza sativa mRNA for RicMT, complete cds
Seq. No.
                   290750
Seq. ID
                   LIB143-034-Q1-E1-H2
Method
                   BLASTX
NCBI GI
                  ฎ629843
BLAST score
                   451
E value
                   5.0e-45
Match length
                   110
% identity
                   83
NCBI Description
                  heat shock protein hsp70-4 - maize (fragment)
                   >gi_498773_emb_CAA55183_ (X78414) heat shock protein 70 kDa
                   [Zea mays]
                   290751
Seq. No.
Seq. ID
                   LIB143-034-Q1-E1-H4
                   BLASTX
Method
                   q112994
NCBI GI
                   394
BLAST score
                   2.0e-38
E value
                   86
Match length
                   92
% identity
                   GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                   >gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                   ABA-inducible gene protein [Zea mays]
                   >gi 226091 prf 1410284A abscisic acid inducible gene [Zea
                   mays]
                   290752
Seq. No.
Seq. ID
                   LIB143-035-Q1-E1-C7
Method
                   BLASTX
NCBI GI
                   g1129145
BLAST score
                   164
                   7.0e-12
E value
Match length
                   38
% identity
                   76
```

40421

NCBI Description (X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

Seq. ID

Method

NCBI GI



```
Seq. No.
                  290753
Seq. ID
                  LIB143-035-Q1-E1-D8
Method
                  BLASTX
NCBI GI
                  g2894534
BLAST score
                  417
E value
                  5.0e-41
Match length
                  101
% identity
NCBI Description (AJ224327) aquaporin [Oryza sativa]
Seq. No.
                  290754
Seq. ID
                  LIB143-035-Q1-E1-E10
Method
                  BLASTN
NCBI GI
                  q949979
BLAST score
                  47
E value
                  2.0e-17
Match length
                  95
                  86
% identity
NCBI Description Z.mays Glossy2 locus DNA
                  290755
Seq. No.
Seq. ID
                  LIB143-035-Q1-E1-F7
Method
                  BLASTX
NCBI GI
                  q445613
BLAST score
                  160
                  2.0e-11
E value
Match length
                  71
% identity
                  45
NCBI Description ribosomal protein L7 [Solanum tuberosum]
                  290756
Seq. No.
Seq. ID
                  LIB143-035-Q1-E1-F8
Method
                  BLASTX
NCBI GI
                  g3123270
                  213
BLAST score
                  1.0e-17
E value
                  41
Match length
% identity
                  93
                  40S RIBOSOMAL PROTEIN S4 (SCAR PROTEIN SS620)
NCBI Description
                  >gi 2463335 emb CAA75242 (Y15009) ribosomal protein S4
                  [Oryza sativa]
                  290757
Seq. No.
Seq. ID
                  LIB143-035-Q1-E1-F9
                  BLASTN
Method
NCBI GI
                  g758352
BLAST score
                  40
                  1.0e-13
E value
                  74
Match length
                  94
% identity
NCBI Description Z.mays mRNA for cysteine synthase
                  290758
Seq. No.
```

40422

LIB143-035-Q1-E1-G12

BLASTX

g322641



```
BLAST score
E value
                  5.0e-09
                  76
Match length
                  37
% identity
                  beta-1,3-glucanase homolog (clone A6) - rape (fragment)
NCBI Description
                  >qi 17738 emb CAA49513 (X69887) beta-1,3-glucanase
                  homologue [Brassica napus]
                  290759
Seq. No.
                  LIB143-036-Q1-E1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g168424
BLAST score
                  207
                  2.0e-16
E value
                  99
Match length
                  52
% identity
                  (M59449) polypeptide chain-binding protein [Zea mays]
NCBI Description
                  290760
Seq. No.
                  LIB143-036-Q1-E1-B2
Seq. ID
                  BLASTX
Method
                  g100883
NCBI GI
BLAST score
                   226
E value
                  1.0e-18
                   86
Match length
% identity
                   56
                  heat shock protein 17.2 - maize >gi_22335_emb_CAA46641_
NCBI Description
                   (X65725) heat shock protein 17.2 [Zea mays]
                   290761
Seq. No.
                   LIB143-036-Q1-E1-C11
Seq. ID
                   BLASTN
Method
                   q1049254
NCBI GI
BLAST score
                   48
                   4.0e-18
E value
Match length
                   144
% identity
                   84
                  Zea mays H+-pyrophosphatase mRNA, partial cds
NCBI Description
                   290762
Seq. No.
                   LIB143-036-Q1-E1-E4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3004949
BLAST score
                   39
                   6.0e-13
E value
Match length
                   171
% identity
                   81
                   Zea mays tonoplast intrinsic protein (ZmTIP1) mRNA,
NCBI Description
                   complete cds
                   290763
Seq. No.
                   LIB143-036-Q1-E1-E6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g466172
```

293

110

2.0e-29

BLAST score

Match length

E value



% identity GTP-BINDING PROTEIN YPTM2 >gi 283056 pir B38202 ypt family NCBI Description - maize >gi_287835_emb_CAA44919_ (X63278) yptm2 [Zea mays] Seq. No. 290764 Seq. ID LIB143-036-Q1-E1-G2 Method BLASTX NCBI GI q1632822 BLAST score 356 E value 3.0e-51 Match length 116 % identity 88 NCBI Description (Y08962) transmembrane protein [Oryza sativa] >gi 1667594 (U77297) transmembrane protein [Oryza sativa] 290765 Seq. No. LIB143-036-Q1-E1-G3 Seq. ID Method BLASTN q575730 NCBI GI BLAST score 56 4.0e-23 E value Match length 108 % identity 88 NCBI Description Z.mays mRNA for transmembrane protein 290766 Seq. No. LIB143-036-01-E1-H1 Seq. ID Method BLASTX NCBI GI q1632822 BLAST score 539 E value 3.0e-55 Match length 117 % identity 86 NCBI Description (Y08962) transmembrane protein [Oryza sativa] >gi 1667594 (U77297) transmembrane protein [Oryza sativa] 290767 Seq. No. LIB143-037-Q1-E1-B7 Seq. ID Method BLASTX NCBI GI g2293568 BLAST score 155 2.0e-10 E value Match length 73 % identity 47 NCBI Description (AF012897) HvB12D homolog [Oryza sativa] Seq. No. 290768 Seq. ID LIB143-037-Q1-E1-C4 Method BLASTX NCBI GI q3298474 BLAST score 208

2.0e-17 E value Match length 103 % identity 56

NCBI Description (AB012765) ovpl [Oryza sativa]

Seq. No. 290769



```
Seq. ID
                  LIB143-037-Q1-E1-F10
Method
                  BLASTX
NCBI GI
                  g629602
BLAST score
                  185
                  8.0e-14
E value
Match length
                  73
% identity
                  48
                  probable imbibition protein - wild cabbage
NCBI Description
                  >gi 488787 emb CAA55893_ (X79330) putative imbibition
                  protein [Brassica oleracea]
Seq. No.
                  290770
Seq. ID
                  LIB143-037-Q1-E1-F8
Method
                  BLASTX
NCBI GI
                  q585202
BLAST score
                  208
E value
                  3.0e-26
Match length
                  65
% identity
                  97
                  GLUTAMINE SYNTHETASE ROOT ISOZYME 2 (GLUTAMATE--AMMONIA
NCBI Description
                  LIGASE) >gi_481807_pir__S39478 glutamate--ammonia ligase
                  (EC 6.3.1.2) 1-2, cytosolic - maize
                  >gi_434326_emb_CAA46720_ (X65927) glutamine synthetase [Zea
                  mays]
                  290771
Seq. No.
                  LIB143-037-Q1-E1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334320
BLAST score
                  460
                  5.0e-46
E value
Match length
                  131
% identity
                  74
                  40S RIBOSOMAL PROTEIN SA (P40) >qi 2444420 (AF020553)
NCBI Description
                  ribosome-associated protein p40 [Glycine max]
                  290772
Seq. No.
Seq. ID
                  LIB143-037-Q1-E1-H1
                  BLASTX
Method
NCBI GI
                  g1362108
                  383
BLAST score
                  5.0e-37
E value
Match length
                  112
                  71
% identity
NCBI Description histone H3 homolog - common tobacco
                  290773
Seq. No.
Seq. ID
                  LIB143-037-Q1-E1-H11
Method
                  BLASTX
NCBI GI
                  q4510349
BLAST score
                  180
                  4.0e-13
E value
```

Match length 74 51 % identity

NCBI Description (AC006921) putative bZIP transcription factor [Arabidopsis

thalianal

NCBI Description



```
Seq. No.
Seq. ID
                  LIB143-037-Q1-E1-H12
Method
                  BLASTX
NCBI GI
                  g4510349
BLAST score
                  143
E value
                  7.0e-09
Match length
                  103
                  40
% identity
NCBI Description
                  (AC006921) putative bZIP transcription factor [Arabidopsis
Seq. No.
                  290775
Seq. ID
                  LIB143-038-Q1-E1-B10
Method
                  BLASTX
NCBI GI
                  q3157944
BLAST score
                  428
E value
                  2.0e-42
Match length
                  104
                  79
% identity
NCBI Description
                  (AC002131) Very strong similarity to aminomethyltransferase
                  precursor gb_U79769 from Mesembryanthemum crystallinum.
                  ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773,
                  gb_N38038, gb_T13742, gb_Z26545, gb_T20753 and gb_W43123
                  come from this ge
Seq. No.
                  290776
Seq. ID
                  LIB143-038-Q1-E1-E4
Method
                  BLASTX
NCBI GI
                  g2191150
BLAST score
                  144
E value
                  6.0e-09
Match length
                  81
% identity
                   (AF007269) similar to mitochondrial carrier family
NCBI Description
                   [Arabidopsis thaliana]
                  290777
Seq. No.
Seq. ID
                  LIB143-038-Q1-E1-F1
Method
                  BLASTX
NCBI GI
                  g4558591
BLAST score
                  160
E value
                  6.0e-11
                  51
Match length
                  57
% identity
                   (AC006555) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                  thaliana]
                  290778
Seq. No.
Seq. ID
                  LIB143-039-Q1-E1-C4
Method
                  BLASTX
NCBI GI
                  g548774
BLAST score
                  181
E value
                  6.0e-14
                  57
Match length
% identity
                  65
```

60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal

protein L7a - rice >gi 303855 dbj BAA02156 (D12631)

BLAST score

221



ribosomal protein L7A [Oryza sativa]

```
290779
Seq. No.
Seq. ID
                  LIB143-039-Q1-E1-C8
Method
                  BLASTX
NCBI GI
                   q4154352
BLAST score
                   144
E value
                   5.0e-09
                   89
Match length
% identity
                   37
                  (AF110333) PrMC3 [Pinus radiata]
NCBI Description
                   290780
Seq. No.
Seq. ID
                   LIB143-039-Q1-E1-F8
Method
                   BLASTN
NCBI GI
                   q440170
BLAST score
                   209
                   1.0e-114
E value
                   296
Match length
                   99
% identity
NCBI Description Z.mays (C6000237) trpA gene
Seq. No.
                   290781
Seq. ID
                  LIB143-039-Q1-E1-G11
Method
                  BLASTX
                                                          ***
NCBI GI
                   g2194119
BLAST score
                   169
E value
                  7.0e-12
Match length
                  87
% identity
                   43
NCBI Description (AC002062) No definition line found [Arabidopsis thaliana]
Seq. No.
                  290782
Seq. ID
                  LIB143-039-Q1-E1-G3
Method
                  BLASTX
NCBI GI
                  q4220479
BLAST score
                  256
E value
                  3.0e-22
                  90
Match length
                  59
% identity
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
                  290783
Seq. No.
Seq. ID
                  LIB143-039-Q1-E1-G7
Method
                  BLASTX
NCBI GI
                  g1296955
BLAST score
                  172
                  1.0e-12
E value
                  52
Match length
                  62
% identity
NCBI Description
                  (X95402) duplicated domain structure protein [Oryza sativa]
Seq. No.
                  290784
                  LIB143-039-Q1-E1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4582787
```



```
E value
                   2.0e-18
Match length
% identity
                   85
NCBI Description
                  (AJ012281) adenosine kinase [Zea mays]
                   290785
Seq. No.
Seq. ID
                  LIB143-040-Q1-E1-A5
Method
                  BLASTN
NCBI GI
                  g1870200
                   121
BLAST score
E value
                   1.0e-61
Match length
                   193
% identity
                   92
NCBI Description Z.mays cyp71c2 gene
                  290786
Seq. No.
                  LIB143-040-01-E1-D3
Seq. ID
Method
                  BLASTX
                  g2293566
NCBI GI
                  199
BLAST score
                   8.0e-27
E value
Match length
                  75
% identity
                  87
NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
                  290787
Seq. No.
                  LIB143-041-Q1-E1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1296955
                  403
BLAST score
E value
                  2.0e-39
Match length
                  115
% identity
                   34
NCBI Description (X95402) duplicated domain structure protein [Oryza sativa]
                  290788
Seq. No.
Seq. ID
                  LIB143-041-Q1-E1-A3
Method
                  BLASTN
NCBI GI
                   q1532070
BLAST score
                   247
E value
                   1.0e-136
Match length
                   335
% identity
                   93
NCBI Description Z.mays grp3 mRNA for glycine-rich protein
                   290789
Seq. No.
Seq. ID
                  LIB143-041-Q1-E1-B11
Method
                  BLASTX
NCBI GI
                  q1009234
BLAST score
                   514
                  2.0e-52
E value
Match length
                  124
                  73
% identity
```

Seq. No. 290790

Seq. ID LIB143-041-Q1-E1-B12

NCBI Description (L38829) SUP2 gene product [Nicotiana tabacum]

Match length

% identity

140

89



```
Method
                  BLASTX
NCBI GI
                  g134598
BLAST score
                  177
                  2.0e-15
E value
Match length
                  65
% identity
                  72
NCBI Description SUPEROXIDE DISMUTASE-4AP (CU-ZN)
Seq. No.
                  290791
Seq. ID
                  LIB143-041-Q1-E1-C12
Method
                  BLASTX
NCBI GI
                  q1814403
BLAST score
                  150
E value
                  3.0e-10
Match length
                  44
                  70
% identity
                  (U84889) methionine synthase [Mesembryanthemum
NCBI Description
                  crystallinum]
Seq. No.
                  290792
Seq. ID
                  LIB143-041-Q1-E1-D10
Method
                  BLASTN
NCBI GI
                  q296593
BLAST score
                  55
E value
                  4.0e-22
Match length
                  75
                  93
% identity
NCBI Description H. vulgare pZE40 gene
                  290793
Seq. No.
Seq. ID
                  LIB143-041-Q1-E1-E7
Method
                  BLASTX
NCBI GI
                  g4185310
BLAST score
                  350
E value
                  3.0e - 33
                  108
Match length
% identity
                  67
NCBI Description (AF090446) gag protein [Zea mays]
                  290794
Seq. No.
Seq. ID
                  LIB143-041-Q1-E1-F4
Method
                  BLASTX
NCBI GI
                  g2827080
BLAST score
                  237
E value
                  7.0e-20
                  57
Match length
                  82
% identity
NCBI Description (AF020271) malate dehydrogenase precursor [Medicago sativa]
                  290795
Seq. No.
Seq. ID
                  LIB143-041-Q1-E1-G12
Method
                  BLASTN
                  g22338
NCBI GI
BLAST score
                  64
E value
                  1.0e-27
```



```
NCBI Description Maize mRNA for an 18kDa heat shock protein
                  290796
Seq. No.
Seq. ID
                  LIB143-041-Q1-E1-H8
Method
                  BLASTX
NCBI GI
                  g3033398
BLAST score
                  285
E value
                  1.0e-25
Match length
                  94
                  59
% identity
                   (AC004238) putative phosphoribosylaminoimidazolecarboxamide
NCBI Description
                  formyltransferase [Arabidopsis thaliana]
                   290797
Seq. No.
                  LIB143-042-Q1-E1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1498055
BLAST score
                   599
                   3.0e-62
E value
                  117
Match length
% identity
NCBI Description (U64437) novel protein [Zea mays]
Seq. No.
                   290798
                   LIB143-042-Q1-E1-H6
Seq. ID
Method
                   BLASTN
                   a1944204
NCBI GI
BLAST score
                   56
E value
                   1.0e-22
Match length
                   68
                   96
% identity
NCBI Description Oryza sativa mRNA for RicMT, complete cds
                   290799
Seq. No.
Seq. ID
                   LIB143-043-Q1-E1-A12
Method
                   BLASTX
                   g1332579
NCBI GI
                   235
BLAST score
E value
                   6.0e-20
Match length
                   64
% identity
                  (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
Seq. No.
                   290800
Seq. ID
                   LIB143-043-Q1-E1-F11
Method
                   BLASTX
                   g3236242
NCBI GI
BLAST score
                   292
                   2.0e-26
E value
Match length
                   89
                   66
% identity
```

NCBI Description

(AC004684) putative ribosomal protein L36 [Arabidopsis

thaliana]

290801 Seq. No.

LIB143-043-Q1-E1-G4 Seq. ID

BLASTX Method

Match length

```
q4115377
NCBI GI
BLAST score
                   174
                   8.0e-13
E value
                   82
Match length
                   51
% identity
                   (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                   290802
Seq. No.
                   LIB143-043-Q1-E1-G5
Seq. ID
Method
                   BLASTN
                   g1944204
NCBI GI
BLAST score
                   56
E value
                   1.0e-22
Match length
                   68
                   96
% identity
NCBI Description Oryza sativa mRNA for RicMT, complete cds
                   290803
Seq. No.
                   LIB143-043-Q1-E1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g439879
BLAST score
                   172
E value
                   2.0e-12
Match length
                   90
% identity
                   41
                   (L15194) [Golden delicious apple fruit expressed mRNA,
NCBI Description
                   complete cds.], gene product [Malus domestica]
Seq. No.
                   290804
                   LIB143-044-Q1-E1-A6
Seq. ID
Method
                   BLASTX
                   g2134102
NCBI GI
BLAST score
                   250
E value
                   2.0e-21
                   137
Match length
% identity
                   kinesin-like protein 1 - African clawed frog
>gi_562793_emb_CAA57539_ (X82012) kinesin-like protein 1
NCBI Description
                    [Xenopus laevis]
Seq. No.
                    290805
Seq. ID
                   LIB143-044-Q1-E1-C2
Method
                   BLASTX
NCBI GI
                   g4510379
BLAST score
                   153
                    5.0e-10
E value
Match length
                    71
% identity
                    42
                   (AC007017) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    290806
Seq. No.
                   LIB143-044-Q1-E1-C4
Seq. ID
                   BLASTX
Method
NCBI GI
                    g2245095
                    283
BLAST score
                    2.0e-25
E value
                    70
```



```
% identity
                   (Z97343) formyltransferase purU homolog [Arabidopsis
NCBI Description
                   thaliana]
                   290807
Seq. No.
                   LIB143-044-Q1-E1-D9
Seq. ID
                   BLASTN
Method
NCBI GI
                   g296593
BLAST score
                   55
                   4.0e-22
E value
                   75
Match length
                   93
% identity
NCBI Description H. vulgare pZE40 gene
                   290808
Seq. No.
                   LIB143-044-Q1-E1-E4
Seq. ID
                   BLASTX
Method
                   g3915131
NCBI GI
BLAST score
                   148
                   7.0e-10
E value
                   78
Match length
                   38
% identity
                   THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1)
NCBI Description
                   >gi_426442_dbj_BAA04864_ (D21836) thioredoxin h [Oryza
                   satīva] >gī_454882_dbj_BAA05546_ (D26547) rice thioredoxin
                   h [Oryza sativa] >\overline{gi}_1\overline{9}30072 (U\overline{9}2541) thioredoxin h [Oryza
                   sativa]
                   290809
Seq. No.
                   LIB143-044-Q1-E1-E5
Seq. ID
                   BLASTX
Method
                   q4102839
NCBI GI
                   220
BLAST score
                   7.0e-18
E value
                   60
Match length
                   67
% identity
                   (AF016713) LeOPT1 [Lycopersicon esculentum]
NCBI Description
                   290810
Seq. No.
Seq. ID
                   LIB143-044-Q1-E1-F1
                   BLASTX
Method
                   g585338
NCBI GI
                   317
BLAST score
                   3.0e-29
E value
Match length
                   109
% identity
                   ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)
NCBI Description
                   >qi 391879 dbj BAA01181 (D10335) adenylate kinase-b [Oryza
                   sativa]
Seq. No.
                   290811
Seq. ID
                   LIB143-044-Q1-E1-G12
Method
```

BLASTX

g4416307 NCBI GI 330 BLAST score 7.0e-31 E value 88 Match length

% identity (AF105716) hypothetical protein [Zea mays] NCBI Description 290812 Seq. No. LIB143-044-Q1-E1-G9 Seq. ID Method BLASTX NCBI GI g2642648 BLAST score 508 E value 9.0e-52 Match length 100 % identity NCBI Description (AF033852) cytosolic heat shock 70 protein; HSC70-3 [Spinacia oleracea] >gi 2660768 (AF034616) cytosolic heat shock 70 protein [Spinacia oleracea] >gi 2660770 (AF034617) cytosolic heat shock 70 protein [Spinacia oleracea] 290813 Seq. No. Seq. ID LIB143-044-Q1-E1-H4 Method BLASTX NCBI GI g2827548 BLAST score 185 E value 8.0e-14 Match length 75 % identity 47 (AL021635) cytochrome P450 - like protein [Arabidopsis NCBI Description thaliana 290814 Seq. No. Seq. ID LIB143-045-Q1-E1-A12 Method BLASTX NCBI GI g1518113

Method BLASTX
NCBI GI g1518113
BLAST score 282
E value 4.0e-25
Match length 121
% identity 53

NCBI Description (U66193) SLL2 [Brassica napus]

Seq. No. 290815

Seq. ID LIB143-045-Q1-E1-C11

Method BLASTX
NCBI GI g2723473
BLAST score 153
E value 2.0e-10
Match length 51
% identity 71

NCBI Description (D89726) defender against apoptotic death 1 protein [Oryza

sativa] >gi 2723883 dbj_BAA24104_ (D89727) defender against

apoptotic death 1 protein [Oryza sativa]

Seq. No. 290816

Seq. ID LIB143-045-Q1-E1-D1

Method BLASTX
NCBI GI g4262242
BLAST score 373
E value 2.0e-44
Match length 121
% identity 72



```
(AC006200) NADC homolog [Arabidopsis thaliana]
NCBI Description
                  290817
Seq. No.
                  LIB143-045-Q1-E1-D12
Seq. ID
Method
                  BLASTN
                  g168462
NCBI GI
BLAST score
                  156
E value
                  1.0e-82
Match length
                  168
                  98
% identity
                  Zea mays defective suppressor-mutator from the
NCBI Description
                  brittle-1-mutable allele
Seq. No.
                  290818
                  LIB143-045-Q1-E1-E10
Seq. ID
                  BLASTN
Method
                  g3015620
NCBI GI
BLAST score
                  68
                  7.0e-30
E value
                  229
Match length
                  83
% identity
                  Zea mays low molecular weight heat shock protein precursor
NCBI Description
                   (hsp22) mRNA, nuclear gene encoding mitochondrial protein,
                   complete cds
Seq. No.
                   290819
                  LIB143-045-Q1-E1-F9
Seq. ID
Method
                  BLASTN
                   g440170
NCBI GI
BLAST score
                   46
                   1.0e-16
E value
                   150
Match length
                   83
% identity
NCBI Description Z.mays (C6000237) trpA gene
Seq. No.
                   290820
Seq. ID
                   LIB143-046-Q1-E1-A12
Method
                   BLASTX
NCBI GI
                   q4582468
BLAST score
                   239
E value
                   3.0e-20
Match length
                   97
                   55
% identity
                   (AC007071) putative 40S ribosomal protein; contains
NCBI Description
                   C-terminal domain [Arabidopsis thaliana]
Seq. No.
                   290821
Seq. ID
                   LIB143-046-Q1-E1-B5
Method
                   BLASTX
NCBI GI
                   g1170937
                   347
BLAST score
                   7.0e-33
E value
                   86
Match length
% identity
                   81
                   S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
```

40434

>gi 450549_emb_CAA81481_ (Z26867) S-adenosyl methionine

NCBI Description



synthetase [Oryza sativa]

```
290822
Seq. No.
                  LIB143-046-Q1-E1-B8
Seq. ID
Method
                  BLASTX
                  g1351840
NCBI GI
BLAST score
                  488
                  2.0e-49
E value
Match length
                  105
                  87
% identity
NCBI Description
                  ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
                  >gi_1084319_pir__S53505 isocitrate lyase - cucumber
                  >gi 1052578 emb CAA84632 (Z35499) isocitrate lyase
                  [Cucumis sativus]
                  290823
Seq. No.
                  LIB143-046-Q1-E1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g122022
BLAST score
                  275
                  2.0e-24
E value
                  95
Match length
                  64
% identity
NCBI Description
                  HISTONE H2B >gi_283025_pir__S22323 histone H2B - wheat
                  >gi 21801 emb CAA42530 (X59873) histone H2B [Triticum
                  aestivum]
                  290824
Seq. No.
                  LIB143-046-Q1-E1-C6
Seq. ID
Method
                  BLASTN
                  q1617470
NCBI GI
                  75
BLAST score
                  5.0e-34
E value
Match length
                  150
% identity
NCBI Description
                  Z.diploperennis DNA for Grandel-4 retrotransposon
                  290825
Seq. No.
                  LIB143-046-Q1-E1-C8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q22334
BLAST score
                  36
E value
                   2.0e-11
Match length
                  80
% identity
                  86
                  Z.mays mRNA for heat shock protein 17.2
NCBI Description
Seq. No.
                   290826
                  LIB143-046-Q1-E1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1352088
BLAST score
                   365
                   5.0e-35
E value
Match length
                   107
% identity
                   67
```

CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR >gi_624676

(U19481) citrate synthase precursor [Citrus maxima]

Seq. ID



```
290827
Seq. No.
Seq. ID
                   LIB143-046-Q1-E1-G1
Method
                   BLASTX
NCBI GI
                   g3420052
BLAST score
                   318
E value
                   2.0e-29
Match length
                   87
% identity
                   70
NCBI Description
                   (AC004680) putative ubiginone reductase [Arabidopsis
                   thaliana]
Seq. No.
                   290828
Seq. ID
                   LIB143-046-Q1-E1-H7
Method
                   BLASTN
NCBI GI
                   q3004949
BLAST score
                   59
E value
                   7.0e-25
Match length
                   91
                   91
% identity
                   Zea mays tonoplast intrinsic protein (ZmTIP1) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   290829
Seq. ID
                   LIB143-047-Q1-E1-A1
Method
                   BLASTX
NCBI GI
                   q2494116
BLAST score
                   194
E value
                   2.0e-15
Match length
                   69
% identity
                   57
                   (AC002376) Similar to Synechocystis hypothetical protein
NCBI Description
                   (gb D90915). [Arabidopsis thaliana]
Seq. No.
                   290830
Seq. ID
                   LIB143-047-Q1-E1-A3
                   BLASTX
Method
NCBI GI
                   g2662310
BLAST score
                   297
                   4.0e-27
E value
                   68
Match length
                   84
% identity
                  (AB009307) bpw1 [Hordeum vulgare]
NCBI Description
                   290831
Seq. No.
Seq. ID
                   LIB143-047-Q1-E1-B1
                   BLASTN
Method
NCBI GI
                   q4140643
BLAST score
                   41
                   9.0e-14
E value
                   57
Match length
                   93
% identity
                   Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                   complete sequence
                   290832
Seq. No.
```

LIB143-047-Q1-E1-B9



```
BLASTX
Method
NCBI GI
                  a4510348
                  180
BLAST score
                  3.0e-13
E value
Match length
                  82
                  46
% identity
NCBI Description
                  (AC006921) unknown protein [Arabidopsis thaliana]
                  290833
Seq. No.
                  LIB143-047-Q1-E1-C10
Seq. ID
Method
                  BLASTN
                  g3004949
NCBI GI
BLAST score
                  58
                  3.0e-24
E value
                  154
Match length
                  85
% identity
                  Zea mays tonoplast intrinsic protein (ZmTIP1) mRNA,
NCBI Description
                  complete cds
                  290834
Seq. No.
                  LIB143-047-Q1-E1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112994
BLAST score
                  457
                  9.0e-46
E value
                  92
Match length
                  98
% identity
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi 22313_emb_CAA31077_ (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi_226091_prf__1410284A abscisic acid inducible gene [Zea
                  mays]
Seq. No.
                   290835
Seq. ID
                  LIB143-047-Q1-E1-F1
Method
                  BLASTX
NCBI GI
                   g2073375
BLAST score
                   186
                   3.0e-14
E value
Match length
                   81
% identity
                   53
                   (D85317) farnesyl pyrophosphate synthase [Oryza sativa]
NCBI Description
                  >gi 4063829 dbj_BAA36276_ (AB021747) farnesyl diphosphate
                   synthase [Oryza sativa]
Seq. No.
                   290836
Seq. ID
                  LIB143-047-Q1-E1-F5
                  BLASTX
Method
NCBI GI
                   g3023751
BLAST score
                   221
                   3.0e-22
E value
Match length
                   95
                   63
% identity
                  70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS
NCBI Description
```

peptidylprolyl isomerase (EC 5.2.1.8) - wheat

ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383

% identity



>gi 854626_emb_CAA60505_ (X86903) peptidylprolyl isomerase [Triticum aestivum]

290837 Seq. No. LIB143-048-Q1-E1-A3 Seq. ID Method BLASTX g3059131 NCBI GI 195 BLAST score 5.0e-15 E value 62 Match length 55 % identity NCBI Description (AJ000478) cytochrome P450 [Helianthus tuberosus] Seq. No. 290838 LIB143-048-Q1-E1-B12 Seq. ID BLASTN Method g902585 NCBI GI 37 BLAST score E value 2.0e-11 Match length 65 89 % identity NCBI Description Zea mays clone MubG9 ubiquitin gene, complete cds 290839 Seq. No. Seq. ID LIB143-048-Q1-E1-E6 Method BLASTX NCBI GI g4585900 BLAST score 139 5.0e-09 E value Match length 47 70 % identity NCBI Description (AC007133) putative histone H2A [Arabidopsis thaliana] 290840 Seq. No. LIB143-049-Q1-E1-B5 Seq. ID Method BLASTX NCBI GI g3413709 338 BLAST score 1.0e-31 E value Match length 108 % identity NCBI Description (AC004747) hypothetical protein [Arabidopsis thaliana] 290841 Seq. No. Seq. ID LIB143-049-Q1-E1-D5 Method BLASTX NCBI GI g1175381 BLAST score 155 E value 3.0e-10 Match length 77

HYPOTHETICAL 44.9 KD PROTEIN C18B11.02C IN CHROMOSOME I NCBI Description >gi_2130286_pir__S58301 hypothetical protein SPAC18B11.02c
- fission yeast (Schizosaccharomyces pombe)

>gi 929888 emb CAA90587 (Z50728) hypothetical protein

[Schizosaccharomyces pombe]



```
290842
Seq. No.
                  LIB143-049-Q1-E1-G4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2331140
BLAST score
                  34
                  8.0e-10
E value
Match length
                  90
                  84
% identity
                  Oryza sativa water-stress inducible protein (WSI) mRNA,
NCBI Description
                  complete cds
                  290843
Seq. No.
                  LIB143-049-Q1-E1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1710563
BLAST score
                  156
                  1.0e-10
E value
Match length
                  47
                   60
% identity
                  60S RIBOSOMAL PROTEIN YL43 >gi_2119153_pir__S71066
NCBI Description
                   ribosomal protein L29.e, cytosolic - yeast (Saccharomyces
                   cerevisiae)
                   290844
Seq. No.
                  LIB143-049-Q1-E1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g122022
BLAST score
                   265
                   4.0e-23
E value
Match length
                   56
                   95
% identity
                  HISTONE H2B >gi_283025_pir__S22323 histone H2B - wheat
NCBI Description
                   >qi 21801 emb CAA42530 (X59873) histone H2B [Triticum
                   aestivum]
                   290845
Seq. No.
                   LIB143-049-Q1-E1-H4
Seq. ID
                   BLASTN
Method
                   g1184775
NCBI GI
BLAST score
                   85
                   3.0e-40
E value
                   217
Match length
                   87
% identity
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC4
NCBI Description
                   (gpc4) mRNA, complete cds
                   290846
Seq. No.
                   LIB143-050-Q1-E1-A10
Seq. ID
                   BLASTN
Method
                   g1944204
NCBI GI
BLAST score
                   56
                   1.0e-22
E value
                   68
Match length
 % identity
NCBI Description Oryza sativa mRNA for RicMT, complete cds
```

40439

290847

Seq. No.



```
LIB143-050-Q1-E1-C6
Seq. ID
                  BLASTX
Method
                  q1184776
NCBI GI
BLAST score
                  235
                  6.0e-20
E value
Match length
                  60
                  78
% identity
                  (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC4 [Zea mays]
                  290848
Seq. No.
                  LIB143-050-Q1-E1-C8
Seq. ID
Method
                  BLASTN
                  g559533
NCBI GI
BLAST score
                  40
                  2.0e-13
E value
Match length
                  86
                  89
% identity
                  Z.mays mRNA for defense-related protein
NCBI Description
Seq. No.
                  290849
                  LIB143-050-Q1-E1-E2
Seq. ID
Method
                  BLASTX
                  g4038471
NCBI GI
BLAST score
                  149
E value
                   4.0e-10
Match length
                   40
% identity
                  70
                  (AF111029) 40S ribosomal protein S27 homolog [Zea mays]
NCBI Description
                   290850
Seq. No.
                  LIB143-050-Q1-E1-F1
Seq. ID
                  BLASTX
Method
                   g1699370
NCBI GI
BLAST score
                   344
                   2.0e-32
E value
                   103
Match length
                   59
% identity
                   (S82620) prolidase=peptidase D/imidopeptidase {EC 3.4.13.9}
NCBI Description
                   [mice, liver, Peptide, 493 aa] [Mus sp.]
                   290851
Seq. No.
                   LIB143-050-Q1-E1-F3
Seq. ID
                   BLASTX
Method
                   g2801433
NCBI GI
BLAST score
                   362
                   1.0e-34
E value
                   77
Match length
                   84
% identity
                   (AF017991) salt stress inducible small GTP binding protein
NCBI Description
                   Ran1 homolog [Arabidopsis thaliana] >gi 3559764 (U75601)
                   unknown [Arabidopsis thaliana]
                   290852
Seq. No.
```

Seq. ID LIB143-050-Q1-E1-H3

Method BLASTN NCBI GI g1944204

% identity

49



```
BLAST score
                  1.0e-22
E value
Match length
                  68
                  96
% identity
NCBI Description Oryza sativa mRNA for RicMT, complete cds
                  290853
Seq. No.
                  LIB143-051-Q1-E1-C11
Seq. ID
                  BLASTN
Method
                  g293888
NCBI GI
                  76
BLAST score
                  5.0e-35
E value
                  172
Match length
% identity
                  87
                  Zea mays, glyceraldehyde-3-phosphate dehydrogenase mRNA, 3'
NCBI Description
                  end (clone GAPC2)
                  290854
Seq. No.
                  LIB143-051-Q1-E1-C6
Seq. ID
Method
                  BLASTN
                  g1617470
NCBI GI
BLAST score
                  36
                  1.0e-10
E value
                  80
Match length
% identity
                  86
NCBI Description Z.diploperennis DNA for Grandel-4 retrotransposon
                  290855
Seq. No.
                  LIB143-051-Q1-E1-D4
Seq. ID
Method
                  BLASTX
                  g4314400
NCBI GI
BLAST score
                   366
                   6.0e-35
E value
                   141
Match length
% identity
                   52
                   (AC006232) putative selenium-binding protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   290856
Seq. ID
                  LIB143-051-Q1-E1-D9
                   BLASTX
Method
                   q1658315
NCBI GI
BLAST score
                   156
                   6.0e-11
E value
Match length
                   42
% identity
                   62
NCBI Description (Y08988) osr40g3 [Oryza sativa]
Seq. No.
                   290857
Seq. ID
                   LIB143-051-Q1-E1-F1
Method
                   BLASTX
NCBI GI
                   q2104681
BLAST score
                   200
E value
                   1.0e-15
Match length
                   101
```

40441

NCBI Description (X97907) transcription factor [Vicia faba]

NCBI GI

BLAST score

g1848281

141



```
290858
Seq. No.
                  LIB143-051-Q1-E1-F8
Seq. ID
Method
                  BLASTN
                  g1870200
NCBI GI
                  49
BLAST score
                  1.0e-18
E value
                  157
Match length
% identity
                  83
NCBI Description Z.mays cyp71c2 gene
                  290859
Seq. No.
                  LIB143-051-Q1-E1-G2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2668742
BLAST score
                  357
                   6.0e - 34
E value
Match length
                  85
                  84
% identity
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]
                   290860
Seq. No.
                   LIB143-051-Q1-E1-H12
Seq. ID
                   BLASTX
Method
                   g3859570
NCBI GI
BLAST score
                   278
                   1.0e-24
E value
Match length
                   78
% identity
                   68
                  (AF098753) unknown [Oryza sativa]
NCBI Description
                   290861
Seq. No.
                   LIB143-052-Q1-E1-B12
Seq. ID
                   BLASTX
Method
                   g4490732
NCBI GI
BLAST score
                   242
                   2.0e-20
E value
                   92
Match length
                   62
% identity
                   (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like
NCBI Description
                   protein [Arabidopsis thaliana]
                   290862
Seq. No.
                   LIB143-052-Q1-E1-E6
Seq. ID
                   BLASTX
Method
                   q2909583
NCBI GI
                   205
BLAST score
                   4.0e-16
E value
                   116
Match length
% identity
                   42
NCBI Description (AL021926) oxcA [Mycobacterium tuberculosis]
                   290863
 Seq. No.
                   LIB143-053-Q1-E1-D8
 Seq. ID
Method
                   BLASTX
```

Match length

% identity

112

81

```
SOURCE OF STREET
```

```
3.0e-09
 E value
 Match length
                   50
                   56
 % identity
                   (U87981) Sorghum bicolor membrane intrinsic (Mip1) protein,
 NCBI Description
                   partial sequence
                   290864
 Seq. No.
                   LIB143-053-Q1-E1-E12
 Seq. ID
                   BLASTX
 Method
                   g4239887
NCBI GI
                   574
 BLAST score
                   2.0e-59
 E value
                   109
 Match length
                   99
 % identity
 NCBI Description (AB016801) MAP kinase 4 [Zea mays]
                   290865
 Seq. No.
                   LIB143-053-Q1-E1-E2
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q3914557
 BLAST score
                   678
                   1.0e-71
 E value
                   132
 Match length
                   98
 % identity
                   RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED
 NCBI Description
                   PROTEIN) >gi 1155265 (U40219) possible apospory-associated
                   protein [Pennisetum ciliare]
                   290866
 Seq. No.
                   LIB143-053-Q1-E1-E4
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                    g440170
 BLAST score
                    134
 E value
                    1.0e-69
 Match length
                    174
                    95
 % identity
 NCBI Description Z.mays (C6000237) trpA gene
                    290867
 Seq. No.
 Seq. ID
                    LIB143-054-Q1-E1-A2
 Method
                    BLASTN
                    q1863998
 NCBI GI
 BLAST score
                    46
                    7.0e-17
 E value
 Match length
                    178
 % identity
                    81
 NCBI Description Maize DNA for Fd VI, complete cds
 Seq. No.
                    290868
 Seq. ID
                    LIB143-054-Q1-E1-A3
 Method
                    BLASTX
                    q3850999
 NCBI GI
 BLAST score
                    455
                    2.0e-45
 E value
```

NCBI Description (AF069908) pyruvate dehydrogenase E1 beta subunit isoform 1 40443

Method

NCBI GI

BLASTX

g2827002



[Zea mays]

```
Seq. No.
                  290869
Seq. ID
                  LIB143-054-Q1-E1-B3
Method
                  BLASTX
NCBI GI
                  q3212854
BLAST score
                  286
                  1.0e-25
E value
                  90
Match length
% identity
                  62
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  290870
Seq. ID
                  LIB143-054-Q1-E1-F4
Method
                  BLASTN
NCBI GI
                  q296593
BLAST score
                  55
E value
                  5.0e-22
Match length
                  75
                  93
% identity
NCBI Description H. vulgare pZE40 gene
Seq. No.
                  290871
Seq. ID
                  LIB143-054-Q1-E1-G2
Method
                  BLASTX
NCBI GI
                  q3183106
BLAST score
                  259
E value
                  2.0e-22
Match length
                  90
                  58
% identity
NCBI Description PROBABLE OXALYL-COA DECARBOXYLASE >gi 1788716 (AE000325)
                  putative enzyme [Escherichia coli]
Seq. No.
                  290872
Seq. ID
                  LIB143-054-Q1-E1-H4
Method
                  BLASTX
NCBI GI
                  g224970
BLAST score
                  260
E value
                  1.0e-22
                  49
Match length
% identity
                  98
NCBI Description heat shock protein hsp70 [Zea mays]
Seq. No.
                  290873
Seq. ID
                  LIB143-054-Q1-E1-H6
Method
                  BLASTX
NCBI GI
                  g3264596
                  209
BLAST score
E value
                  2.0e-20
Match length
                  96
                  61
% identity
NCBI Description (AF057183) putative tonoplast aquaporin [Zea mays]
                  290874
Seq. No.
Seq. ID
                  LIB143-054-Q1-E1-H8
```

BLAST score

% identity

E value Match length 42 2.0e-14

54 94



```
BLAST score
E value
                  6.0e-43
Match length
                  88
                  92
% identity
                  (AF005993) HSP70 [Triticum aestivum]
NCBI Description
Seq. No.
                  290875
                  LIB143-055-Q1-E1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q123553
BLAST score
                  473
E value
                  1.0e-47
Match length
                  100
% identity
                  96
                  17.8 KD CLASS II HEAT SHOCK PROTEIN >gi 100884_pir__S14997
NCBI Description
                  heat shock protein, 18K - maize >gi 22337_emb_CAA38012_
                  (X54075) 18kDa heat shock protein [Zea mays]
Seq. No.
                  290876
                  LIB143-055-Q1-E1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g832928
BLAST score
                  150
E value
                  1.0e-09
Match length
                  134
% identity
                  27
NCBI Description (M19469) ORF [Dictyostelium discoideum]
Seq. No.
                  290877
                  LIB143-055-Q1-E1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3924611
BLAST score
                  197
E value
                  2.0e-15
Match length
                  53
% identity
                  66
NCBI Description
                  (AF069442) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  290878
Seq. ID
                  LIB143-055-Q1-E1-H3
Method
                  BLASTX
NCBI GI
                  g1632822
BLAST score
                  207
E value
                  6.0e-17
Match length
                  45
% identity
                  87
NCBI Description
                  (Y08962) transmembrane protein [Oryza sativa] >gi 1667594
                  (U77297) transmembrane protein [Oryza sativa]
                  290879
Seq. No.
Seq. ID
                  LIB143-056-Q1-E1-C9
Method
                  BLASTN
                  g1944204
NCBI GI
```



```
NCBI Description Oryza sativa mRNA for RicMT, complete cds
                   290880
Seq. No.
                   LIB143-056-Q1-E1-D8
Seq. ID
Method
                   BLASTX
                   g927428
NCBI GI
                   159
BLAST score
                   9.0e-11
E value
                   29
Match length
% identity
                   93
                   (X86733) fis1 [Linum usitatissimum]
NCBI Description
                   290881
Seq. No.
                   LIB143-056-Q1-E1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2384675
BLAST score
                   397
                   1.0e-38
E value
                   122
Match length
                   70
% identity
                   (AF012659) putative potassium transporter AtKT4p
NCBI Description
                   [Arabidopsis thaliana]
                   290882
Seq. No.
                   LIB143-056-Q1-E1-G10
Seq. ID
Method
                   BLASTX
                   g3746431
NCBI GI
BLAST score
                   535
E value
                   7.0e-55
                   118
Match length
                   90
% identity
                   (AF038585) pyruvate dehydrogenase kinase isoform 1; PDK1
NCBI Description
                    [Zea mays]
                   290883
Seq. No.
                   LIB143-057-Q1-E1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1408222
BLAST score
                    323
E value
                   5.0e-30
Match length
                   112
                    61
% identity
                   (U60764) pathogenesis-related protein [Sorghum bicolor]
NCBI Description
Seq. No.
                   290884
                   LIB143-057-Q1-E1-B10
Seq. ID
                   BLASTX
Method
                    g112994
NCBI GI
BLAST score
                    220
                    4.0e-18
E value
Match length
                    68
                    69
% identity
                   GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                   >gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
```

40446

>gi 226091 prf__1410284A abscisic acid inducible gene [Zea

ABA-inducible gene protein [Zea mays]



mays]

```
Seq. No.
                   290885
Seq. ID
                   LIB143-057-Q1-E1-C1
Method
                   BLASTN
NCBI GI
                   g4204375
BLAST score
                   113
E value
                   1.0e-56
Match length
                   269
                   85
% identity
NCBI Description
                   Zea mays acidic ribosomal protein P2a-4 (rpp2a-4) mRNA,
                   partial cds
                   290886
Seq. No.
                   LIB143-057-Q1-E1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2668742
BLAST score
                   357
E value
                   4.0e-34
Match length
                   80
% identity
                   85
                   (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
Seq. No.
                   290887
                   LIB143-057-Q1-E1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4539677
BLAST score
                   306
E value
                   5.0e-28
Match length
                   101
% identity
                   (AF061282) patatin-like protein [Sorghum bicolor]
NCBI Description
                   290888
Seq. No.
Seq. ID
                   LIB143-057-Q1-E1-D9
Method
                   BLASTX
                   g122022
NCBI GI
                   222
BLAST score
E value
                   3.0e-18
Match length
                   69
% identity
                   68
                   HISTONE H2B >gi 283025 pir S22323 histone H2B - wheat
NCBI Description
                   >gi_21801_emb_CAA42530_ (X59873) histone H2B [Triticum
                   aestivum]
Seq. No.
                   290889
Seq. ID
                   LIB143-057-Q1-E1-F4
                   BLASTX
Method
NCBI GI
                   g3915053
BLAST score
                   215
                   1.0e-17
E value
Match length
                   64
% identity
                   70
                   SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)
NCBI Description
                   >gi_2129479_pir__S71494 sucrose synthase (EC 2.4.1.13) -
```

40447

synthase [Beta vulgaris]

beet (fragment) >gi_1488570_emb_CAA57499_ (X81974) sucrose

Match length

% identity

111

77



```
290890
Seq. No.
                  LIB143-057-Q1-E1-G12
Seq. ID
Method
                  BLASTX
                  g266578
NCBI GI
                  210
BLAST score
                  7.0e-17
E value
                  56
Match length
% identity
                  68
                  METALLOTHIONEIN-LIKE PROTEIN 1 >gi_100898_pir__S17560
NCBI Description
                  metallothionein-like protein - maize >gi_236730_bbs_57629
                  (S57628) metallothionein homologue [Zea mays, Peptide, 76
                  aa] [Zea mays] >gi_559536_emb_CAA57676_ (X82186)
                  metallothionein- like protein [Zea mays]
                  >gi 228095 prf 1717215A metallothionein-like protein [Zea
                  mays]
                  290891
Seq. No.
                  LIB143-057-Q1-E1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131772
BLAST score
                  227
                  4.0e-19
E value
                  49
Match length
                  92
% identity
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
NCBI Description
                  >gi 82723 pir A30097 ribosomal protein S14 (clone MCH1) -
                  maize
                  290892
Seq. No.
                  LIB143-057-Q1-E1-H3
Seq. ID
Method
                  BLASTN
                  g1944204
NCBI GI
                  44
BLAST score
E value
                  2.0e-15
                  68
Match length
                  91
% identity
NCBI Description Oryza sativa mRNA for RicMT, complete cds
                  290893
Seq. No.
                  LIB143-057-Q1-E1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g169755
                   206
BLAST score
E value
                   2.0e-16
Match length
                   61
                   64
% identity
                  (M24287) alpha-amylase (EC 3.2.1.1) [Oryza sativa]
NCBI Description
                   290894
Seq. No.
Seq. ID
                  LIB143-058-Q1-E1-G6
Method
                  BLASTX
NCBI GI
                   q3135543
BLAST score
                   448
E value
                   1.0e-44
```

% identity

NCBI Description

58



```
(AF062393) aquaporin [Oryza sativa]
NCBI Description
                  290895
Seq. No.
                  LIB143-058-Q1-E1-G7
Seq. ID
                  BLASTX
Method
                  g1709563
NCBI GI
BLAST score
                  139
                  9.0e-09
E value
                  53
Match length
                  57
% identity
                  PHENYLALANINE AMMONIA-LYASE >gi_2130081_pir__$66313
NCBI Description
                  phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
                  >gi 871494 emb CAA61198 (X87946) phenylalanine
                  ammonia-lyase [Oryza sativa]
                  290896
Seq. No.
                  LIB143-059-Q1-E1-B10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q22458
BLAST score
                  60
                  1.0e-25
E value
                  80
Match length
                  94
% identity
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)
                  290897
Seq. No.
                  LIB143-059-Q1-E1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1408222
BLAST score
                  174
                  1.0e-12
E value
Match length
                  88
                   47
% identity
                  (U60764) pathogenesis-related protein [Sorghum bicolor]
NCBI Description
                   290898
Seq. No.
Seq. ID
                  LIB143-059-Q1-E1-C11
Method
                  BLASTX
NCBI GI
                   q1346559
BLAST score
                   417
E value
                   5.0e-41
Match length
                   100
                   73
% identity
NCBI Description
                  DNA-BINDING PROTEIN MNB1A >gi 2130126 pir S66358
                   DNA-binding protein MNB1a - maize >gi 517258 emb CAA46875
                   (X66076) DNA-binding protein [Zea mays]
Seq. No.
                   290899
                   LIB143-059-Q1-E1-E4
Seq. ID
Method
                  BLASTX
                   q1408222
NCBI GI
                   261
BLAST score
                   8.0e-23
E value
                   93
Match length
```

(U60764) pathogenesis-related protein [Sorghum bicolor]

Seq. No.

Seq. ID

290905

LIB143-060-Q1-E1-D5



```
290900
Seq. No.
Seq. ID
                   LIB143-059-Q1-E1-F4
Method
                   BLASTX
NCBI GI
                   q3004950
BLAST score
                   226
                   5.0e-19
E value
Match length
                   58
                   79
% identity
NCBI Description
                   (AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays]
                   290901
Seq. No.
Seq. ID
                   LIB143-059-Q1-E1-G1
Method
                   BLASTN
                   g22263
NCBI GI
BLAST score
                   124
E value
                   3.0e-63
Match length
                   212
                   90
% identity
NCBI Description Z.mays Ds insertion element
                   290902
Seq. No.
                   LIB143-060-Q1-E1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2119187
BLAST score
                   356
E value
                   5.0e-34
Match length
                   92
                   77
% identity
                   transmembrane protein, glucose starvation-induced - maize
NCBI Description
                   >gi 575731 emb CAA57955 (X82633) transmembrane protein
                   [Zea mays]
Seq. No.
                   290903
Seq. ID
                   LIB143-060-Q1-E1-A7
Method
                   BLASTX
NCBI GI
                   g134613
BLAST score
                   292
E value
                   2.0e-26
Match length
                   69
% identity
                   81
                   SUPEROXIDE DISMUTASE-2 (CU-ZN) >gi_82727_pir_A29077 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 2 - maize
NCBI Description
                   >gi_168620 (M54936) superoxide dismutase 2 [Zea mays]
                   >gi_168622 (M15175) SOD2 protein [Zea mays]
Seq. No.
                   290904
Seq. ID
                   LIB143-060-Q1-E1-B2
Method
                   BLASTN
NCBI GI
                   q296593
BLAST score
                   56
E value
                   1.0e-22
Match length
                   76
% identity
                   93
NCBI Description H. vulgare pZE40 gene
```

% identity

54

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A STATE OF THE PARTY OF THE PAR
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```
BLASTX
Method
                  g4582450
NCBI GI
                  170
BLAST score
                  4.0e-12
E value
                  91
Match length
                  46
% identity
                  (AC007071) putative APG protein [Arabidopsis thaliana]
NCBI Description
                  290906
Seq. No.
                  LIB143-060-Q1-E1-F12
Seq. ID
Method
                  BLASTX
                  g1292710
NCBI GI
BLAST score
                  208
                  1.0e-16
E value
Match length
                  56
% identity
                  73
                  (X97558) calmodulin-1 [Capsicum annuum]
NCBI Description
                  290907
Seq. No.
                  LIB143-060-Q1-E1-H11
Seq. ID
Method
                  BLASTX
                  g729771
NCBI GI
                  193
BLAST score
                   5.0e-15
E value
                  97
Match length
                   47
% identity
NCBI Description HEAT SHOCK PROTEIN
                   290908
Seq. No.
                   LIB143-060-Q1-E1-H9
Seq. ID
Method
                  BLASTX
                   g4309969
NCBI GI
BLAST score
                   162
                   4.0e-11
E value
Match length
                   59
                   51
% identity
                  (AC002983) putative phosphoglyceride transfer protein
NCBI Description
                   [Arabidopsis thaliana]
                   290909
Seq. No.
                   LIB143-061-Q1-E1-A10
Seq. ID
Method
                   BLASTX
                   g4539009
NCBI GI
                   299
BLAST score
E value
                   3.0e-27
Match length
                   116
% identity
                   51
                  (AL049481) putative protein [Arabidopsis thaliana]
NCBI Description
                   290910
Seq. No.
Seq. ID
                   LIB143-061-Q1-E1-A11
Method
                   BLASTX
NCBI GI
                   g461929
BLAST score
                   146
                   2.0e-14
E value
Match length
                   83
```



NCBI Description PROBABLE TONOPLAST INTRINSIC PROTEIN DIP >qi 1076688 pir S51781 integral membrane protein - garden snapdragon >gi_414088_emb_CAA49854_ (X70417) integral membrane protein [Antirrhinum majus] 290911 Seq. No. LIB143-061-Q1-E1-A6 Seq. ID Method BLASTX NCBI GI g67155 BLAST score 152 E value 4.0e-10 Match length 91 % identity 46 pyruvate, orthophosphate dikinase (EC 2.7.9.1) precursor -NCBI Description maize 290912 Seq. No. LIB143-061-Q1-E1-B12 Seq. ID Method BLASTX NCBI GI q3377509 BLAST score 448 E value 2.0e-46 Match length 115 86 % identity (AF056027) auxin transport protein REH1 [Oryza sativa] NCBI Description 290913 Seq. No. Seq. ID LIB143-061-Q1-E1-H10 Method BLASTX g4163997 NCBI GI BLAST score 574 E value 2.0e-59 Match length 127 % identity 80 (AF087483) alpha-xylosidase precursor [Arabidopsis NCBI Description thaliana] 290914 Seq. No. LIB143-061-Q1-E1-H11 Seq. ID BLASTX Method g1076797 NCBI GI BLAST score 233 1.0e-19 E value 68 Match length 69 % identity cysteine proteinase inhibitor precursor - maize NCBI Description >gi_809608_emb_CAA60610_ (X87126) cysteine proteinase inhibitor [Zea mays] 290915 Seq. No.

Seq. ID LIB143-061-Q1-E1-H12

Method BLASTX
NCBI GI g1076797
BLAST score 291
E value 8.0e-27
Match length 70
% identity 79



cysteine proteinase inhibitor precursor - maize NCBI Description >gi_809608_emb_CAA60610_ (X87126) cysteine proteinase inhibitor [Zea mays] 290916 Seq. No. LIB143-061-Q1-E1-H4 Seq. ID BLASTX Method g4191782 NCBI GI 150 BLAST score 7.0e-10 E value 73 Match length 42 % identity (AC005917) WD-40 repeat protein [Arabidopsis thaliana] NCBI Description 290917 Seq. No. LIB143-062-Q1-E1-B6 Seq. ID BLASTX Method g3024122 NCBI GI 276 BLAST score 8.0e-25 E value 85 Match length 66 % identity S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa] 290918 Seq. No. LIB143-062-Q1-E1-E4 Seq. ID BLASTX Method g2511541 NCBI GI BLAST score 321 8.0e-30 E value 73 Match length 84 % identity (AF020787) DNA-binding protein GBP16 [Oryza sativa] NCBI Description 290919 Seq. No. LIB143-062-Q1-E1-F4 Seq. ID Method BLASTX NCBI GI g286124 231 BLAST score 8.0e-22 E value 79 Match length 72 % identity NCBI Description (D14577) glutamine synthetase [Zea mays]

290920 Seq. No.

LIB143-062-Q1-E1-F7 Seq. ID

Method BLASTX q3914423 NCBI GI BLAST score 315 4.0e-29 E value 79 Match length % identity 75

NCBI Description PROFILIN 4 >gi_2642324 (AF032370) profilin [Zea mays]

290921 Seq. No.

Method

NCBI GI

BLASTX

g1707017



```
Seq. ID
                  LIB143-062-Q1-E1-H4
Method
                  BLASTX
                  g100883
NCBI GI
BLAST score
                  340
                  4.0e-32
E value
Match length
                  86
                  78
% identity
NCBI Description
                  heat shock protein 17.2 - maize >gi 22335 emb CAA46641
                  (X65725) heat shock protein 17.2 [Zea mays]
                  290922
Seq. No.
                  LIB143-063-Q1-E1-A4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g296593
                  56
BLAST score
                  1.0e-22
E value
Match length
                  76
                  93
% identity
NCBI Description H. vulgare pZE40 gene
                  290923
Seq. No.
                  LIB143-063-Q1-E1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2642441
BLAST score
                  208
                  1.0e-16
E value
Match length
                  103
% identity
                  45
                  (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  290924
                  LIB143-063-Q1-E1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g125065
BLAST score
                  232
                  2.0e-19
E value
                  85
Match length
% identity
                  60
                  60 KD JASMONATE-INDUCED PROTEIN >gi 419795 pir S25092
NCBI Description
                  jasmonate-induced protein - barley >gi 19011 emb CAA47017
                   (X66376) jasmonate-induced protein [Hordeum vulgare]
Seq. No.
                  290925
                  LIB143-063-Q1-E1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g399854
BLAST score
                  349
                  5.0e-33
E value
Match length
                  100
% identity
                  74
NCBI Description
                  HISTONE H2B.2 >gi_283042_pir__S28049 histone H2B - maize
                  >gi 22325 emb CAA40565 (X57313) H2B histone [Zea mays]
Seq. No.
                  290926
Seq. ID
                  LIB143-063-Q1-E1-G1
```

NCBI Description



```
BLAST score
E value
                   5.0e-10
Match length
                   40
                   72
% identity
                  (U78721) RNA helicase isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  290927
                  LIB143-063-Q1-E1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2196671
BLAST score
                  109
E value
                  2.0e-54
Match length
                  175
% identity
                   92
NCBI Description Z.mays mRNA for HMG protein
Seq. No.
                   290928
Seq. ID
                  LIB143-063-Q1-E1-G5
Method
                  BLASTX
                   g1707017
NCBI GI
BLAST score
                   146
E value
                   8.0e-10
Match length
                   58
% identity
                   52
NCBI Description (U78721) RNA helicase isolog [Arabidopsis thaliana]
                   290929
Seq. No.
Seq. ID
                  LIB143-063-Q1-E1-H4
Method
                  BLASTX
NCBI GI
                   g3747046
BLAST score
                   321
                   7.0e-30
E value
Match length
                   69
% identity
                   90
                  (AF093538) voltage-dependent anion-selective channel
NCBI Description
                   protein [Zea mays]
Seq. No.
                   290930
Seq. ID
                   LIB143-064-Q1-E1-B6
Method
                   BLASTX
NCBI GI
                   q4454452
                   277
BLAST score
E value
                   1.0e-24
Match length
                   138
% identity
                   43
NCBI Description
                  (AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.
                   290931
                   LIB143-064-Q1-E1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2493494
BLAST score
                   189
E value
                   2.0e-14
                   53
Match length
% identity
                   66
```

40455

SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2)

>gi_619351_bbs_153537 CP-MII.2=serine carboxypeptidase



[Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436 aa]

Seq. No. 290932
Seq. ID LIB143

q. ID LIB143-064-Q1-E1-F12

Method BLASTX
NCBI GI 94539315
BLAST score 278
E value 1.0e-24
Match length 61
% identity 79

NCBI Description (AL035679) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 290933

Seq. ID LIB143-064-Q1-E1-F2

Method BLASTX
NCBI GI g2499708
BLAST score 167
E value 1.0e-11
Match length 36
% identity 92

NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)

(PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)

>gi_1020409_dbj_BAA11135_ (D73410) phospholipase D [Zea

mays]

Seq. No. 290934

Seq. ID LIB143-064-Q1-E1-F6

Method BLASTX
NCBI GI g2497259
BLAST score 384
E value 4.0e-37
Match length 130
% identity 65

NCBI Description ISOCITRATE DEHYDROGENASE (NADP), CHLOROPLAST PRECURSOR

(OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC ICDH)

(IDP) >gi_166386 (M93672) isocitrate dehydrogenase

[Medicago sativa]

Seq. No. 290935

Seq. ID LIB143-065-Q1-E1-A6

Method BLASTX
NCBI GI g2668742
BLAST score 396
E value 1.0e-38
Match length 85
% identity 91

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 290936

Seq. ID LIB143-065-Q1-E1-A7

Method BLASTX
NCBI GI g1076678
BLAST score 276
E value 4.0e-25
Match length 71

Match length

% identity

124 94

NCBI Description Zea mays lipase (LIP) mRNA, complete cds



```
% identity
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)
                  290937
Seq. No.
                  LIB143-065-Q1-E1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82733
BLAST score
                  463
                  2.0e-46
E value
                  122
Match length
                  80
% identity
                  ubiquitin fusion protein UBF9 - maize >gi_168651 (M68937)
NCBI Description
                  ubiquitin fusion protein [Zea mays] >gi_902527 (U29161)
                  ubiquitin fusion protein [Zea mays]
                  >gi 1589388 prf 2211240B ubiquitin fusion protein [Zea
                  mays]
                  290938
Seq. No.
                  LIB143-065-Q1-E1-B11
Seq. ID
Method
                  BLASTX
                  g3135543
NCBI GI
                  474
BLAST score
                  1.0e-47
E value
                  116
Match length
% identity
                  78
NCBI Description (AF062393) aquaporin [Oryza sativa]
                  290939
Seq. No.
                  LIB143-065-Q1-E1-B12
Seq. ID
                  BLASTX
Method
                  g3135543
NCBI GI
                  288
BLAST score
                  6.0e-26
E value
                  111
Match length
                  52
% identity
NCBI Description (AF062393) aquaporin [Oryza sativa]
Seq. No.
                  290940
                  LIB143-065-Q1-E1-E11
Seq. ID
Method
                  BLASTN
                  g3821780
NCBI GI
BLAST score
                  36
E value
                   9.0e-11
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  290941
Seq. No.
                  LIB143-065-Q1-E1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g532622
BLAST score
                   45
                   4.0e-16
E value
```



```
290942
Seq. No.
                  LIB143-065-Q1-E1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2924772
BLAST score
                  392
                  5.0e-38
E value
Match length
                  112
                  70
% identity
                  (AC002334) unknown protein [Arabidopsis thaliana]
NCBI Description
                  290943
Seq. No.
                  LIB143-065-Q1-E1-G8
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2286150
BLAST score
                  269
E value
                  1.0e-150
Match length
                  269
                  100
% identity
                  Zea mays translation initiation factor (eIF-4A) mRNA,
NCBI Description
                  complete cds
                  290944
Seq. No.
                  LIB143-065-Q1-E1-H4
Seq. ID
                  BLASTN
Method
                  g426441
NCBI GI
BLAST score
                  46
                  1.0e-16
E value
Match length
                  94
                  87
% identity
                  Rice mRNA for thioredoxin h, complete cds
NCBI Description
                  290945
Seq. No.
                  LIB143-066-Q1-E1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g13920
BLAST score
                  43
                  3.0e-15
E value
Match length
                  133
% identity
                  84
                  Z.mays NCS3 mutant DNA for mitochondrial L16-like and
NCBI Description
                  S3-like ribosomal proteins
                  290946
Seq. No.
                  LIB143-066-Q1-E1-D10
Seq. ID
Method
                  BLASTN
                  g1944204
NCBI GI
BLAST score
                  36
E value
                  9.0e-11
Match length
                  56
% identity
                  91
NCBI Description Oryza sativa mRNA for RicMT, complete cds
```

290947 Seq. No.

LIB143-066-Q1-E1-D5 Seq. ID

Method BLASTX NCBI GI g4337207 BLAST score 144



E value 2.0e-09
Match length 81
% identity 43
NCBI Description (AC0064
thalian
C2H2 zi

I Description (AC006403) putative zinc-finger protein [Arabidopsis thaliana] >gi_4585205_gb_AAD25324.1_AF095588_1 (AF095588) C2H2 zinc finger protein FZF [Arabidopsis thaliana]

Seq. No. 290948

Seq. ID LIB143-066-Q1-E1-E7

Method BLASTX
NCBI GI g567893
BLAST score 141
E value 4.0e-09
Match length 63
% identity 49

NCBI Description (L37382) beta-galactosidase-complementation protein

[Cloning vector]

Seq. No. 290949

Seq. ID LIB143-066-Q1-E1-E9

Method BLASTX
NCBI GI g2493650
BLAST score 149
E value 5.0e-17
Match length 109
% identity 57

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD

CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)

>gi_1167858_emb_CAA93139_ (Z68903) chaperonin [Secale

cereale]

Seq. No. 290950

Seq. ID LIB143-067-Q1-E1-B12

Method BLASTN
NCBI GI g296593
BLAST score 38
E value 5.0e-12
Match length 65
% identity 92

NCBI Description H. vulgare pZE40 gene

Seq. No. 290951

Seq. ID LIB143-067-Q1-E1-B9

Method BLASTN
NCBI GI g13920
BLAST score 120
E value 2.0e-61
Match length 154
% identity 95

NCBI Description Z.mays NCS3 mutant DNA for mitochondrial L16-like and

S3-like ribosomal proteins

Seq. No. 290952

Seq. ID LIB143-067-Q1-E1-C5

Method BLASTN NCBI GI g1491773

BLAST score 49

```
1.0e-18
E value
Match length
                  157
% identity
                  83
NCBI Description Z.mays mRNA for cysteine proteinase, See1
                  290953
Seq. No.
                  LIB143-067-Q1-E1-D10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1944204
BLAST score
                  44
                  1.0e-15
E value
Match length
                  68
                  91
% identity
NCBI Description Oryza sativa mRNA for RicMT, complete cds
                  290954
Seq. No.
                  LIB143-067-Q1-E1-E9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1944204
BLAST score
                  52
                  2.0e-20
E value
Match length
                  68
```

% identity 94
NCBI Description Oryza sativa mRNA for RicMT, complete cds

 Seq. No.
 290955

 Seq. ID
 LIB143-067-Q1-E1-F4

 Method
 BLASTN

 NCBI GI
 g2062705

 BLAST score
 39

 E value
 1 0e-12

E value 1.0e-12 Match length 51 % identity 68

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

 Seq. No.
 290956

 Seq. ID
 LIB143-067-Q1-E1-H1

 Method
 BLASTX

 NCBI GI
 g4512666

 BLAST score
 392

 E value
 5.0e-38

E value 5.0e-Match length 124 % identity 60

NCBI Description (AC006931) putative mei2 protein [Arabidopsis thaliana]

Seq. No. 290957

Seq. ID LIB143-068-Q1-E1-B11 Method BLASTN

NCBI GI g1870202
BLAST score 36
E value 9.0e-11
Match length 64
% identity 89

NCBI Description Z.mays cyp71c3 gene

Seq. No. 290958

Seq. ID LIB143-068-Q1-E1-D7



```
Method
                  BLASTN
                  g440170
NCBI GI
BLAST score
                  172
                  5.0e-92
E value
                  228
Match length
                  94
% identity
NCBI Description Z.mays (C6000237) trpA gene
                  290959
Seq. No.
                  LIB143-068-Q1-E1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g129916
BLAST score
                  346
E value
                  7.0e-33
Match length
                  74
                  93
% identity
NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY
                  phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                  >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                  (AA 1 - 401) [Triticum aestivum]
                  290960
Seq. No.
                  LIB148-001-Q1-E1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3461822
                  418
BLAST score
                  4.0e-41
E value
                  134
Match length
                  57
% identity
NCBI Description (AC004138) hypothetical protein [Arabidopsis thaliana]
                  290961
Seq. No.
                  LIB148-002-Q1-E1-A7
Seq. ID
Method
                  BLASTX
                  g1491638
NCBI GI
BLAST score
                  296
                  8.0e-27
E value
Match length
                  105
% identity
                  55
NCBI Description (X99922) male sterility protein 2 [Brassica napus]
                  290962
Seq. No.
                  LIB148-002-Q1-E1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q484531
                  184
BLAST score
E value
                  7.0e-14
Match length
                  44
% identity
NCBI Description H3.3 like histone MH321 - mouse
                  290963
Seq. No.
                  LIB148-002-Q1-E1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g600117
BLAST score
                  348
```

40461

0.0e+00

E value



```
Match length
% identity
                  60
NCBI Description Z.mays (B73) gene for extensin-like protein
                  290964
Seq. No.
                  LIB148-002-Q1-E1-D2
Seq. ID
Method
                  BLASTX
                  g629852
NCBI GI
BLAST score
                  430
                  4.0e-43
E value
Match length
                  122
                  77
% identity
NCBI Description
                  polygalacturonase - maize >gi_288367_emb_CAA46680_ (X65845)
                  polygalacturonase [Zea mays]
                  290965
Seq. No.
                  LIB148-002-Q1-E1-D7
Seq. ID
Method
                  BLASTX
                  g2459424
NCBI GI
BLAST score
                  203
                  2.0e-23
E value
                  114
Match length
                  50
% identity
                  (AC002332) unknown protein [Arabidopsis thaliana]
NCBI Description
                  290966
Seq. No.
Seq. ID
                  LIB148-002-Q1-E1-E2
Method
                  BLASTN
                  g309569
NCBI GI
BLAST score
                  71
                  1.0e-31
E value
                  123
Match length
                  45
% identity
NCBI Description
                  Zea mays transcriptional activator for anthocyanin
                  synthesis gene, complete cds
Seq. No.
                  290967
Seq. ID
                  LIB148-002-Q1-E1-F12
Method
                  BLASTX
NCBI GI
                  q1076820
BLAST score
                  173
E value
                  2.0e-12
Match length
                  37
% identity
                  95
NCBI Description phosphoglycerate mutase (EC 5.4.2.1) - maize
Seq. No.
                  290968
Seq. ID
                  LIB148-003-Q1-E1-B8
Method
                  BLASTN
NCBI GI
                  g22155
BLAST score
                   44
                  7.0e-16
E value
Match length
                  92
                  87
% identity
```

40462

NCBI Description Z.mays mRNA for alpha-tubulin

290969

Seq. No.

Match length

72



```
LIB148-004-Q1-E1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2811224
                  272
BLAST score
                  5.0e-24
E value
Match length
                  65
                  78
% identity
                  (AF042668) fimbrin 1 [Arabidopsis thaliana]
NCBI Description
                  290970
Seq. No.
                  LIB148-004-Q1-E1-C2
Seq. ID
Method
                  BLASTX
                  g2245138
NCBI GI
BLAST score
                  144
E value
                  5.0e-09
Match length
                  59
% identity
                  51
                  (Z97344) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  290971
Seq. No.
                  LIB148-004-Q1-E1-E3
Seq. ID
                  BLASTX
Method
                  g2239262
NCBI GI
BLAST score
                  233
                  2.0e-19
E value
Match length
                  72
% identity
                  61
                  (Y13285) pectin methylesterase-like protein [Zea mays]
NCBI Description
                  290972
Seq. No.
                  LIB148-005-Q1-E1-A1
Seq. ID
Method
                  BLASTX
                  g3236246
NCBI GI
BLAST score
                  160
E value
                  6.0e-11
                  74
Match length
                  42
% identity
NCBI Description
                  (AC004684) putative expansin protein [Arabidopsis thaliana]
Seq. No.
                  290973
                  LIB148-005-Q1-E1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g464470
                  208
BLAST score
E value
                  3.0e-19
Match length
                  64
                  81
% identity
                  PROFILIN 3 >gi_422033_pir__S35798 profilin 3 - maize
NCBI Description
                  >gi 313142 emb CAA51720 (X73281) profilin 3 [Zea mays]
Seq. No.
                  290974
                  LIB148-005-Q1-E1-A9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g416731
BLAST score
                  140
E value
                  8.0e-17
```

NCBI Description



```
% identity
                  POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi 82655 pir JQ1107
NCBI Description
                  18.3K protein precursor, pollen - maize
                  >gi 255569 bbs 113677 (S44171) pollen specific protein [Zea
                  mays=corn, Peptide, 170 aa] [Zea mays]
                  >gi_1588669_prf__2209273A Zm13 [Zea mays]
                  290975
Seq. No.
                  LIB148-005-Q1-E1-B3
Seq. ID
                  BLASTX
Method
                  q3212877
NCBI GI
                  333
BLAST score
                  3.0e-31
E value
                  81
Match length
% identity
NCBI Description (AC004005) Lea-like protein [Arabidopsis thaliana]
                  290976
Seq. No.
                LIB148-005-Q1-E1-D7
Seq. ID
                  BLASTX
Method
                  g2290681
NCBI GI
                  152
BLAST score
                  6.0e-10
E value
                  48
Match length
% identity
NCBI Description (AF000135) acidic cellulase [Citrus sinensis]
                  290977
Seq. No.
                  LIB148-005-Q1-E1-F9
Seq. ID
                  BLASTX
Method
                   q3402722
NCBI GI
                   163
BLAST score
                   1.0e-11
E value
                   68
Match length
                   47
% identity
                  (AC004261) CPDK-related protein [Arabidopsis thaliana]
NCBI Description
                   290978
Seq. No.
                   LIB148-005-Q1-E1-H2
Seq. ID
                   BLASTX
Method
                   g2760326
NCBI GI
BLAST score
                   175
E value
                   1.0e-12
Match length
                   73
                   49
 % identity
                   (AC002130) F1N21.11 [Arabidopsis thaliana]
NCBI Description
                   290979
 Seq. No.
                   LIB148-006-Q1-E1-A3
 Seq. ID
                   BLASTX
 Method
                   q118011
 NCBI GI
                   260
 BLAST score
 E value
                   6.0e-23
 Match length
                   67
                   70
 % identity
                  CYTOCHROME C >gi 625189 pir__CCRZ cytochrome c - rice
```

40464

>gi 169786 (M63704) cytochrome c [Oryza sativa]

NCBI Description



>gi 218249 dbj_BAA02159_ (D12634) 'cytochrome C' [Oryza

```
290980
Seq. No.
                  LIB148-006-Q1-E1-B1
Seq. ID
                  BLASTN
Method
                  g313141
NCBI GI
BLAST score
                  38
                  1.0e-12
E value
                  54
Match length
% identity
                  93
NCBI Description Z.mays ZmPRO3 mRNA for profilin
                   290981
Seq. No.
Seq. ID
                  LIB148-006-Q1-E1-B6
Method
                  BLASTX
                   q128592
NCBI GI
BLAST score
                   200
                   1.0e-15
E value
                   71
Match length
% identity
                   POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR
NCBI Description
                   >gi 82190_pir__S22495 pollen-specific protein precursor -
                   common tobacco >gi 19902_emb_CAA43454_ (X61146) pollen
                   specific protein [Nicotiana tabacum]
Seq. No.
                   290982
                   LIB148-006-Q1-E1-B7
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2239261
BLAST score
                   192
                   1.0e-104
E value
Match length
                   411
                   87
% identity
NCBI Description Zea Mays mRNA for pectin methylesterase-like protein
                   290983
Seq. No.
                   LIB148-006-Q1-E1-D11
Seq. ID
                   BLASTN
Method
                   g1808693
NCBI GI
                   40
BLAST score
                   2.0e-13
E value
                   52
Match length
                   94
% identity
NCBI Description S.stapfianus pSD.34 mRNA
                   290984
Seq. No.
                   LIB148-006-Q1-E1-D4
Seq. ID
                   BLASTX
Method
                   g629852
NCBI GI
                   165
BLAST score
E value
                   1.0e-11
                   68
Match length
                   49
 % identity
                   polygalacturonase - maize >gi_288367_emb_CAA46680_ (X65845)
```

polygalacturonase [Zea mays]



```
290985
Seq. No.
                  LIB148-006-Q1-E1-E10
Seq. ID
                  BLASTX
Method
                  q4006835
NCBI GI
BLAST score
                  233
E value
                  2.0e-19
                  118
Match length
                  10
% identity
NCBI Description (AC005970) hypothetical protein [Arabidopsis thaliana]
                  290986
Seq. No.
                  LIB148-006-Q1-E1-E4
Seq. ID
                  BLASTX
Method
                  q3236246
NCBI GI
                  237
BLAST score
                  8.0e-20
E value
Match length
                  83
% identity
NCBI Description (AC004684) putative expansin protein [Arabidopsis thaliana]
                  290987
Seq. No.
Seq. ID
                  LIB148-006-Q1-E1-G9
Method
                  BLASTX
                  q283049
NCBI GI
BLAST score
                  190
                  6.0e-15
E value
Match length
                  63
% identity
NCBI Description polygalacturonase (EC 3.2.1.15) precursor (clone W2247) -
                  maize (fragment) >gi_481079_pir__S37718 polygalacturonase -
                  maize >qi 22426 emb CAA44248 (X62384) polygalacturonase
                   [Zea mays] >gi_287830_emb_CAA47234 (X66692)
                   polygalacturonase [Zea mays]
Seq. No.
                   290988
                  LIB148-007-Q1-E1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3193298
BLAST score
                   147
                   3.0e-09
E value
Match length
                   89
% identity
                   (AF069298) T14P8.17 gene product [Arabidopsis thaliana]
NCBI Description
                   290989
Seq. No.
                   LIB148-007-Q1-E1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4581116
BLAST score
                   431
                   1.0e-42
E value
                   120
Match length
% identity
                   63
                   (AC005825) putative beta-galactosidase [Arabidopsis
NCBI Description
                   thaliana]
```

40466

290990

LIB148-007-Q1-E1-E2

Seq. No. Seq. ID

NCBI GI



```
BLASTN
Method
                  q4416300
NCBI GI
BLAST score
                  40
                  4.0e-13
E value
Match length
                  116
% identity
                   42
                  Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                  region, complete sequence
                  290991
Seq. No.
Seq. ID
                  LIB148-007-Q1-E1-E6
                  BLASTX
Method
                  g585551
NCBI GI
                   219
BLAST score
                   4.0e-37
E value
                   97
Match length
% identity
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                   >gi 629798 pir S43330 nucleoside-diphosphate kinase (EC
                   2.7.4.6) - rice >gi 303849_dbj_BAA03798_ (D16292)
                   nucleoside diphosphate kinase [Oryza sativa]
                   290992
Seq. No.
                   LIB148-007-Q1-E1-F11
Seq. ID
                   BLASTX
Method
                   q3297815
NCBI GI
BLAST score
                   290
                   1.0e-29
E value
                   89
Match length
% identity
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]
Seq. No.
                   290993
                   LIB148-007-Q1-E1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2459424
BLAST score
                   176
E value
                   9.0e-13
Match length
                   106
% identity
                  (AC002332) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   290994
                   LIB148-007-Q1-E1-G7
Seq. ID
                   BLASTX
Method
                   g2506328
NCBI GI
                   293
BLAST score
                   3.0e - 35
E value
                   112
Match length
% identity
                   CYTOCHROME C >gi_1235929 (L77113) cytochrome c [Helianthus
NCBI Description
                   annuus]
                   290995
Seq. No.
                   LIB148-007-Q1-E1-H9
Seq. ID
                   BLASTX
Method
```

40467

g3386614



```
BLAST score
                  2.0e-18
E value
                  101
Match length
                  47
% identity
NCBI Description (AC004665) putative transcription factor SF3 [Arabidopsis
                  thaliana]
                  290996
Seq. No.
                  LIB148-008-Q1-E1-D4
Seq. ID
                  BLASTX
Method
                  q481432
NCBI GI
                  200
BLAST score
                  1.0e-15
E value
                  85
Match length
                  41
% identity
NCBI Description allergen Phl pI - common timothy >gi_1582250_prf__2118271A
                  allergen PhI p I [Phleum pratense]
                  290997
Seq. No.
                  LIB148-008-Q1-E1-D5
Seq. ID
                  BLASTN
Method
                  g22458
NCBI GI
                  156
BLAST score
                  2.0e-82
E value
                  261
Match length
                  95
% identity
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)
                  290998
Seq. No.
                  LIB148-009-Q1-E1-A11
Seq. ID
                  BLASTX
Method
                  q629852
NCBI GI
BLAST score
                  368
                  2.0e-35
E value
                  108
Match length
% identity
NCBI Description polygalacturonase - maize >gi_288367_emb_CAA46680_ (X65845)
                  polygalacturonase [Zea mays]
Seq. No.
                   290999
                   LIB148-009-Q1-E1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3036807
BLAST score
                   430
                   1.0e-42
E value
                   126
Match length
% identity
NCBI Description (AL022373) putative protein [Arabidopsis thaliana]
                   291000
Seq. No.
                   LIB148-009-Q1-E1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4417291
BLAST score
                   271
                   7.0e-24
E value
                   97
Match length
                   55
 % identity
```



```
NCBI Description (AC007019) hypothetical protein [Arabidopsis thaliana]
                  291001
Seq. No.
Seq. ID
                  LIB148-010-Q1-E1-D4
                  BLASTN
Method
NCBI GI
                  q1314382
                  121
BLAST score
                   1.0e-61
E value
                   133
Match length
                   98
% identity
NCBI Description Tripsacum laxum de Wet 3766 ITS1, 5.8S ribosomal RNA, ITS2
                   291002
Seq. No.
                   LIB148-010-Q1-E1-F2
Seq. ID
                   BLASTN
Method
                   g3341647
NCBI GI
BLAST score
                   59
                   1.0e-24
E value
                   99
Match length
                   90
% identity
NCBI Description Zea mays Ama gene encoding single-subunit RNA polymerase
                   291003
Seq. No.
                   LIB148-011-Q1-E1-A3
Seq. ID
                   BLASTX
Method
                   g626029
NCBI GI
                   171
BLAST score
                   3.0e-12
E value
                   48
Match length
                   69
% identity
                   pollen allergen Lol p XI - perennial ryegrass
NCBI Description
                   >gi_1582249_prf__2118270A allergen Lol p XI [Lolium
                   perenne]
                   291004
Seq. No.
                   LIB148-011-Q1-E1-B1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1519253
                   322
BLAST score
                   4.0e-30
E value
                   71
Match length
 % identity
                   (U65958) GF14-d protein [Oryza sativa]
 NCBI Description
                   291005
 Seq. No.
                   LIB148-012-Q1-E1-B12
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q422032
                    309
 BLAST score
                    2.0e-28
 E value
                    98
 Match length
                    63
 % identity
                   profilin 2 - maize >gi_313140_emb_CAA51719_ (X73280)
 NCBI Description
                   profilin 2 [Zea mays]
```

291006

LIB148-012-Q1-E1-B2

Seq. No.

Seq. ID

E value

Match length

316



```
BLASTX
Method
                  g100638
NCBI GI
BLAST score
                   175
                   1.0e-12
E value
Match length
                   93
                   38
% identity
                  pollen allergen Lol p I precursor (clone 5A) - perennial
NCBI Description
                   ryegrass >gi_168316 (M57474) pollen allergen [Lolium
                  perenne]
                   291007
Seq. No.
                   LIB148-012-Q1-E1-E10
Seq. ID
                   BLASTN
Method
                   g255568
NCBI GI
                   59
BLAST score
E value
                   2.0e-24
Match length
                   83
% identity
                   93
NCBI Description pollen specific protein [Zea mays=corn, mRNA, 943 nt]
                   291008
Seq. No.
                   LIB148-012-Q1-E1-E4
Seq. ID
                   BLASTX
Method
                   g3702323
NCBI GI
BLAST score
                   262
                   9.0e-23
E value
Match length
                   85
% identity
                   (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
                   291009
Seq. No.
                   LIB148-012-Q1-E1-F7
Seq. ID
Method
                   BLASTX
                   g4049353
NCBI GI
BLAST score
                   258
                   2.0e-22
E value
Match length
                   95
% identity
                   52
                   (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
                   291010
Seq. No.
                   LIB148-012-Q1-E1-G7
Seq. ID
Method
                   BLASTX
                   q886130
NCBI GI
                   233
 BLAST score
                   2.0e-19
 E value
                   123
Match length
 % identity
                   41
                   (U28148) putative pectinesterase [Medicago sativa]
 NCBI Description
                   291011
 Seq. No.
                   LIB148-013-Q1-E1-A3
 Seq. ID
 Method
                   BLASTN
                    g3264606
 NCBI GI
                    157
 BLAST score
                    5.0e-83
```



```
% identity
NCBI Description Zea mays shaggy kinase homolog mRNA, partial cds
                  291012
Seq. No.
Seq. ID
                  LIB148-013-Q1-E1-A6
Method
                  BLASTN
NCBI GI
                  g22458
BLAST score
                  192
E value "
                  1.0e-104
                  259
Match length
% identity
                  95
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)
                  291013
Seq. No.
                  LIB148-013-Q1-E1-B3
Seq. ID
Method
                  BLASTX
                  g2529707
NCBI GI
BLAST score
                  241
                  2.0e-20
E value
Match length
                  102
                  43
% identity
NCBI Description (AF001434) Hpast [Homo sapiens]
                  291014
Seq. No.
                  LIB148-013-Q1-E1-C10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4567310
BLAST score
                  248
                  3.0e-21
E value
Match length
                  72
% identity
                  72
NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]
                  291015
Sea. No.
                  LIB148-014-Q1-E1-A4
Seq. ID
                  BLASTX
Method
                  g548492
NCBI GI
                  153
BLAST score
                  5.0e-10
E value
                  121
Match length
% identity
                  26
                 EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                   (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi 629853 pir S30066 polygalacturonase - maize
                  >qi 288379 emb CAA45751 (X64408) polygalacturonase [Zea
                  mays]
                  291016
Seq. No.
                  LIB148-014-Q1-E1-G9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g416731
BLAST score
                  259
```

2.0e-22 E value Match length 74 % identity 68

NCBI Description POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi 82655 pir JQ1107

18.3K protein precursor, pollen - maize



>gi 255569 bbs 113677 (S44171) pollen specific protein [Zea mays=corn, Peptide, 170 aa] [Zea mays] >gi_1588669_prf__2209273A Zm13 [Zea mays]

Seq. No. 291017 LIB148-015-Q1-E1-B6 Seq. ID Method BLASTX NCBI GI q425194 BLAST score 458 E value 8.0e-46 Match length 130

% identity

(L26243) heat shock protein [Spinacia oleracea] >gi 2660772 NCBI Description

(AF034618) cytosolic heat shock 70 protein [Spinacia

oleracea]

291018 Seq. No.

Seq. ID LIB148-015-Q1-E1-E2

Method BLASTX NCBI GI g2961378 BLAST score 362 E value 2.0e-36 121 Match length % identity

NCBI Description (AL022141) putative protein [Arabidopsis thaliana]

291019 Seq. No.

LIB148-015-Q1-E1-H9 Seq. ID

Method BLASTX g4587567 NCBI GI BLAST score 173 2.0e-12 E value 79 Match length

% identity 41

NCBI Description (AC006550) F1003.7 [Arabidopsis thaliana]

291020 Seq. No.

LIB148-017-Q1-E1-B1 Seq. ID

BLASTX Method g3850581 NCBI GI BLAST score 215 3.0e-17 E value Match length 70 57 % identity

NCBI Description (AC005278) EST gb N96383 comes from this gene. [Arabidopsis

thaliana]

291021 Seq. No.

LIB148-017-Q1-E1-B7 Seq. ID

Method BLASTX NCBI GI g2827631 BLAST score 351 E value 3.0e-33 Match length 134 % identity

NCBI Description (AL021636) putative protein [Arabidopsis thaliana]



```
291022
Seq. No.
                  LIB148-017-Q1-E1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2459424
BLAST score
                  312
                  1.0e-28
E value
                  109
Match length
                  60
% identity
NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]
Seq. No.
                  291023
                  LIB148-017-Q1-E1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q639722
                  332
BLAST score
E value
                  5.0e-31
                  86
Match length
% identity
                  80
NCBI Description (L27484) calcium-dependent protein kinase [Zea mays]
                  291024
Seq. No.
Seq. ID
                  LIB148-017-Q1-E1-D10
Method
                  BLASTX
NCBI GI
                  g1352460
BLAST score
                  321
E value
                  7.0e-44
Match length
                  106
% identity
                  94
NCBI Description IN2-1 PROTEIN >gi 100896 pir S17743 In2-1 protein - maize
                  >gi_22347_emb_CAA41447_ (X58573) In2-1 [Zea mays]
                  291025
Seq. No.
                  LIB148-017-Q1-E1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2673918
BLAST score
                  180
E value
                  3.0e-13
Match length
                  48
% identity
                  69
NCBI Description (AC002561) unknwon protein [Arabidopsis thaliana]
                  291026
Seq. No.
Seq. ID
                  LIB148-017-Q1-E1-E11
Method
                  BLASTX
NCBI GI
                  q3047085
                  434
BLAST score
E value
                   6.0e-43
Match length
                  142
% identity
NCBI Description (AF058914) No definition line found [Arabidopsis thaliana]
Seq. No.
                  291027
                  LIB148-017-Q1-E1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1332579
```

40473

502

8.0e-58

BLAST score

E value

```
128
Match length
% identity
                 (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
Seq. No.
                  291028
                  LIB148-017-Q1-E1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4204257
BLAST score
                  164
E value
                  6.0e-18
                                               4
Match length
                  112
                  52
% identity
NCBI Description (AC005223) 5493 [Arabidopsis thaliana]
                  291029
Seq. No.
Seq. ID
                  LIB148-018-Q1-E1-D3
Method
                  BLASTN
NCBI GI
                  g293901
BLAST score
                  51
                  6.0e-20
E value
                  67
Match length
% identity
                  96
NCBI Description Zea mays Zea mI gene, complete cds
Seq. No.
                  291030
Seq. ID
                  LIB148-019-Q1-E1-C11
Method
                  BLASTN
NCBI GI
                  g4519188
BLAST score
                  37
                  2.0e-11
E value
Match length
                  133
% identity
                  82
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K21L19, complete sequence
Seq. No.
                  291031
Seg. ID
                  LIB148-019-Q1-E1-C6
Method
                  BLASTX
```

٠٧.

Method BLASTX
NCBI GI g4587513
BLAST score 201
E value 1.0e-15
Match length 123
% identity 37

NCBI Description (AC007060) Contains eukaryotic protein kinase domain

PF_00069. [Arabidopsis thaliana]

Seq. No. 291032

Seq. ID LIB148-019-Q1-E1-E7

Method BLASTX
NCBI GI 94049353
BLAST score 337
E value 1.0e-31
Match length 134
% identity 56

NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

Seq. No. 291033

Method

NCBI GI

BLASTX

g129949



```
Seq. ID
                   LIB148-019-Q1-E1-F4
 Method
                   BLASTX
                   g3702323
 NCBI GI
 BLAST score
                   402
 E value
                   3.0e-39
 Match length
                   127
 % identity
                   61
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
 Seq. No.
                   291034
                   LIB148-019-Q1-E1-F8
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q4490707
 BLAST score
                   366
 E value
                   5.0e-35
                   129
 Match length
                   53
 % identity
 NCBI Description (AL035680) putative protein [Arabidopsis thaliana]
                   291035
 Seq. No.
 Seq. ID
                   LIB148-019-01-E1-H12
 Method
                   BLASTX
 NCBI GI
                   g4580398
 BLAST score
                   286
                   6.0e-26
 E value
 Match length
                   84
 % identity
                   64
 NCBI Description (AC007171) putative protein kinase APK1A [Arabidopsis
                   thaliana]
 Seq. No.
                   291036
 Seq. ID
                   LIB148-020-Q1-E1-A11
 Method
                   BLASTX
 NCBI GI
                   g1174380
 BLAST score
                   618
 E value
                   2.0e-64
                   133
 Match length
                   89
 % identity
 NCBI Description SUPEROXIDE DISMUTASE PRECURSOR (MN)
 Seq. No.
                   291037
                   LIB148-020-Q1-E1-B10
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g1699167
 BLAST score
                   497
                   2.0e-50
 E value
 Match length
                   94
                   99
 % identity
 NCBI Description (S82407) IgG2a heavy chain constant region {CH1-CH3
                   domains, hinge region} [cattle, Holstein-Friesian, A2/A2
                   allotype, peripheral blood leukocytes, Peptide Partial, 326
                   aa] [Bos taurus]
 Seq. No.
                   291038
 Seq. ID
                   LIB148-020-Q1-E1-C10
```



```
BLAST score
                  4.0e-77
E value
Match length
                  144
% identity
                  99
                  BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN)
NCBI Description
                  >gi 89740 pir S06280 decorin precursor - bovine
                  >qi 619 emb CAA68702 (Y00712) precursor polypeptide (AA
                  -30 to 330) [Bos taurus]
                                                                  ž. · ·
Seq. No.
                  291039
                  LIB148-020-Q1-E1-C9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g31176
BLAST score
                  62
                  3.0e-26
E value
Match length
                  94
% identity
                  91
                  H.sapiens alpha-enolase gene for non-neuronal enolase (EC
NCBI Description
                  4.2.1.11) exons 4-12
                  291040
Seq. No.
                  LIB148-020-Q1-E1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3660117
BLAST score
                  317
E value
                  3.0e-29
Match length
                  61
                  98
% identity
                  Structural And Functional Consequences Of Point Mutations
NCBI Description
                  Of Variants A And B Of Bovine Beta-Lactoglobulin
                  >gi_4388846_pdb_1B00_ Bovine Beta-Lactoglobulin Complexed
                  With Palmitate , Lattice Z
                  291041
Seq. No.
                  LIB148-020-Q1-E1-D9
Seq. ID
                  BLASTN
Method
                  g3483581
NCBI GI
                  37
BLAST score
                  3.0e-11
E value
                  68
Match length
% identity
                  88
NCBI Description Homo sapiens full length insert cDNA clone ZD20E11
                  291042
Seq. No.
                  LIB148-020-Q1-E1-E12
Seq. ID
                  BLASTN
Method
NCBI GI
                   g182734
                   332
BLAST score
                   0.0e+00
E value
                   413
Match length
```

95 % identity

NCBI Description Human fos proto-oncogene (c-fos), complete cds

291043 Seq. No.

LIB148-020-Q1-E1-F12 Seq. ID

Method BLASTX NCBI GI g4507237



```
AST score
                   3.0e-27
  value
 itch length
                   76
  identity
                   80
                   signal sequence receptor, alpha (translocon-associated
NCBI Description
                   protein alpha) >gi_1174449_sp_P43307_SSRA_HUMAN
TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR
                   (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT)
                   (SSR-ALPHA) >gi_551638_emb_CAA78290_ (Z12830) SSR alpha
                   subunit [Homo sapiens]
                   291044
Seq. No.
                   LIB148-020-Q1-E1-F9
Seq. ID
                   BLASTN
Method
NCBI GI
                   q509215
BLAST score
                   51
                   1.0e-19
E value
Match length
                   151
                   83
% identity
NCBI Description B.taurus microsatellite sequence INRA082
Seq. No.
                   291045
                   LIB148-020-Q1-E1-G9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g452070
BLAST score
                   61
                   1.0e-25
E value
Match length
                   172
                   84
% identity
NCBI Description Human MHC class III HLA-RP gene, complete cds
Seq. No.
                   291046
                   LIB148-020-Q1-E1-H12
Seq. ID
                   BLASTN
Method
                   g2182268
NCBI GI
                   99
BLAST score
                   2.0e-48
E value
                   102
Match length
                   99
% identity
NCBI Description Ovis aries beta actin mRNA, complete cds
                   291047
Seq. No.
                   LIB148-020-Q1-E1-H5
Seq. ID
                   BLASTX
Method
                   q3928084
NCBI GI
                   234
BLAST score
                   2.0e-19
E value
                   141
Match length
% identity
                   42
                   (AC005770) retrotransposon-like protein [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. ID LIB148-020-Q1-E1-H7

Method BLASTX
NCBI GI g1362010
BLAST score 336



1.0e-31 E value Match length 88 % identity ubiquitin-like protein 9 - Arabidopsis thaliana NCBI Description Seq. No. 291049 LIB148-021-Q1-E1-A2 Seq. ID BLASTX Method NCBĮ GI q416731 215 BLAST score 1.0e-17 E value 89 Match length 54 % identity POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi_82655_pir__JQ1107 NCBI Description 18.3K protein precursor, pollen - maize >gi 255569 bbs_113677 (S44171) pollen specific protein [Zea mays=corn, Peptide, 170 aa] [Zea mays] >gi 1588669 prf 2209273A Zm13 [Zea mays] 291050 Seq. No. LIB148-021-Q1-E1-B4 Seq. ID BLASTX Method q1703147 NCBI GI 169 BLAST score 2.0e-22 E value 119 Match length 53 % identity NCBI Description ACTIN, ALPHA ANOMALOUS >gi 1335837 (U38962) alpha actin [Fugu rubripes] 291051 Seq. No. Seq. ID LIB148-021-Q1-E1-E12 Method BLASTX NCBI GI q4164408 BLAST score 327 2.0e-30 E value 100 Match length % identity 58 NCBI Description (AJ132228) amino acid carrier [Ricinus communis] 291052 Seq. No. Seq. ID LIB148-021-Q1-E1-H5 Method BLASTX NCBI GI q4104060 BLAST score 229 E value 5.0e-19 Match length 120 % identity 42 NCBI Description (AF031231) S222 [Triticum aestivum]

291053 Seq. No.

LIB148-022-Q1-E1-H8 Seq. ID

Method BLASTN q4240040 NCBI GI 374 BLAST score 0.0e + 00E value 374 Match length

```
% identity
                  Zea mays ZmGR2c mRNA, complete cds
NCBI Description
                   291054
Seq. No.
Seq. ID
                  LIB148-023-Q1-E1-B10
Method
                   BLASTX
                   g2529677
NCBI GI
                   186
BLAST score
                   6.0e-14
E value
                   89.
Match length
                   48
% identity
                   (AC002535) kinesin-like protein, heavy chain [Arabidopsis
NCBI Description
                   thaliana]
                   291055
Seq. No.
Seq. ID
                   LIB148-023-Q1-E1-B5
                   BLASTX
Method
                   g3236246
NCBI GI
BLAST score
                   218
                   1.0e-17
.E value
                   74
Match length
                   47
% identity
                  (AC004684) putative expansin protein [Arabidopsis thaliana]
NCBI Description
                   291056
Seq. No.
Seq. ID
                   LIB148-023-Q1-E1-C4
                   BLASTX
Method
                   g639722
NCBI GI
BLAST score
                   364
                   7.0e-35
E value
                   109
Match length
% identity
                   65
                   (L27484) calcium-dependent protein kinase [Zea mays]
NCBI Description
                   291057
Seq. No.
                   LIB148-023-Q1-E1-C6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3281853
BLAST score
                   207
                   8.0e-17
E value
Match length
                   79
% identity
                   57
                   (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                   291058
Seq. No.
                   LIB148-023-Q1-E1-D4
Seq. ID
                   BLASTX
Method
                   g1076632
NCBI GI
                   145
BLAST score
                   6.0e-15
E value
                   102
Match length
                   47
 % identity
                   protein kinase - common tobacco >gi_506534_emb_CAA50374_
 NCBI Description
                    (X71057) protein kinase [Nicotiana tabacum]
```

291059

LIB148-023-Q1-E1-E2

Seq. No.

Seq. ID

Seq. ID Method

NCBI GI



```
BLASTX
Method
                  g2809232
NCBI GI
                  289
BLAST score
                  2.0e-29
E value
                  136
Match length
                  54
% identity
NCBI Description (AC002560) F21B7.1 [Arabidopsis thaliana]
                  291060
Seq. No.
                  LIB148-023-Q1-E1-E4
Seq. ID
                  BLASTX
Method
                  g1076632
NCBI GI
                  376
BLAST score
                  2.0e-36
E value
                  105
Match length
                  73
% identity
                  protein kinase - common tobacco >gi_506534 emb_CAA50374_
NCBI Description
                  (X71057) protein kinase [Nicotiana Tabacum]
                  291061
Seq. No.
                  LIB148-023-Q1-E1-F2
Seq. ID
Method
                  BLASTX
                  g1871186
NCBI GI
                  156
BLAST score
                  2.0e-10
E value
                  108
Match length
                   40
% identity
                  (U90439) protein kinase isolog [Arabidopsis thaliana]
NCBI Description
                   291062
Seq. No.
                  LIB148-023-Q1-E1-G12
Seq. ID
                  BLASTX
Method
                   q4337196
NCBI GI
BLAST score
                   203
                   7.0e-16
E value
                   138
Match length
% identity
                   (AC006403) putative serine/threonine receptor kinase
NCBI Description
                   [Arabidopsis thaliana]
                   291063
Seq. No.
Seq. ID
                   LIB148-024-Q1-E1-A8
                   BLASTX
Method
NCBI GI
                   g231509
                   142
BLAST score
                   5.0e-09
E value
                   51
Match length
                   57
% identity
                  ACTIN DEPOLYMERIZING FACTOR (ADF) >gi_419809_pir__S30935
NCBI Description
                   actin-depolymerizing factor - trumpet lily
                   >gi_22748_emb_CAA78483_ (Z14110) actin depolymerizing
                   factor [Lilium longiflorum]
 Seq. No.
                   291064
```

40480

LIB148-024-Q1-E1-C7

BLASTX q3335372



```
BLAST score
                  1.0e-35
E value
                  126
Match length
                  57
% identity
                  (AC003028) putative SRG1 protein [Arabidopsis thaliana]
NCBI Description
                  291065
Seq. No.
                  LIB148-024-Q1-E1-D6
Seq. ID
                  BLASTN
Method
                  q255568
NCBI GI
BLAST score
                   42
                   2.0e-14
E value
                   98
Match length
                   86
% identity
NCBI Description pollen specific protein [Zea mays=corn, mRNA, 943 nt]
                   291066
Seq. No.
Seq. ID
                   LIB148-024-Q1-E1-G10
                   BLASTX
Method
                   q3006187
NCBI GI
                   242
BLAST score
                   1.0e-20
E value
                   79
Match length
                   51
% identity
                  (AL022304) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                   291067
Seq. No.
                   LIB148-024-Q1-E1-H5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4468993
BLAST score
                   209
                   1.0e-16
E value
Match length
                   77
% identity
                   52
                  (AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
                   291068
Seq. No.
                   LIB148-025-Q1-E1-B1
Seq. ID
Method
                   BLASTN
                   g22458
NCBI GI
BLAST score
                   188
                   1.0e-101
E value
Match length
                   267
% identity
                   93
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)
                   291069
Seq. No.
                   LIB148-025-Q1-E1-B3
Seq. ID
                   BLASTX
Method
                   g405533
NCBI GI
BLAST score
                   466
                   9.0e-47
E value
Match length
                   83
 % identity
                   99
NCBI Description (L20139) homology with pectate lyase [Zea mays]
```

291070

Seq. No.



```
LIB148-025-Q1-E1-D11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2398679
BLAST score
                  194
                  5.0e-15
E value
Match length
                  91
% identity
                  45
                  (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate
NCBI Description
                  synthase [Morinda citrifolia]
Seq. No.
                  291071
Seq. ID
                  LIB148-025-Q1-E1-E8
                  BLASTX
Method
                  g1086989
NCBI GI
BLAST score
                  182
                  2.0e-13
E value
Match length
                  73
                  55
% identity
                  (S79323) plasma membrane H(+)-ATPase [Vicia faba, Otafuku,
NCBI Description
                  abaxial epidermis, guard cell protoplasts, Peptide, 963 aa]
                   [Vicia faba]
Seq. No.
                  291072
Seq. ID
                  LIB148-025-Q1-E1-G5
Method
                  BLASTN
                  g255568
NCBI GI
BLAST score
                  101
E value
                  8.0e-50
Match length
                  203
% identity
                   89
NCBI Description pollen specific protein [Zea mays=corn, mRNA, 943 nt]
                   291073
Seq. No.
                  LIB148-026-Q1-E1-C5
Seq. ID
                   BLASTN
Method
NCBI GI
                   g309569
BLAST score
                   98
E value
                   7.0e-48
Match length
                   106
                   49
% identity
                   Zea mays transcriptional activator for anthocyanin
NCBI Description
                   synthesis gene, complete cds
                   291074
Seq. No.
                   LIB148-026-Q1-E1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q586078
BLAST score
                   297
                   2.0e-27
E value
Match length
                   55
% identity
                   96
                   TUBULIN BETA CHAIN >gi 1076736 pir JC2518 beta-tubulin
NCBI Description
                   pTUB22 - rice >gi_303842_dbj_BAA02505_ (D13224)
                   beta-tubulin [Oryza sativa]
```

Seq. ID LIB148-026-Q1-E1-D2



```
Method
                  g1170504
NCBI GI
                  144
BLAST score
                  4.0e-09
E value
                  34
Match length
                  79
% identity
                  EUKARYOTIC INITIATION FACTOR (ISO) 4F SUBUNIT P82
NCBI Description
                  (IEIF-(ISO)4F P82) >gi_452440 (M95747) initiation factor
                  (iso)4f p82 subunit [Triticum aestivum]
                  291076
Seq. No.
                  LIB148-026-Q1-E1-D4
Seq. ID
                  BLASTX
Method
                  g1737218
NCBI GI
                  365
BLAST score
                  3.0e-35
E value
                  82
Match length
                  71
% identity
                  (U79959) vacuolar sorting receptor homolog [Arabidopsis
NCBI Description
                  thaliana]
                  291077
Seq. No.
                  LIB148-026-Q1-E1-E3
Seq. ID
                  BLASTN
Method
                  q22458
NCBI GI
                  37
BLAST score
                  1.0e-11
E value
                  41
Match length
% identity
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)
                   291078
Seq. No.
Seq. ID
                   LIB148-026-Q1-E1-E9
                   BLASTX
Method
                   q481432
NCBI GI
                   253
BLAST score
                   8.0e-22
E value
Match length
                   78
% identity
                   54
NCBI Description allergen Phl pI - common timothy >gi_1582250_prf__2118271A
                   allergen PhI p I [Phleum pratense]
Seq. No.
                   291079
                   LIB148-026-Q1-E1-F11
Seq. ID
                   BLASTX
Method
                   q3550985
NCBI GI
BLAST score
                   355
                   9.0e-34
E value
Match length
                   100
                   67
 % identity
NCBI Description (AB010740) OsS5a [Oryza sativa]
                   291080
```

LIB148-026-Q1-E1-G5 Seq. ID

BLASTX Method g1076531 NCBI GI 166 BLAST score



```
1.0e-11
E value
Match length
                  46
                  63
% identity
                  hypothetical protein, pollen allergen homolog - garden pea
NCBI Description
                  >gi 2129891_pir__S65056 pollen allergen homolog precursor
                  (clone PPA1) - garden pea >gi_732905_emb_CAA59470_ (X85187)
                  homology with pollen allergens [Pisum sativum]
                  291081
Seq. No.
                  LIB148-026-Q1-E1-H1
Seq. ID
                  BLASTX
Method
                  g4510345
NCBI GI
BLAST score
                  160
                  5.0e-11
E value
                  57
Match length
                  51
% identity
                 (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  291082
                  LIB148-027-Q1-E1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g416731
                  252
BLAST score
E value
                  3.0e - 33
                  113
Match length
                  67
% identity
                  POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi 82655_pir JQ1107
NCBI Description
                  18.3K protein precursor, pollen - maize
                  >gi_255569_bbs_113677 (S44171) pollen specific protein [Zea
                  mays=corn, Peptide, 170 aa] [Zea mays]
                  >gi 1588669_prf _2209273A Zm13 [Zea mays]
                  291083
Seq. No.
                  LIB148-027-Q1-E1-C3
Seq. ID
                  BLASTX
Method
                  q639722
NCBI GI
BLAST score
                  311
                  1.0e-28
E value
Match length
                  77
                   82
% identity
NCBI Description (L27484) calcium-dependent protein kinase [Zea mays]
                   291084
Seq. No.
Seq. ID
                   LIB148-027-Q1-E1-D12
                   BLASTX
Method
NCBI GI
                   q464466
                   194
BLAST score
                   5.0e-15
E value
Match length
                   63
% identity
NCBI Description PROFILIN 1 >gi_422031_pir__S35796 profilin 1 - maize
                   >gi_313138_emb_CAA51718_ (X73279) profilin 1 [Zea mays]
```

Seq. ID LIB148-027-Q1-E1-E1

Method BLASTN NCBI GI g22458



```
BLAST score
                  1.0e-178
E value
                  321
Match length
                  100
% identity
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)
                  291086
Seq. No.
                  LIB148-027-Q1-E1-E2
Seq. ID
                  BLASTX
Method
                  g3236246
NCBI GI
                  273
BLAST score
                  4.0e-24
E value
                  85
Match length
                  53
% identity
                  (AC004684) putative expansin protein [Arabidopsis thaliana]
NCBI Description
                  291087
Seq. No.
                  LIB148-027-Q1-E1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4646217
BLAST score
                   615
                  3.0e-64
E value
                  122
Match length
                   92
% identity
                  (AC007290) putative phosphoprotein phosphatase [Arabidopsis
NCBI Description
                   thaliana]
                   291088
Seq. No.
                   LIB148-028-Q1-E1-A7
Seq. ID
                   BLASTX
Method
                   q2288887
NCBI GI
BLAST score
                   363
                   8.0e-35
E value
                   93
Match length
% identity
                  (Y14325) mevalonate diphosphate decarboxylase [Arabidopsis
NCBI Description
                   thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate
                   diphosphate decarboxylase [Arabidopsis thaliana]
                   >gi_3786002 (AC005499) mevalonate diphosphate decarboxylase
                   [Arabidopsis thaliana]
Seq. No.
                   291089
Seq. ID
                   LIB148-028-Q1-E1-B12
Method
                   BLASTX
                   g1778015
NCBI GI
BLAST score
                   326
                   2.0e-30
E value
                   113
Match length
 % identity
                   57
                  (U59508) osmotic stress-induced proline dehydrogenase
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. ID LIB148-028-Q1-E1-F7

Method BLASTX
NCBI GI g4455364
BLAST score 165



```
E value
                  1.0e-11
Match length
% identity
                  (AL035524) senescence-associated protein-like [Arabidopsis
NCBI Description
                  thaliana]
                  291091
Seq. No.
                  LIB148-028-Q1-E1-G3
Seq. ID
                  BLASTX
Method
                  q4098321
NCBI GI
BLAST score
                  525
                  9.0e-54
E value
                  100
Match length
                   98
% identity
                  (U76745) beta-tubulin 2 [Triticum aestivum]
NCBI Description
                   291092
Seq. No.
Seq. ID
                  LIB148-029-Q1-E1-B6
Method
                  BLASTX
                   q4235430
NCBI GI
                   235
BLAST score
                   6.0e-20
E value
                   60
Match length
                   75
% identity
NCBI Description (AF098458) latex-abundant protein [Hevea brasiliensis]
                   291093
Seq. No.
Seq. ID
                   LIB148-029-Q1-E1-B7
                   BLASTX
Method
NCBI GI
                   q1168345
                   297
BLAST score
                   3.0e-27
E value
                   73
Match length
                   81
% identity
NCBI Description ACTIN DEPOLYMERIZING FACTOR (ADF) >gi_929918_emb_CAA56786_
                   (X80820) actin-depolymerizing factor [Zea mays]
Seq. No.
                   291094
                   LIB148-029-Q1-E1-D10
Seq. ID
                   BLASTN
Method
NCBI GI
                   g313137
BLAST score
                   60
E value
                   4.0e-25
Match length
                   80
% identity
                   94
NCBI Description Z.mays ZmPRO1 mRNA for profilin
Seq. No.
                   291095
                   LIB148-029-Q1-E1-G11
Seq. ID
                   BLASTX
Method
                   g629849
NCBI GI
                   278
BLAST score
E value
                   7.0e-25
                   108
Match length
                   51
% identity
                   pectate lyase (EC 4.2.2.2) - maize >gi 405535 (L20140)
NCBI Description
```

homology with pectate lyase [Zea mays]

Match length

NCBI Description

% identity

97 88

complete sequence



```
291096
Seq. No.
                  LIB148-029-Q1-E1-H6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3702323
BLAST score
                  261
                  6.0e-23
E value
                  77
Match length
% identity
                  (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
                  291097
Seq. No.
                  LIB148-029-Q1-E1-H7
Seq. ID
                  BLASTX
Method
                  g3015488
NCBI GI
BLAST score
                  248
                  2.0e-21
E value
                  89
Match length
% identity
                   53
                  (U58474) receptor-like protein kinase [Lycopersicon
NCBI Description
                  esculentum]
Seq. No.
                   291098
Seq. ID
                  LIB148-030-Q1-E1-D2
                  BLASTX
Method
                   g731834
NCBI GI
BLAST score
                   148
                   1.0e-09
E value
                   49
Match length
% identity
                  HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION
NCBI Description
                   >gi_1077790_pir__S49797 hypothetical protein YIL083c -
                   yeast (Saccharomyces cerevisiae) >gi 577131_emb_CAA86711.1_
                   (Z46728) YI9910.13c, unknown orf, len: 365, CAI: 0.17
                   [Saccharomyces cerevisiae]
Seq. No.
                   291099
                   LIB148-030-Q1-E1-E4
Seq. ID
Method
                   BLASTX
                   g3021336
NCBI GI
BLAST score
                   273
                   3.0e-24
E value
Match length
                   117
% identity
                   47
                  (AJ224957) RGA-like [Arabidopsis thaliana]
NCBI Description
                   291100
Seq. No.
                   LIB148-030-Q1-E1-E6
Seq. ID
                   BLASTN
Method
                   g4140643
NCBI GI
BLAST score
                   49
E value
                   2.0e-18
```

40487

Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,



```
291101
Seq. No.
Seq. ID
                  LIB148-031-Q1-E1-D5
                  BLASTN
Method
                  g3341647
NCBI GI
BLAST score
                  36
E value
                  7.0e-11
                  72
Match length
                  88
% identity
                  Zea mays Ama gene encoding single-subunit RNA polymerase
NCBI Description
                  291102
Seq. No.
                  LIB148-031-Q1-E1-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4567310
BLAST score
                  156
                   1.0e-10
E value
Match length
                   56
                   57
% identity
                  (AC005956) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   291103
Seq. ID
                  LIB148-031-Q1-E1-E11
Method
                   BLASTX
NCBI GI
                   g4582467
BLAST score
                   378
                   2.0e-36
E value
                   116
Match length
                   62
% identity
                   (AC007071) putative calcium dependent protein kinase;
NCBI Description
                   contains protein kinase domain [Arabidopsis thaliana]
                   >gi 4589951_gb AAD26469.1 AC007169 1 (AC007169) putative
                   calcium-dependent protein kinase [Arabidopsis thaliana]
                   291104
Seq. No.
                   LIB148-031-Q1-E1-F11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4191791
BLAST score
                   314
E value
                   4.0e-29
Match length
                   80
% identity
                   68
                   (AC005917) putative sf21 {Helianthus annuus} protein
NCBI Description
                   [Arabidopsis thaliana]
                   291105
Seq. No.
                   LIB148-032-Q1-E1-B4
Seq. ID
                   BLASTX
Method
                   g4580398
NCBI GI
                   357
BLAST score
                   6.0e - 34
E value
                   122
Match length
% identity
                   (AC007171) putative protein kinase APK1A [Arabidopsis
NCBI Description
                   thaliana]
```

291106

LIB148-032-Q1-E1-B9

Seq. No.

Seq. ID

Seq. ID

Method



```
BLASTX
Method
                  g4538930
NCBI GI
                  170
BLAST score
                  2.0e-12
E value
                  55
Match length
                  53
% identity
NCBI Description (AL049483) putative peroxidase [Arabidopsis thaliana]
                  291107
Seq. No.
                  LIB148-032-Q1-E1-H2
Seq. ID
                  BLASTX
Method
                  g1171005
NCBI GI
BLAST score
                  346
                   1.0e-32
E value
                   127
Match length
                   49
% identity
                  MAJOR POLLEN ALLERGEN HOL L 1 PRECURSOR (HOL L I)
NCBI Description
                   >gi 1085628 pir__S38581 allergen Hol-II - Holcus lanatus
                   >gi 414703 emb CAA81610 (Z27084) allergen Hol-II [Holcus
                   lanatus]
                   291108
Seq. No.
                   LIB148-033-Q1-E1-A11
Seq. ID
                   BLASTX
Method
                   g3249086
NCBI GI
                   331
BLAST score
                   6.0e-31
E value
                   86
Match length
                   73
% identity
                   (AC004473) Contains similarity to 21 KD subunit of the
NCBI Description
                   Arp2/3 protein complex (ARC21) gb_AF006086 from Homo
                   sapiens. EST gb Z37222 comes [Arabidopsis thaliana]
                   291109
Seq. No.
                   LIB148-033-Q1-E1-A6
Seq. ID
                   BLASTN
Method
                   g433043
NCBI GI
BLAST score
                   55
                   4.0e-22
E value
                   63
Match length
                   97
% identity
                   Zea mays W-22 clone PREM-1E retroelement PREM-1, partial
NCBI Description
                   sequence
                   291110
Seq. No.
                   LIB148-033-Q1-E1-B4
Seq. ID
                   BLASTN
Method
NCBI GI
                   g255568
BLAST score
                   55
                   2.0e-22
E value
Match length
                   87
                   91
 % identity
NCBI Description pollen specific protein [Zea mays=corn, mRNA, 943 nt]
 Seq. No.
                   291111
```

40489

LIB148-033-Q1-E1-C1

BLASTX



```
g4539330
NCBI GI
                  477
BLAST score
                  5.0e-48
E value
                  120
Match length
                  74
% identity
                  (AL035679) putative receptor-like protein kinase (fragment)
NCBI Description
                  [Arabidopsis thaliana]
                  291112
Seq. No.
                  LIB148-034-Q1-E1-C8
Seq. ID
                  BLASTX
Method
                  g1935000
NCBI GI
                  299
BLAST score
E value
                   4.0e-27
                  106
Match length
                   54
% identity
                  (Y12314) GTPase [Schizosaccharomyces pombe]
NCBI Description
Seq. No.
                   291113
                  LIB148-034-Q1-E1-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2459424
                   237
BLAST score
                   7.0e-20
E value
                   125
Match length
                   42
% identity
                  (AC002332) unknown protein [Arabidopsis thaliana]
NCBI Description
                   291114
Seq. No.
                   LIB148-034-Q1-E1-G2
Seq. ID
                   BLASTX
Method
                   g4581150
NCBI GI
                   209
BLAST score
E value
                   3.0e-17
                   72
Match length
                   61
% identity
                  (AC006919) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   291115
Seq. No.
                   LIB148-034-Q1-E1-H1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1931645
BLAST score
                   271
E value
                   5.0e-24
                   87
Match length
                   62
% identity
                  (U95973) Fe(II) transporter isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   291116
                   LIB148-035-Q1-E1-D3
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2239261
BLAST score
                   313
E value
                   1.0e-176
Match length
                   340
                   99
% identity
NCBI Description Zea Mays mRNA for pectin methylesterase-like protein
```

```
291117
Seq. No.
                  LIB148-036-Q1-E1-C1
Seq. ID
                  BLASTX
Method
                  g1091678
NCBI GI
                  219
BLAST score
                  8.0e-18
E value
Match length
                  80
% identity
                  51
NCBI Description activator-like transposable element [Pennisetum glaucum]
                  291118
Seq. No.
                  LIB148-036-Q1-E1-E3
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2239261
                   251
BLAST score
                   1.0e-139
E value
                   390
Match length
% identity
                   92
                  Zea Mays mRNA for pectin methylesterase-like protein
NCBI Description
                   291119
Seq. No.
                   LIB148-036-Q1-E1-E7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4587571
                   277
BLAST score
                   1.0e-24
E value
                   83
Match length
                   57
% identity
                   (AC006550) Belongs to the PF 01027 Uncharacterized protein
NCBI Description
                   family UPF0005 with 7 transmembrane domains. [Arabidopsis
                   thaliana]
                   291120
Seq. No.
                   LIB148-036-Q1-E1-F12
Seq. ID
                   BLASTN
Method
                   g405534
NCBI GI
                   181
BLAST score
                   1.0e-97
E value
                   189
Match length
                   99
% identity
                   Zea mays pollen specific pectate lyase homologue gene,
NCBI Description
                   complete cds
 Seq. No.
                   291121
                   LIB148-037-Q1-E1-A10
Seq. ID
                   BLASTX
Method
                   g548492
NCBI GI
BLAST score
                   251
                   2.0e-21
E value
                   89
Match length
                   55
 % identity
                  EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
 NCBI Description
                   (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                   >gi_629853_pir__S30066 polygalacturonase - maize
```

mays]

>gi 288379 emb CAA45751 (X64408) polygalacturonase [Zea



LIB148-037-Q1-E1-A12

Seq. No.

Seq. ID

```
BLASTN
Method
                  g3821780
NCBI GI
                  37
BLAST score
                  2.0e-11
E value
                  37
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  291123
Seq. No.
                  LIB148-037-Q1-E1-A3
Seq. ID
                  BLASTX
Method
                  g629849
NCBI GI
                  270
BLAST score
                   5.0e-24
E value
                   80
Match length
                   70
% identity
                  pectate lyase (EC 4.2.2.2) - maize >gi_405535 (L20140)
NCBI Description
                   homology with pectate lyase [Zea mays]
                   291124
Seq. No.
                   LIB148-037-Q1-E1-B10
Seq. ID
                   BLASTX
Method
                   g1399303
NCBI GI
                   360
BLAST score
                   2.0e-34
E value
                   133
Match length
                   54
% identity
                   (U41473) phosphoinositide-specific phospholipase C P12
NCBI Description
                   [Glycine max]
                   291125
Seq. No.
                   LIB148-037-Q1-E1-E3
Seq. ID
                   BLASTX
Method
                   g729944
NCBI GI
BLAST score
                   223
                   2.0e-18
E value
                   41
Match length
 % identity
                   POLLEN ALLERGEN ZEA M 1 (ZEA M I) >gi_478272_pir__JC1524
 NCBI Description
                   major allergen mI protein - maize >gi_293902 (L14271) Zea
                   mI [Zea mays]
                   291126
 Seq. No.
                   LIB148-037-Q1-E1-E5
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g4416301
                   342
 BLAST score
                   3.0e-32
 E value
                   140
 Match length
                   70
 % identity
                   (AF105716) gag protein [Zea mays]
 NCBI Description
                   291127
 Seq. No.
                   LIB148-037-Q1-E1-F11
 Seq. ID
```

BLAST score

E value

276 2.0e-24



```
BLASTX
  Method
  NCBI GI
                     g3785983
                     160
BLAST score
                     7.0e-11
  E value
                     66
  Match length
                     45
  % identity
  NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana]
  Seq. No.
                     291128
                     LIB148-037-Q1-E1-F9
  Seq. ID
                     BLASTX
  Method
                     g2143942
  NCBI GI
                     208
  BLAST score
                     1.0e-16
  E value
                     94
  Match length
                     46
  % identity
  NCBI Description prostaglandin G/H synthase 1 - rat (fragment)
  Seq. No.
                     291129
                     LIB148-038-Q1-E1-C12
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     q4099090
                     219
  BLAST score
                     7.0e-18
  E value
  Match length
                     83
                     48
  % identity
  NCBI Description (U83178) unknown [Arabidopsis thaliana]
                     291130
  Seq. No.
                     LIB148-038-Q1-E1-D9
  Seq. ID
                     BLASTX
  Method
  NCBI GI
                     g2642213
                     226
  BLAST score
                     1.0e-18
  E value
  Match length
                     83
                     55
  % identity
                    (AF030385) nitrate-induced NOI protein [Zea mays]
  NCBI Description
                     >gi 2895781 (AF045033) nitrate-induced NOI protein [Zea
                     mays]
                     291131
  Seq. No.
  Seq. ID
                     LIB148-038-Q1-E1-E1
                     BLASTX
  Method
  NCBI GI
                     g3461821
  BLAST score
                     183
                     1.0e-13
  E value
                     129
  Match length
                     36
  % identity
                     (AC004138) putative nucleoside triphosphatase [Arabidopsis
  NCBI Description
                     thaliana]
                     291132
  Seq. No.
  Seq. ID
                     LIB148-038-Q1-E1-E10
  Method
                     BLASTX
  NCBI GI
                     q576773
```



```
Match length
                  116
                  11
% identity
                  (U16956) polyubiquitin [Filobasidiella neoformans]
NCBI Description
                  291133
Seq. No.
                  LIB148-038-Q1-E1-F7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q416731
BLAST score
                  476
E value
                  7.0e-48
                  101
Match length
                  90
% identity
                  POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi 82655 pir JQ1107
NCBI Description
                  18.3K protein precursor, pollen - maize
                  >gi_255569_bbs_113677 (S44171) pollen specific protein [Zea
                  mays=corn, Peptide, 170 aa] [Zea mays]
                  >gi 1588669 prf 2209273A Zm13 [Zea mays]
                  291134
Seq. No.
                  LIB148-038-Q1-E1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2642213
                  192
BLAST score
                  1.0e-14
E value
Match length
                   68
                   57
% identity
                   (AF030385) nitrate-induced NOI protein [Zea mays]
NCBI Description
                   >gi 2895781 (AF045033) nitrate-induced NOI protein [Zea
                  mays]
                   291135
Seq. No.
                   LIB148-039-Q1-E1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1706551
                   309
BLAST score
                   3.0e-28
E value
                   128
Match length
                   48
% identity
                   GLUCAN ENDO-1, 3-BETA-GLUCOSIDASE PRECURSOR
NCBI Description
                   ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
                   (BETA-1, 3-ENDOGLUCANASE) >gi 924953 (U30323) beta
                   1,3-glucanase [Triticum aestivum]
                   291136
Seq. No.
                   LIB148-039-Q1-E1-B2
Seq. ID
                   BLASTX
Method
                   q4581508
NCBI GI
                   578
BLAST score
                   7.0e-60
E value
Match length
                   138
```

77 % identity

(AL049558) putative phosphatidylinositol-kinase NCBI Description

[Schizosaccharomyces pombe]

Seq. No. 291137

LIB148-039-Q1-E1-B5 Seq. ID

BLASTN Method



```
g175854
NCBI GI
                  82
BLAST score
                  3.0e-38
E value
                  82
Match length
                  100
% identity
NCBI Description O.sativa 28S large subunit rRNA, 5' end
                  291138
Seq. No.
                  LIB148-039-Q1-E1-D6
Seq. ID
Method
                  BLASTX
                  g84373
NCBI GI
                  296
BLAST score
                   5.0e-33
E value
Match length
                  119
                   62
% identity
NCBI Description tubulin alpha chain - Stylonychia lemnae (SGC5)
                   291139
Seq. No.
                   LIB148-039-Q1-E1-D8
Seq. ID
                   BLASTX
Method
                   g3335372
NCBI GI
                   289
BLAST score
                   4.0e-26
E value
                   119
Match length
                   50
% identity
                  (AC003028) putative SRG1 protein [Arabidopsis thaliana]
NCBI Description
                   291140
Seq. No.
                   LIB148-040-Q1-E1-E5
Seq. ID
                   BLASTN
Method
                   g3341647
NCBI GI
                   99
BLAST score
                   2.0e-48
E value
                   207
Match length
                   87
% identity
NCBI Description Zea mays Ama gene encoding single-subunit RNA polymerase
                   291141
Seq. No.
                   LIB148-041-Q1-E1-A10
 Seq. ID
                   BLASTN
Method
                   g34544
NCBI GI
                   34
BLAST score
                   1.0e-09
E value
                   34
Match length
 % identity
                   100
NCBI Description Human malignant melanoma cell amplification unit (mel/HPV9)
                   291142
 Seq. No.
 Seq. ID
                   LIB148-041-Q1-E1-B5
                   BLASTX
 Method
                   g1304599
 NCBI GI
                   177
 BLAST score
                   8.0e-13
 E value
 Match length
                   61
 % identity
                   46
```

NCBI Description (U41315) ZNF127-Xp [Homo sapiens]

E value

Match length

% identity

72

49



```
Seq. No.
Seq. ID
                   LIB148-041-Q1-E1-D10
                   BLASTX
Method
NCBI GI
                   g548492
                   226
BLAST score
E value
                   9.0e-19
Match length
                   101
                   40
% identity
                   EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                   (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                   >gi 629853_pir S30066 polygalacturonase - maize
                   >gi 288379 emb CAA45751 (X64408) polygalacturonase [Zea
                   mays]
                   291144
 Seq. No.
 Seq. ID
                   LIB148-041-Q1-E1-G12
                   BLASTX
Method
                   g2239262
NCBI GI
BLAST score
                   559
                   1.0e-57
E value
                   109
Match length.
                   94
 % identity
                   (Y13285) pectin methylesterase-like protein [Zea mays]
 NCBI Description
                   291145
 Seq. No.
 Seq. ID
                   LIB148-041-Q1-E1-H10
                   BLASTX
Method
'NCBI GI
                   q4572671
 BLAST score
                   169
                   2.0e-14
 E value
 Match length
                   102
                   42
 % identity
                   (AC006954) putative cyclic nucleotide regulated ion channel
 NCBI Description
                   [Arabidopsis thaliana]
                   291146
 Seq. No.
 Seq. ID
                   LIB148-041-Q1-E1-H7
 Method
                   BLASTX
                   g416731
 NCBI GI
 BLAST score
                   274
                   3.0e-24
 E value
 Match length
                   58
 % identity
                   POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi 82655 pir JQ1107
 NCBI Description
                    18.3K protein precursor, pollen - maize
                    >gi 255569 bbs 113677 (S44171) pollen specific protein [Zea
                    mays=corn, Peptide, 170 aa] [Zea mays]
                    >gi 1588669_prf 2209273A Zm13 [Zea mays]
                    291147
 Seq. No.
                   LIB148-042-Q1-E1-B4
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    g416731
                    143
 BLAST score
                    6.0e-09
```



POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi_82655_pir__JQ1107 NCBI Description 18.3K protein precursor, pollen - maize >gi 255569 bbs 113677 (S44171) pollen specific protein [Zea mays=corn, Peptide, 170 aa] [Zea mays] >gi_1588669_prf__2209273A Zm13 [Zea mays] Seq. No. 291148 LIB148-042-Q1-E1-C12 . Seq. ID Method BLASTN NCBI GI g600117 176 BLAST score 1.0e-94 E value 196 Match length % identity 78 NCBI Description Z.mays (B73) gene for extensin-like protein 291149 Seq. No. LIB148-042-Q1-E1-D11 Seq. ID Method BLASTX g115420 NCBI GI 293 BLAST score E value 5.0e-27 64 Match length % identity 84 MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT NCBI Description MALIC ENZYME) (NADP-ME) >gi 65940 pir DEFBC cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - kidney bean >gi 169327 (J03825) NADP-dependent malic enzyme [Phaseolus vulgaris] 291150 Seq. No. LIB148-042-Q1-E1-G1 Seq. ID BLASTN Method NCBI GI g3341647 BLAST score 60 3.0e-25 E value 84 Match length 93 % identity NCBI Description Zea mays Ama gene encoding single-subunit RNA polymerase 291151 Seq. No. LIB148-042-Q1-E1-G3 Seq. ID BLASTX Method NCBI GI g3776536 232 BLAST score 9.0e-36 E value 107 Match length % identity NCBI Description (AF095794) polyubiquitin [Schizosaccharomyces pombe] 291152 Seq. No.

LIB148-043-Q1-E1-C11 Seq. ID Method BLASTX

NCBI GI g4454039 BLAST score 219 7.0e-21 E value Match length 124



```
% identity
                  (AL035394) putative Na+/H+-exchanging protein [Arabidopsis
NCBI Description
                  thaliana]
                  291153
Seq. No.
Seq. ID
                  LIB148-043-Q1-E1-D10
                  BLASTX
Method
                  g1171161
NCBI GI
                  151
BLAST score
                  2.0e-10
E value
Match length
                  54
% identity
                  46
NCBI Description (U41472) pectate lyase homolog [Medicago sativa]
                  291154
Seq. No.
Seq. ID
                  LIB148-043-Q1-E1-D3
Method
                  BLASTX
NCBI GI
                  q2829898
                  175
BLAST score
E value
                   9.0e-13
                  54
Match length
% identity
NCBI Description (AC002311) Hypothetical protein [Arabidopsis thaliana]
                  291155
Seq. No.
                  LIB148-043-Q1-E1-E2
Seq. ID
Method
                  BLASTX
                   q4337202
NCBI GI
BLAST score
                   170
E value
                   5.0e-12
Match length
                   112
                   35
% identity
                  (AC006403) putative endosperm-specific protein [Arabidopsis
NCBI Description
                   thaliana]
                   291156
Seq. No.
Seq. ID
                  LIB148-043-Q1-E1-F4
Method
                   BLASTX
                   g3702333
NCBI GI
BLAST score
                   189
E value
                   2.0e-14
Match length
                   59
% identity
                   47
                  (AC005397) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   291157
Seq. No.
                   LIB148-043-Q1-E1-G6
Seq. ID
Method
                   BLASTX
                   g4539304
NCBI GI
                   266
```

NCBI GI g4539304
BLAST score 266
E value 2.0e-23
Match length 125
% identity 42

NCBI Description (AL049480) putative protein [Arabidopsis thaliana]

Seq. No. 291158

Seq. ID LIB148-043-Q1-E1-H7



```
BLASTX
Method
                  q4467125
NCBI GI
BLAST score
                  586
                   8.0e-61
E value
                  134
Match length
% identity
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]
                   291159
Seq. No.
                  LIB148-044-Q1-E1-A2
Seq. ID
                  BLASTN
Method
NCBI GI
                   g433038
BLAST score
                   62
                   3.0e-26
E value
                   93
Match length
                   91
% identity
                   Zea mays W-22 clone cDNA7 retroelement PREM-1-containing
NCBI Description
                   291160
Seq. No.
                   LIB148-044-Q1-E1-A4
Seq. ID
                   BLASTN
Method
NCBI GI
                   g22420
                   236
BLAST score
                   1.0e-130
E value
                   382
Match length
                   98
% identity
NCBI Description Z.mays mRNA for polygalacturonase (clone PG2)
                   291161
Seq. No.
Seq. ID
                   LIB148-044-Q1-E1-A7
                   BLASTX
Method
NCBI GI
                   g2130028
                   241
BLAST score
E value
                   2.0e-20
                   78
Match length
                   59
% identity
                   B12D protein - barley >gi_471319_emb_CAA54065.1_ (X76604)
NCBI Description
                   HvB12D [Hordeum vulgare] >gi_3445292_emb_CAA70936_ (Y09805)
                   B12Dg1 [Hordeum vulgare]
Seq. No.
                   291162
Seq. ID
                   LIB148-044-Q1-E1-B3
Method
                   BLASTX
NCBI GI
                   q2230959
BLAST score
                   155
E value
                   3.0e-10
Match length
                   111
 % identity
                   38
                   (Y10149) subtilisin-like protease [Lycopersicon esculentum]
NCBI Description
                   >gi_4200336_emb_CAA76725_ (Y17276) P69B protein
                   [Lycopersicon esculentum]
 Seq. No.
                   291163
                   LIB148-044-Q1-E1-C1
 Seq. ID
```

BLASTX

q2583123

Method NCBI GI



BLAST score 279 E value 7.0e-25 69 Match length 75 % identity (AC002387) putative nucleotide sugar epimerase [Arabidopsis NCBI Description thaliana] 291164 Seq. No. Seq. ID LIB148-044-Q1-E1-G4 Method BLASTX NCBI GI q22422 BLAST score 206 E value 3.0e-16 Match length 44 % identity 89 NCBI Description (X57743) polygalacturonase [Zea mays] 291165 Seq. No. LIB148-044-Q1-E1-G5 Seq. ID BLASTX Method NCBI GI g1864024 BLAST score 349 E value 5.0e-33 78 Match length 88 % identity (U35683) calcium-binding pollen allergen [Cynodon dactylon] NCBI Description >gi_1871507_emb_CAA62634_ (X91256) calcium-binding pollen allergen [Cynodon dactylon] Seq. No. 291166 Seq. ID LIB148-045-Q1-E1-H9 Method BLASTX NCBI GI g1834353 BLAST score 142 5.0e-09 E value 85 Match length % identity 45 NCBI Description (Y10986) hypothetical protein 194 [Arabidopsis thaliana] 291167 Seq. No. Seq. ID LIB148-046-Q1-E1-A10 Method BLASTX g2191152 NCBI GI 175 BLAST score E value 9.0e-19 82 Match length 55 % identity NCBI Description (AF007269) A IG002N01.31 gene product [Arabidopsis thaliana] 291168 Seq. No. Seq. ID LIB148-046-Q1-E1-F1

BLASTX Method NCBI GI g4415931 BLAST score 321 E value 9.0e-30 Match length 118



% identity

NCBI Description

(AC006418) unknown protein [Arabidopsis thaliana]

>qi 4559393 gb AAD23053.1 AC006526_18 (AC006526) unknown

protein [Arabidopsis thaliana]

Seq. No.

291169

Seq. ID

LIB148-047-Q1-E1-A8

Method NCBI GI BLASTX q3668084

BLAST score E value

142

Match length

9.0e-09 43

% identity

56

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.

291170

Seq. ID

LIB148-047-Q1-E1-E11 BLASTX

Method NCBI GI

g2529707

BLAST score E value

264 4.0e-23

Match length

87

% identity

55 NCBI Description (AF001434) Hpast [Homo sapiens]

Seq. No.

291171

Seq. ID

LIB148-047-Q1-E1-E5

Method NCBI GI BLASTX g3776559

BLAST score

145

E value

4.0e-09

Match length % identity

68

NCBI Description

(AC005388) Strong similarity to gene F14J9.26 gi 3482933

cdc2 protein kinase homolog from A. thaliana BAC

qb AC003970. ESTs qb Z35332 and gb F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No.

291172

Seq. ID

LIB148-047-Q1-E1-G4

Method NCBI GI BLASTX

q3182927

BLAST score

182

E value Match length

2.0e-13 125

% identity

38 NCBI Description HYDROXYATRAZINE HYDROLASE >gi 1732206 (U66917) AtzB

[Pseudomonas sp. ADP]

Seq. No.

291173

Seq. ID

LIB148-047-Q1-E1-H4

Method NCBI GI BLASTX

BLAST score

g1171008

E value

341

Match length

4.0e-32

% identity

111 58





NCBI Description POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I) >gi_629812_pir__S44182 allergen Phl p I - common timothy >gi 473360 emb CAA55390 (X78813) Phl p I allergen [Phleum pratense] Seq. No. 291174 Seq. ID LIB148-048-Q1-E1-B5 Method BLASTN NCBI GI g2239261 BLAST score 37 2.0e-11 E value Match length 61 90 % identity NCBI Description Zea Mays mRNA for pectin methylesterase-like protein Seq. No. 291175 Seq. ID LIB148-048-Q1-E1-D9 Method BLASTX NCBI GI g4325324 BLAST score 380 E value 1.0e-36 Match length 95 % identity 69 (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis NCBI Description thaliana] Seq. No. 291176 Seq. ID LIB148-048-Q1-E1-H4 Method BLASTX NCBI GI g4415931 BLAST score 408 E value 1.0e-43 Match length 143 60 % identity NCBI Description (AC006418) unknown protein [Arabidopsis thaliana] >gi_4559393_gb_AAD23053.1_AC006526 18 (AC006526) unknown protein [Arabidopsis thaliana] Seq. No. 291177 Seq. ID LIB148-049-Q1-E1-C11 Method BLASTX NCBI GI g4218011 BLAST score 297 E value 6.0e-27 88 Match length % identity 64 NCBI Description (AC006135) putative protein kinase [Arabidopsis thaliana] >gi_4309721_gb_AAD15491 (AC006439) putative serine/threonine protein kinase [Arabidopsis thaliana] Seq. No. 291178

Seq. ID LIB148-049-Q1-E1-H12

Method BLASTX NCBI GI g2245066 BLAST score 254 E value 4.0e-22 Match length 98

% identity (Z97342) Beta-Amylase [Arabidopsis thaliana] NCBI Description Seq. No. 291179 LIB148-050-Q1-E1-A1 Seq. ID BLASTX Method q4581150 NCBI GI 226 BLAST score E value 1.0e-18 94 Match length 53 % identity (AC006919) hypothetical protein [Arabidopsis thaliana] NCBI Description 291180 Seq. No. LIB148-050-Q1-E1-A9 Seq. ID BLASTN Method g22458 NCBI GI 83 BLAST score 5.0e-39 E value Match length 127 91 % identity NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7) 291181 Seq. No. LIB148-050-Q1-E1-C8 Seq. ID BLASTX Method q3193316 NCBI GI 253 BLAST score 7.0e-22 E value 106 Match length 52 % identity (AF069299) contains similarity to nucleotide sugar NCBI Description epimerases [Arabidopsis thaliana] 291182 Seq. No. LIB148-050-Q1-E1-D3 Seq. ID Method BLASTX g464849 NCBI GI 265 BLAST score 3.0e-23 E value 120 Match length 54 % identity TUBULIN ALPHA CHAIN >gi_486847 pir S36232 tubulin alpha NCBI Description chain - almond >gi_20413_emb_CAA47635 (X67162) alpha-tubulin [Prunus dulcis] 291183 Seq. No. LIB148-050-Q1-E1-F1 Seq. ID BLASTN Method g255568 NCBI GI BLAST score 56 9.0e-23 E value 181 Match length 88 % identity NCBI Description pollen specific protein [Zea mays=corn, mRNA, 943 nt]

Seq. No. 291184

```
LIB148-050-Q1-E1-G11
Seq. ID
                  BLASTX
Method
                  g695411
NCBI GI
BLAST score
                  277
E value
                  1.0e-24
                  59
Match length
                  95
% identity
                  (D49475) glutamate dehydrogenase [Zea mays]
NCBI Description
Seq. No.
                  291185
                  LIB148-051-Q1-E1-A8
Seq. ID
                  BLASTN
Method
                  g1518673
NCBI GI
BLAST score
                  55
E value
                  4.0e-22
Match length
                  111
                  87
% identity
                  Zea mays beta-D-glucosidase (glu1) gene, intron 4
NCBI Description
                  transposon 1, complete sequence
Seq. No.
                  291186
                  LIB148-051-Q1-E1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4218010
BLAST score
                   173
E value
                   2.0e-12
Match length
                   97
% identity
                   41
                   (AC006135) putative sugar transporter [Arabidopsis
NCBI Description
                   thaliana] >gi 4309720 gb AAD15490 (AC006439) putative
                   sugar transporter [Arabidopsis thaliana]
                   291187
Seq. No.
                   LIB148-051-Q1-E1-G4
Seq. ID
Method
                   BLASTX
                   q4104056
NCBI GI
BLAST score
                   510
E value
                   7.0e-52
                   136
Match length
                   68
% identity
                  (AF031194) S276 [Triticum aestivum]
NCBI Description
                   291188
Seq. No.
                   LIB148-051-Q1-E1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1518540
BLAST score
                   369
E value
                   2.0e-35
Match length
                   117
```

% identity 62

NCBI Description

(U53418) UDP-glucose dehydrogenase [Glycine max]

291189 Seq. No.

Seq. ID LIB148-052-Q1-E1-F9

Method BLASTX NCBI GI g2190992 BLAST score 379



```
2.0e - 36
E value
Match length
                  127
% identity
                  54
                  (AF004358) glutathione S-transferase TSI-1 [Aegilops
NCBI Description
                  tauschii]
                  291190
Seq. No.
                  LIB148-052-Q1-E1-G1
Seq. ID
                  BLASTX
Method
                  g2463509
NCBI GI
BLAST score
                  178
                  1.0e-13
E value
                  53
Match length
% identity
                  62
                  (Y09541) pectate lyase [Zinnia elegans]
NCBI Description
                  291191
Seq. No.
                  LIB148-052-Q1-E1-G9
Seq. ID
                  BLASTX
Method
                   q2088647
NCBI GI
BLAST score
                   275
                   3.0e-24
E value
                   128
Match length
% identity
                   43
                   (AF002109) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3158394 (AF036340) LRR-containing F-box protein
                   [Arabidopsis thaliana]
                   291192
Seq. No.
                   LIB148-052-Q1-E1-H8
Seq. ID
                   BLASTN
Method
                   g2245648
NCBI GI
                   106
BLAST score
                   1.0e-52
E value
                   122
Match length
% identity
                   97
                   Zea mays discolored-1 (mutant allele dsc1-Ref::Mul) gene,
NCBI Description
                   partial sequence
                   291193
Seq. No.
                   LIB148-053-Q1-E1-A1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1706082
BLAST score
                   143
                   4.0e-09
E value
                   79
```

Match length 42 % identity

SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3) NCBI Description

>gi_629787_pir__S44191 serine-type carboxypeptidase (EC

3.4.16.1) II-3 - barley >gi_619350_bbs_153536

CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley,

cv. Alexis, aleurone, Peptide, 516 aa]

>gi 474392 emb CAA55478 (X78877) serine carboxylase II-3

[Hordeum vulgare]

Seq. No. 291194

LIB148-053-Q1-E1-F8 Seq. ID

```
BLASTX
Method
                  g4544422
NCBI GI
BLAST score
                  565
E value
                  2.0e-58
Match length
                  136
% identity
                  78
NCBI Description (AC006955) putative fimbrin [Arabidopsis thaliana]
                  291195
Seq. No.
Seq. ID
                  LIB148-056-Q1-E1-F1
Method
                  BLASTX
NCBI GI
                  g4191774
BLAST score
                  444
E value
                   4.0e-44
Match length
                  142
% identity
                  (AC005917) putative beta-1,3-endoglucanase [Arabidopsis
NCBI Description
                  thaliana]
                  291196
Seq. No.
Seq. ID
                  LIB148-056-Q1-E1-H8
Method
                  BLASTX
NCBI GI
                  g4538923
BLAST score
                  159
E value
                   9.0e-11
Match length
                   99
% identity
                   48
                  (AL049483) predicted protein destination factor
NCBI Description
                   [Arabidopsis thaliana]
                   291197
Seq. No.
                   LIB148-057-Q1-E1-A8
Seq. ID
                   BLASTN
Method
                   g288378
NCBI GI
BLAST score
                  122
                   4.0e-62
E value
                   317
Match length
                   85
% identity
NCBI Description Z.mays gene PG for polygalacturonase
                   291198
Seq. No.
                   LIB148-057-Q1-E1-B6
Seq. ID
                   BLASTX
Method
                   g2723471
NCBI GI
                   146
BLAST score
                   2.0e-09
E value
                   57
Match length
                   49
% identity
NCBI Description (D87819) sucrose transporter [Oryza sativa]
```

Seq. ID LIB148-057-Q1-E1-C2

Method BLASTX
NCBI GI g3913427
BLAST score 659
E value 2.0e-69
Match length 132



% identity 100
NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)

(SAMDC) >gi_1532073_emb_CAA69075_ (Y07767) S-adenosylmethionine decarboxylase [Zea mays]

Seq. No. 291200

Seq. ID LIB148-057-Q1-E1-C4

Method BLASTN
NCBI GI g1532072
BLAST score 42
E value 2.0e-14
Match length 86
% identity 87

NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase

Seq. No. 291201

Seq. ID LIB148-057-Q1-E1-D11

Method BLASTX
NCBI GI g4210504
BLAST score 193
E value 2.0e-15
Match length 70
% identity 53

NCBI Description (AC002392) putative cadmium-transporting ATPase

[Arabidopsis thaliana]

Seq. No. 291202

Seq. ID LIB148-057-Q1-E1-D12

Method BLASTX
NCBI GI g3063468
BLAST score 166
E value 1.0e-11
Match length 70
% identity 56

NCBI Description (AC003981) F22013.30 [Arabidopsis thaliana]

Seq. No. 291203

Seq. ID LIB148-057-Q1-E1-D7

Method BLASTX
NCBI GI g1586940
BLAST score 230
E value 4.0e-19
Match length 65
% identity 71

NCBI Description Ser/Thr kinase [Lycopersicon esculentum]

Seq. No. 291204

Seq. ID LIB148-057-Q1-E1-G7

Method BLASTX
NCBI GI g3175990
BLAST score 260
E value 3.0e-29
Match length 94
% identity 71

NCBI Description (AJ005836) GDP dissociation inhibitor [Cicer arietinum]

Seq. No. 291205

```
LIB148-057-Q1-E1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4567283
                  214
BLAST score
                  3.0e-17
E value
                  88
Match length
                  52
% identity
                  (AC006841) unknown protein [Arabidopsis thaliana]
NCBI Description
                  291206
Seq. No.
                  LIB148-058-Q1-E1-A5
Seq. ID
                  BLASTX
Method
                  g422032
NCBI GI
BLAST score
                  165
                  3.0e-19
E value
                  66
Match length
                  71
% identity
                  profilin 2 - maize >gi 313140_emb_CAA51719_ (X73280)
NCBI Description
                  profilin 2 [Zea mays]
                  291207
Seq. No.
                  LIB148-058-Q1-E1-B3
Seq. ID
                  BLASTN
Method
NCBI GI
                  g255568
BLAST score
                  249
                  1.0e-138
E value
Match length
                  249
                  100
% identity
NCBI Description pollen specific protein [Zea mays=corn, mRNA, 943 nt]
                  291208
Seq. No.
                  LIB148-058-Q1-E1-D8
Seq. ID
                  BLASTN
Method
                  g1185553
NCBI GI
BLAST score
                   62
                  2.0e-26
E value
                  133
Match length
% identity
                   47
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2)
                  gene, complete cds
                   291209
Seq. No.
                  LIB148-058-Q1-E1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3152590
                   197
BLAST score
                   1.0e-15
E value
                   83
Match length
% identity
                   47
```

NCBI Description

Seq. ID LIB148-058-Q1-E1-F1

Method BLASTX
NCBI GI g3355780
BLAST score 155

(ACO02986) Similar to protein serine/threonine kinase NPK15

gb D31737 from Nicotiana tabacum. [Arabidopsis thaliana]

```
E value
Match length
                  44
% identity
                   64
                  (AJ004997) expansin18 [Lycopersicon esculentum]
NCBI Description
                  291211
Seq. No.
                  LIB148-058-Q1-E1-H2
Seq. ID
Method
                  BLASTX
                  g1523800
NCBI GI
                  198
BLAST score
                  1.0e-15
E value
                   52
Match length
                  73
% identity
                  (Y07694) MAP kinase kinase alpha protein kinase
NCBI Description
                   [Arabidopsis thaliana]
```

 Seq. No.
 291212

 Seq. ID
 LIB148-058-Q1-E1-H3

 Method
 BLASTX

 NCBI GI
 g135449

 PLAST score
 405

NCBI GI g135449
BLAST score 405
E value 9.0e-40
Match length 91
% identity 85

NCBI Description TUBULIN BETA-1 CHAIN >gi_100932_pir__S14701 tubulin beta-1 chain - maize >gi_295851_emb_CAA37060_ (X52878) beta 1

tubulin [Zea mays]

 Seq. No.
 291213

 Seq. ID
 LIB148-058-Q1-E1-H6

 Method
 BLASTX

 MCPL CI
 2729944

NCBI GI g729944
BLAST score 139
E value 7.0e-09
Match length 40
% identity 60

NCBI Description POLLEN ALLERGEN ZEA M 1 (ZEA M I) >gi_478272_pir__JC1524 major allergen mI protein - maize >gi_293902 (L14271) Zea

mI [Zea mays]

Seq. No. 291214

Seq. ID LIB148-058-Q1-E1-H8

Method BLASTX
NCBI GI g4510345
BLAST score 154
E value 3.0e-10
Match length 47
% identity 57

NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 291215

Seq. ID LIB148-059-Q1-E1-C2

Method BLASTX
NCBI GI g3559811
BLAST score 328
E value 1.0e-30
Match length 92



% identity 68 NCBI Description (AJ010735) gr1-protein [Arabidopsis thaliana]

Seq. No. 291216

Seq. ID LIB148-059-Q1-E1-D2

Method BLASTX
NCBI GI g2980770
BLAST score 249
E value 3.0e-28
Match length 118
% identity 63

NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 291217

Seq. ID LIB148-059-Q1-E1-H11

Method BLASTN
NCBI GI g312180
BLAST score 135
E value 6.0e-70
Match length 179
% identity 94

NCBI Description Z.mays GapC4 gene

Seq. No. 291218

Seq. ID LIB148-059-Q1-E1-H12

Method BLASTN

NCBI GI g312180

BLAST score 104

E value 2.0e-51

Match length 160

% identity 91

NCBI Description Z.mays GapC4 gene

Seq. No. 291219

Seq. ID LIB148-060-Q1-E1-B1

Method BLASTN
NCBI GI g600117
BLAST score 71
E value 1.0e-31
Match length 196
% identity 60

NCBI Description Z.mays (B73) gene for extensin-like protein

Seq. No. 291220

Seq. ID LIB148-060-Q1-E1-B10

Method BLASTX
NCBI GI g3786000
BLAST score 142
E value 9.0e-09
Match length 135
% identity 30

NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No. 291221

Seq. ID LIB148-060-Q1-E1-C1

Method BLASTX NCBI GI g1711508



BLAST score 2.0e-32 E value 121 Match length 57 % identity NCBI Description

SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 1 (SRP54) >gi 1020000 (L48284) signal recognition particle 54 kDa

subunit [Hordeum vulgare]

291222 Seq. No.

LIB148-060-Q1-E1-C2 Seq. ID

BLASTX Method g3236246 NCBI GI 282 BLAST score 4.0e-25 E value 89 Match length 53 % identity

(AC004684) putative expansin protein [Arabidopsis thaliana] NCBI Description

Seq. No.

291223 LIB148-060-Q1-E1-D1 Seq. ID

Method BLASTX g2673912 NCBI GI 311 BLAST score 1.0e-28 E value 85 Match length 71 % identity

(AC002561) unknown protein [Arabidopsis thaliana] NCBI Description

291224 Seq. No.

LIB148-060-Q1-E1-H8 Seq. ID

Method BLASTX g1076802 NCBI GI 268 BLAST score 2.0e-23 E value 89 Match length 58 % identity

extensin-like protein - maize >gi_600118_emb_CAA84230_ NCBI Description

(Z34465) extensin-like protein [Zea mays]

>gi 1096557_prf 2111476A extensin-like domain [Zea mays]

Seq. No. 291225

LIB148-061-Q1-E1-A2 Seq. ID

Method BLASTX q1839597 NCBI GI BLAST score 431 E value 1.0e-42 139 Match length 65 % identity

(S82324) calcium/calmodulin-dependent protein kinase NCBI Description

homolog_CaM kinase homolog_MCK1 [Zea mays=maize, cv. Merit,

root caps, Peptide, 625 aa [Zea mays]

291226 Seq. No.

LIB148-061-Q1-E1-B5 Seq. ID

BLASTX Method NCBI GI g508526 BLAST score 289

```
E value
  Match length
                     68
  % identity
                    82
                    (L31642) calmodulin [Mus musculus]
  NCBI Description
  Seq. No.
                    291227
                    LIB148-061-Q1-E1-E5
  Seq. ID
  Method
                    BLASTN
  NCBI GI
                    g22458
  BLAST score
                    53
                     5.0e-21
  E value
                    133
  Match length
                     85
  % identity
  NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)
                    291228
  Seq. No.
                    LIB148-061-Q1-E1-F12
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q2739382
BLAST score
                    291
  E value
                     2.0e-26
  Match length
                     108
  % identity
                     59
  NCBI Description
                    (AC002505) myosin heavy chain-like protein [Arabidopsis
                     thaliana]
                     291229
  Seq. No.
                     LIB148-061-Q1-E1-G1
  Seq. ID
  Method
                     BLASTX
                     g629852
  NCBI GI
                     307
  BLAST score
                     3.0e-28
  E value
  Match length
                     103
  % identity
                     64
  NCBI Description polygalacturonase - maize >gi_288367_emb_CAA46680_ (X65845)
                     polygalacturonase [Zea mays]
                     291230
  Seq. No.
  Seq. ID
                     LIB148-061-Q1-E1-H12
  Method
                     BLASTX
  NCBI GI
                     q1568480
  BLAST score
                     188
  E value
                     3.0e-14
  Match length
                     46
  % identity
  NCBI Description
                    (Z71703) cdc2-like protein kinase [Beta vulgaris]
                     291231
  Seq. No.
  Seq. ID
                     LIB148-062-Q1-E1-E8
  Method
                     BLASTX
  NCBI GI
                     g3355465
  BLAST score
                     206
                     7.0e-17
  E value
  Match length
                     61
  % identity
                     (AC004218) putative Ser/Thr protein kinase [Arabidopsis
  NCBI Description
```

thaliana]



```
Seq. No.
                     291232
                     LIB148-063-Q1-E1-A9
  Seq. ID
  Method
                     BLASTX
                     g422032
  NCBI GI
                     438
  BLAST score
  E value
                     2.0e-43
  Match length
                     118
                     73
  % identity
                    profilin 2 - maize >gi_313140_emb_CAA51719_ (X73280)
  NCBI Description
                     profilin 2 [Zea mays]
  Seq. No.
                     291233
  Seq. ID
                     LIB148-063-Q1-E1-E12
  Method
                     BLASTX
                     g3894197
  NCBI GI
  BLAST score
                     224
  E value
                     3.0e-18
Match length
                     55
                     78
  % identity
  NCBI Description (AC005662) hypothetical protein [Arabidopsis thaliana]
                     291234
  Seq. No.
  Seq. ID
                     LIB148-063-Q1-E1-F11
  Method
                     BLASTX
  NCBI GI
                     g567890
  BLAST score
                     221
                     6.0e-18
  E value
  Match length
                     86
  % identity
                     55
                     (L37352) beta-galactosidase-complementation protein
  NCBI Description
                     [Cloning vector]
  Seq. No.
                     291235
  Seq. ID
                     LIB148-063-Q1-E1-F7
  Method
                     BLASTX
  NCBI GI
                     q22160
  BLAST score
                     151
  E value
                     4.0e-10
  Match length
                     70
   % identity
  NCBI Description (X02842) put. ATP/ADP translocator [Zea mays]
  Seq. No.
                     291236
  Seq. ID
                     LIB148-063-Q1-E1-H3
  Method
                     BLASTX
  NCBI GI
                     q4512703
  BLAST score
                     186
  E value
                     5.0e-14
  Match length
                     114
   % identity
                     39
                    (AC006569) unknown protein [Arabidopsis thaliana]
  NCBI Description
                     291237
  Seq. No.
  Seq. ID
                     LIB148-064-Q1-E1-B3
```

40513

BLASTX

g3660469

Method NCBI GI



BLAST score 169 E value 2.0e-12 Match length 56 % identity 57

NCBI Description (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis

thaliana] >gi_4512693_gb_AAD21746.1_ (AC006569)

succinyl-CoA ligase beta subunit [Arabidopsis thaliana]

Seq. No. 291238

. . .

Seq. ID LIB148-064-Q1-E1-B9

Method BLASTX
NCBI GI g559807
BLAST score 249
E value 3.0e-21
Match length 66
% identity 77

NCBI Description (U15994) histone H3 [Plasmodium falciparum]

Seq. No. 291239

Seq. ID LIB148-064-Q1-E1-C10

Method BLASTX
NCBI GI g1419370
BLAST score 177
E value 7.0e-13
Match length 110
% identity 38

NCBI Description (X97726) actin depolymerizing factor [Zea mays]

Seq. No. 291240

Seq. ID LIB148-064-Q1-E1-C11

Method BLASTX
NCBI GI g2497200
BLAST score 350
E value 4.0e-33
Match length 123
% identity 58

NCBI Description HYPOTHETICAL 34.2 KD PROTEIN IN CUS1-RPL18A1 INTERGENIC

REGION >gi_1084770_pir__S56055 hypothetical protein YMR241w - yeast (Saccharomyces cerevisiae) >gi_736307_emb_CAA88651_

(Z48756) unknown [Saccharomyces cerevisiae]

Seq. No. 291241

Seq. ID LIB148-064-Q1-E1-C12

Method BLASTX
NCBI GI g4056457
BLAST score 305
E value 8.0e-28
Match length 125
% identity 49

NCBI Description (AC005990) ESTs gb_234051 and gb_F13722 come from this

gene. [Arabidopsis thaliana]

Seq. No. 291242

Seq. ID LIB148-064-Q1-E1-D10

Method BLASTX NCBI GI g1749466 BLAST score 179



E value 4.0e-13

Match length 60 % identity 55

NCBI Description (D89129) similar to Saccharomyces cerevisiae

aspartate-semialdehyde dehydrogenase, SWISS-PROT Accession

Number P13663 [Schizosaccharomyces pombe]

Seq. No. 291243

Seq. ID LIB148-064-Q1-E1-G5

Method BLASTX
NCBI GI g4455338
BLAST score 501
E value 7.0e-51
Match length 121
% identity 80

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 291244

Seq. ID LIB148-064-Q1-E1-G9

Method BLASTX
NCBI GI g548492
BLAST score 276
E value 2.0e-24
Match length 108
% identity 56

NCBI Description EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)

(GALACTURAN 1,4-ALPHA-GALACTURONIDASE)

>gi 629853 pir S30066 polygalacturonase - maize

>gi_288379_emb_CAA45751_ (X64408) polygalacturonase [Zea

mays]

Seq. No. 291245

Seq. ID LIB148-064-Q1-E1-H6

Method BLASTX
NCBI GI g893294
BLAST score 531
E value 2.0e-54
Match length 125
% identity 82

NCBI Description (L43362) 4-coumarate:CoA ligase isoform 2 [Oryza sativa]

Seq. No. 291246

Seq. ID LIB148-065-Q1-E1-B6

Method BLASTX
NCBI GI g4417304
BLAST score 336
E value 2.0e-31
Match length 106
% identity 55

NCBI Description (AC006446) putative beta-1,4-mannosyl-glycoprotein

beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis

thaliana]

Seq. No. 291247

Seq. ID LIB148-065-Q1-E1-E9

Method BLASTX NCBI GI g3420055



```
BLAST score
                  3.0e-16
E value
                  69
Match length
                  61
% identity
                  (AC004680) cyclophilin [Arabidopsis thaliana]
NCBI Description
                  291248
Seq. No.
                  LIB148-066-Q1-E1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1326022
BLAST score
                  155
                  2.0e-10
E value
                  79
Match length
                  25
% identity
                  (X01474) polyubiquitin precursor fragment [Saccharomyces
NCBI Description
                  cerevisiae]
                  291249
Seq. No.
                  LIB189-001-Q1-E1-A11
Seq. ID
                  BLASTX
Method
                  g2407279
NCBI GI
BLAST score
                  471
                  2.0e-47
E value
                  93
Match length
% identity
NCBI Description (AF017362) aldolase [Oryza sativa]
                   291250
Seq. No.
                  LIB189-001-Q1-E1-A5
Seq. ID
Method
                  BLASTX
                   q2262105
NCBI GI
BLAST score
                   239
E value
                   4.0e-20
Match length
                   84
% identity
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
Seq. No.
                   291251
                   LIB189-001-Q1-E1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2191136
BLAST score
                   202
E value
                   8.0e-16
Match length
                   94
                   46
% identity
                   (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                   coded for by A. thaliana cDNA T46230; coded for by A.
```

thaliana cDNA H76538; coded for by A. thaliana cDNA H76290

[Arabidopsis thaliana]

291252 Seq. No.

LIB189-001-Q1-E1-E10 Seq. ID

Method BLASTN g4138731 NCBI GI BLAST score 65 2.0e-28 E value 145 Match length



```
% identity
NCBI Description Zea mays mRNA for proline-rich protein
Seq. No.
                  291253
                  LIB189-001-Q1-E1-F10
Seq. ID
                  BLASTX
Method
                  q3582335
NCBI GI
                  153
BLAST score
                  1.0e-10
E value
Match length
                  65
% identity
                  49
```

NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

291254 Seq. No. LIB189-001-Q1-E1-F5 Seq. ID Method BLASTX g2443878 NCBI GI BLAST score 246 6.0e-21 E value

Match length 99 % identity 58

NCBI Description (AC002294) Unknown protein [Arabidopsis thaliana]

291255 Seq. No.

LIB189-001-Q1-E1-G2 Seq. ID

Method BLASTX q2492754 NCBI GI BLAST score 198 E value 4.0e-16 Match length 112 % identity 46

SORBITOL UTILIZATION PROTEIN SOU1 >gi 2183243 (AF002134) NCBI Description

Soulp [Candida albicans]

291256 Seq. No.

LIB189-002-Q1-E1-A3 Seq. ID

Method BLASTX NCBI GI g3810596 BLAST score 224 E value 2.0e-18 127 Match length % identity 38

(AC005398) reverse-transcriptase-like protein [Arabidopsis NCBI Description

thaliana]

291257 Seq. No.

LIB189-002-Q1-E1-B10 Seq. ID

Method BLASTX NCBI GI g400803 BLAST score 461 E value 2.0e-46 Match length 92 100 % identity

NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE

(PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi 283033_pir__A42807 phosphoglycerate mutase (EC 5.4.2.1), 2, 3-bisphosphoglycerate-independent - maize





>gi_168588 (M80912) 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Zea mays]

Seq. No. 291258

Seq. ID LIB189-002-Q1-E1-B8

Method BLASTX
NCBI GI g3080440
BLAST score 147
E value 2.0e-09
Match length 35

NCBI Description (AL022605) hypothetical protein [Arabidopsis thaliana]

Seq. No. 291259

% identity

Seq. ID LIB189-002-Q1-E1-C9

83

Method BLASTX
NCBI GI g129949
BLAST score 207
E value 1.0e-16
Match length 79
% identity 54

NCBI Description BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN)

>gi 89740 pir S06280 decorin precursor - bovine

>gi 619 emb CAA68702 (Y00712) precursor polypeptide (AA

-30 to 330) [Bos taurus]

Seq. No. 291260

Seq. ID LIB189-002-Q1-E1-D1

Method BLASTX
NCBI GI g4096786
BLAST score 141
E value 1.0e-16
Match length 82
% identity 61

NCBI Description (U39958) NADP-malic enzyme [Zea mays]

Seq. No. 291261

Seq. ID LIB189-002-Q1-E1-E9

Method BLASTN
NCBI GI g2984708
BLAST score 285
E value 1.0e-159
Match length 340
% identity 96

NCBI Description Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete

cds

Seq. No. 291262

Seq. ID LIB189-002-Q1-E1-F8

Method BLASTX
NCBI GI g2621798
BLAST score 227
E value 8.0e-19
Match length 78
% identity 53

NCBI Description (AE000850) transcriptional regulator [Methanobacterium

thermoautotrophicum]

NCBI Description



```
Seq. No.
                  291263
                  LIB189-002-Q1-E1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4510348
BLAST score
                  149
                  1.0e-09
E value
Match length
                  54
                  52
% identity
                  (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                  291264
Seq. No.
                  LIB189-002-Q1-E1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g631955
BLAST score
                  470
E value
                  3.0e-47
Match length
                  103
% identity
                  83
                  chlorophyll a/b binding protein type II (LHCI) - Lolium
NCBI Description
                  temulentum L
                  291265
Seq. No.
                  LIB189-003-Q1-E1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3341693
BLAST score
                  178
E value
                  6.0e-13
                  77
Match length
% identity
                  55
                  (AC003672) unknown protein [Arabidopsis thaliana]
NCBI Description
                  291266
Seq. No.
                  LIB189-003-Q1-E1-A4
Seq. ID
Method
                  BLASTX
                  g1703029
NCBI GI
BLAST score
                  297
E value
                  6.0e-27
                  126
Match length
% identity
                  47
                  CLATHRIN COAT ASSEMBLY PROTEIN AP47 HOMOLOG 2 (CLATHRIN
NCBI Description
                  COAT ASSOCIATED PROTEIN AP47 HOMOLOG 2) (GOLGI ADAPTOR AP-1
                  47 KD PROTEIN HOMOLOG 2) (HA1 47 KD SUBUNIT HOMOLOG 2)
                   (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX...
                  >gi 468382 (L07074) clathrin-associated adaptor protein
                   [Rattus norvegicus]
Seq. No.
                  291267
Seq. ID
                  LIB189-003-Q1-E1-B10
Method
                  BLASTX
NCBI GI
                  q2967835
BLAST score
                  236
E value
                  8.0e-20
Match length
                  67
% identity
                  60
```

(AF052061) polygalacturonase [Ophiostoma novo-ulmi]



```
Seq. No.
                  291268
                  LIB189-003-Q1-E1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2232017
BLAST score
                  300
E value
                  3.0e-27
                  100
Match length
                  59
% identity
NCBI Description (U95953) viviparous-14 [Zea mays]
Seq. No.
                  291269
Seq. ID
                  LIB189-003-Q1-E1-D4
                  BLASTX
Method
                  g4558558
NCBI GI
BLAST score
                  213
E value
                  5.0e-17
Match length
                  111
                  45
% identity
                  (AC007138) putative polygalacturonidase [Arabidopsis
NCBI Description
                  thaliana]
                  291270
Seq. No.
                  LIB189-003-Q1-E1-E7
Seq. ID
Method
                  BLASTX
                  g2062676
NCBI GI
BLAST score
                  144
E value
                  5.0e-09
Match length
                  54
% identity
NCBI Description (U88909) inhibitor of apoptosis protein 2 [Mus musculus]
                  291271
Seq. No.
                  LIB189-003-Q1-E1-G5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1212995
BLAST score
                   65
E value
                   4.0e-28
Match length
                   93
% identity
                   92
NCBI Description H.vulgare mRNA for UDP-glucose pyrophosphorylase
                   291272
Seq. No.
                  LIB189-003-Q1-E1-G9
Seq. ID
                  BLASTX
Method
                   q1710565
NCBI GI
                   369
BLAST score
                   2.0e-47
E value
Match length
                   100
% identity
                   95
                  60S RIBOSOMAL PROTEIN L44 (L41) >gi_1255906_dbj_BAA11057_
NCBI Description
                   (D67040) ribosomal protein L41 [Candida utilis]
                   291273
Seq. No.
```

LIB189-004-Q1-E1-A12 Seq. ID

BLASTN Method NCBI GI g2687357 BLAST score 208



```
1.0e-113
E value
                  253
Match length
                  95
% identity
                  Zea mays nonphototropic hypocotyl 1 (nph1) mRNA, complete
NCBI Description
                  cds
Seq. No.
                  291274
                  LIB189-004-Q1-E1-C10
Seq. ID
                  BLASTN
Method
                  q4185305
NCBI GI
                  295
BLAST score
                  1.0e-165
E value
                  384
Match length
                  95
% identity
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                  (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes
                  291275
Seq. No.
                  LIB189-004-Q1-E1-D5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2880048
                  227
BLAST score
                  1.0e-18
E value
                  93
Match length
% identity
                  (AC002340) unknown protein [Arabidopsis thaliana]
NCBI Description
                  291276
Seq. No.
Seq. ID
                  LIB189-004-Q1-E1-F7
                  BLASTN
Method
NCBI GI
                  q1185553
                  60
BLAST score
                  5.0e-25
E value
                  111
Match length
                   53
% identity
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2)
NCBI Description
                   gene, complete cds
                   291277
Seq. No.
                   LIB189-004-Q1-E1-H11
Seq. ID
Method
                   BLASTX
                   g3062801
NCBI GI
BLAST score
                   155
                   3.0e-10
E value
Match length
                   37
                   70
% identity
                  (AB012873) arginine decarboxylase [Nicotiana sylvestris]
NCBI Description
                   291278
Seq. No.
```

Seq. ID LIB189-005-Q1-E1-A7

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 8.0e-11
Match length 36

```
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  291279
Seq. No.
Seq. ID
                  LIB189-005-Q1-E1-B9
Method
                  BLASTX
                  g2244888
NCBI GI
                  236
BLAST score
                  8.0e-20
E value
                  120
Match length
% identity
                  39
                  (Z97338) similarity to cytochrome P450 [Arabidopsis
NCBI Description
                  thaliana]
                  291280
Seq. No.
Seq. ID
                  LIB189-005-Q1-E1-H11
Method
                  BLASTX
NCBI GI
                  g629861
BLAST score
                  157
                  2.0e-10
E value
                  91
Match length
                  40
% identity
NCBI Description zein Zd1, 19K - maize >gi 535020 emb CAA47639 (X67203)
                  zein Zdl (19 kDa zein) [Zea mays]
                  291281
Seq. No.
Seq. ID
                  LIB189-006-Q1-E1-B7
                  BLASTX
Method
NCBI GI
                  g3004555
BLAST score
                  170
                  5.0e-12
E value
                  117
Match length
% identity
                  29
                  (AC003673) similar to salt inducible protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  291282
                  LIB189-006-Q1-E1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4336436
BLAST score
                  172
E value
                  2.0e-12
Match length
                  56
% identity
                  57
NCBI Description (AF092432) protein phosphatase type 2C [Lotus japonicus]
                  291283
Seq. No.
```

Seq. ID LIB189-006-Q1-E1-D4

Method BLASTX
NCBI GI g115608
BLAST score 640
E value 4.0e-67
Match length 127
% identity 98

NCBI Description PHOSPHOENOLPYRUVATE CARBOXYLASE 1 (PEPCASE)

>gi_22563_emb_CAA33316_ (X15238) phosphoenolpyruvate

carboxylase (AA 1 - 970) [Zea mays]



```
291284
  Seq. No.
  Seq. ID
                    LIB189-006-Q1-E1-D5
                    BLASTX
  Method
  NCBI GI
                    g4581122
  BLAST score
                    233
  E value
                    2.0e-19
  Match length
                    96
                    47
% identity
                    (AC005825) putative glucokinase [Arabidopsis thaliana]
  NCBI Description
                    291285
  Seq. No.
  Seq. ID
                    LIB189-006-Q1-E1-F2
                    BLASTX
  Method
  NCBI GI
                    g2735428
  BLAST score
                    269
  E value
                    1.0e-23
  Match length
                    128
  % identity
                    44
                   (U94913) H-K-ATPase alpha 2b subunit [Rattus norvegicus]
  NCBI Description
                    291286
  Seq. No.
                    LIB189-006-Q1-E1-H6
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q2052383
  BLAST score
                    222
                    5.0e-27
  E value
  Match length
                    68
  % identity
  NCBI Description (U66345) calreticulin [Arabidopsis thaliana]
                    291287
  Seq. No.
  Seq. ID
                    LIB189-007-Q1-E1-B2
                    BLASTX
  Method
  NCBI GI
                    q468517
  BLAST score
                    216
  E value
                    2.0e-17
  Match length
                    70
                    67
  % identity
  NCBI Description
                    (X14334) zein [Zea mays]
  Seq. No.
                    291288
  Seq. ID
                    LIB189-007-Q1-E1-B4
  Method
                    BLASTX
                    q120657
  NCBI GI
  BLAST score
                    205
  E value
                    2.0e-16
  Match length
                    81
  % identity
                    GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
  NCBI Description
                    CHLOROPLAST >gi 66024 pir DEZMG3
                    glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                     (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
```

40523

maize >gi_168479 (M18976) glyceraldehyde-3-phosphate
dehydrogenase [Zea mays] >gi_763035_emb_CAA33455_ (X15408)

glyceraldehyde-3-phosphate dehydrogenase [Zea mays]



```
Seq. No.
Seq. ID
                  LIB189-007-Q1-E1-B6
Method
                  BLASTX
NCBI GI
                  g3406742
BLAST score
                  146
E value
                  3.0e-09
Match length
                  126
% identity
                  36
                  (AF017990) Fkbp39p [Schizosaccharomyces pombe]
NCBI Description
                  >gi 4456817 emb CAB37433.1 (AL035548) Peptidyl Prolyl
                  cis-trans isomerase [Schizosaccharomyces pombe]
                  291290
Seq. No.
Seq. ID
                  LIB189-007-Q1-E1-B9
Method
                  BLASTX
NCBI GI
                  g3249071
BLAST score
                  203
E value
                  5.0e-34
Match length
                  126
                  52
% identity
NCBI Description
                  (AC004473) Contains similarity to protein-tyrosine
                  phosphatase 2 gb L15420 from Dictyostelium discoideum. EST
                  gb N38718 comes from this g [Arabidopsis thaliana]
Seq. No.
                  291291
                  LIB189-007-Q1-E1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4102727
BLAST score
                  280
                  6.0e-25
E value
                  97
Match length
% identity
NCBI Description
                   (AF015782) blight-associated protein pl2 precursor [Citrus
                  jambhiri]
Seq. No.
                  291292
Seq. ID
                  LIB189-007-Q1-E1-C7
Method
                  BLASTX
NCBI GI
                  g141617
BLAST score
                  283
E value
                  3.0e-25
Match length
                  132
% identity
                  48
                  ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                  >gi 100941 pir S12140 zein Zc1 - maize
                  >gi_100945_pir B29017 zein 2 - maize
                  >gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                  >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
Seq. No.
                  291293
Seq. ID
                  LIB189-007-Q1-E1-C8
```

Method BLASTX NCBI GI g2979555 BLAST score 262 E value 8.0e-23 Match length 115 % identity 47





```
(AC003680) unknown protein [Arabidopsis thaliana]
NCBI Description
                  291294
Seq. No.
Seq. ID
                  LIB189-007-Q1-E1-D5
Method
                  BLASTN
NCBI GI
                   q3821780
BLAST score
                   36
                   4.0e-11
E value
                   36
Match length
                   100
% identity
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
                   291295
Seq. No.
Seq. ID
                   LIB189-007-Q1-E1-F7
                   BLASTX
Method
NCBI GI
                   g118104
BLAST score
                   463
                   2.0e-46
E value
Match length
                   111
                   81
% identity
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                   >gi 68408 pir CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                   maize >gi 168461 (M55021) cyclophilin [Zea mays]
                   >gi 82914\overline{8} emb CAA48638 (X68678) cyclophilin [Zea mays]
                   291296
Seq. No.
Seq. ID
                   LIB189-007-Q1-E1-G7
                   BLASTN
Method
NCBI GI
                   q22336
BLAST score
                   254
                   1.0e-141
E value
Match length
                   311
                   95
% identity
                  Maize mRNA for an 18kDa heat shock protein
NCBI Description
Seq. No.
                   291297
                   LIB189-007-Q1-E1-H10
Seq. ID
Method
                   BLASTX
                   g3702326
NCBI GI
BLAST score
                   499
E value
                   1.0e-50
Match length
                   114
% identity
                   81
                  (AC005397) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   291298
Seq. No.
                   LIB189-007-Q1-E1-H8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2773154
                   235
BLAST score
E value
                   8.0e-20
Match length
                   86
```

52

[Oryza sativa]

% identity

NCBI Description

(AF039573) abscisic acid- and stress-inducible protein



49

% identity

```
291299
Seq. No.
                  LIB189-008-Q1-E1-B11
Seq. ID
                  BLASTX
Method
                  q4337200
NCBI GI
BLAST score
                  192
E value
                  1.0e-14
                  52
Match length
% identity
                  (AC006403) putative NAM protein [Arabidopsis thaliana]
NCBI Description
                  291300
Seq. No.
                  LIB189-008-Q1-E1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g266578
BLAST score
                  241
                  2.0e-20
E value
Match length
                  56
% identity
                  METALLOTHIONEIN-LIKE PROTEIN 1 >gi_100898_pir__S17560
NCBI Description
                  metallothionein-like protein - maize >gi 236730 bbs 57629 -
                   (S57628) metallothionein homologue [Zea mays, Peptide, 76
                  aa] [Zea mays] >gi 559536_emb_CAA57676_ (X82186)
                  metallothionein- like protein [Zea mays]
                  >gi_228095_prf__1717215A metallothionein-like protein [Zea
                  mays]
                  291301
Seq. No.
                  LIB189-008-Q1-E1-C3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3810827
                   454
BLAST score
                   7.0e-46
E value
Match length
                   126
                   74
% identity
                  (AL032684) 60s ribosomal protein 12 [Schizosaccharomyces
NCBI Description
                   pombe]
Seq. No.
                   291302
                   LIB189-008-Q1-E1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g548763
                   173
BLAST score
E value
                   1.0e-12
                   60
Match length
                   60
% identity
                   60S RIBOSOMAL PROTEIN L2 >gi_312177_emb_CAA51666_ (X73146)
NCBI Description
                   ribosomal protein L2 [Schizosaccharomyces pombe]
                   291303
Seq. No.
                   LIB189-008-Q1-E1-D7
Seq. ID
                   BLASTX
Method
                   g4160292
NCBI GI
BLAST score
                   326
                   3.0e-30
E value
Match length
                   140
```

NCBI Description (Y18209) alpha-N-acetylglucosaminidase [Nicotiana tabacum]



```
291304
Seq. No.
Seq. ID
                  LIB189-008-Q1-E1-E12
Method
                  BLASTX
NCBI GI
                  g3548808
BLAST score
                  209
                  1.0e-16
E value
                  126
Match length
                  37
% identity
                  (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
                  291305
Seq. No.
Seq. ID
                  LIB189-008-Q1-E1-E3
Method
                  BLASTX
                  g4185308
NCBI GI
BLAST score
                  183
E value
                  1.0e-13
Match length
                  46
% identity
NCBI Description (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
Seq. No.
                  291306
                  LIB189-008-Q1-E1-F8
Seq. ID
                  BLASTX
Method
                  g2190992
NCBI GI
BLAST score
                  203
E value
                  7.0e-16
Match length
                  76
                  49
% identity
                  (AF004358) glutathione S-transferase TSI-1 [Aegilops
NCBI Description
                  tauschii]
Seq. No.
                  291307
                  LIB189-008-Q1-E1-G11
Seq. ID
Method
                  BLASTX
                  g224508
NCBI GI
BLAST score
                  354
E value
                  3.0e-42
Match length
                  115
% identity
                  84
NCBI Description zein A20 [Zea mays]
                  291308
Seq. No.
                  LIB189-009-Q1-E1-A4
Seq. ID
Method
                  BLASTN
                  g3821780
NCBI GI
BLAST score
                  36
                  1.0e-10
E value
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
```

Seq. No. 291309

Seq. ID LIB189-009-Q1-E1-A7

Method BLASTX NCBI GI g141603 BLAST score 430



```
2.0e-42
E value
Match length
                  125
                  77
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                  >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
Seq. No.
                  291310
Seq. ID
                  LIB189-009-Q1-E1-B5
                  BLASTX
Method
NCBI GI
                  q3298551
BLAST score
                  347
                  9.0e-33
E value
                  138
Match length
                  7
% identity
                  (AC004681) putative salt-inducible protein [Arabidopsis
NCBI Description
                  thaliana]
                  291311
Seq. No.
Seq. ID
                  LIB189-009-Q1-E1-B7
                  BLASTN
Method
NCBI GI
                  q3821780
                  37
BLAST score
                  2.0e-11
E value
                  49
Match length
                  67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  291312
Seq. No.
Seq. ID
                  LIB189-009-Q1-E1-C11
Method
                  BLASTX
NCBI GI
                  q4454018
BLAST score
                  174
E value
                  1.0e-12
Match length
                  93
% identity
                  41
NCBI Description (AL035396) SRG1-like protein [Arabidopsis thaliana]
                  291313
Seq. No.
                  LIB189-009-Q1-E1-D12
Seq. ID
Method
                  BLASTX
                  q2058284
NCBI GI
BLAST score
                  159
                  9.0e-11
E value
Match length
                  75
% identity
                  44
                  (X97378) atranbp1b [Arabidopsis thaliana]
NCBI Description
                  291314
Seq. No.
                  LIB189-009-Q1-E1-D6
Seq. ID
```

Method BLASTX
NCBI GI g1237250
BLAST score 267
E value 7.0e-25
Match length 143
% identity 47

NCBI Description (X96784) cytochrome P450 [Nicotiana tabacum]

% identity

NCBI Description

60



```
291315
Seq. No.
                  LIB189-009-Q1-E1-E11
Seq. ID
                  BLASTX
Method
                  g1177047
NCBI GI
BLAST score
                  146
E value
                  3.0e-09
Match length
                  43
                  63
% identity
                  14 KD ZINC-BINDING PROTEIN (PROTEIN KINASE C INHIBITOR)
NCBI Description
                  (PKCI) >gi_629857_pir__S44158 protein kinase C inhibitor -
                  maize >gi_473187_emb_CAA82751_ (Z29643) protein kinase C
                  inhibitor [Zea mays]
                  291316
Seq. No.
Seq. ID
                  LIB189-009-Q1-E1-E6
Method
                  BLASTN
                  g3821780
NCBI GI
                  37
BLAST score
                  2.0e-11
E value
                  49
Match length
                  67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  291317
Seq. No.
Seq. ID
                  LIB189-009-Q1-E1-F3
                  BLASTX
Method
NCBI GI
                  g1350986
BLAST score
                  176
                  2.0e-13
E value
                  73
Match length
% identity
                  63
                  40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
NCBI Description
                  >gi 483431 dbj BAA05059 (D26060) cyc07 [Oryza sativa]
                  291318
Seq. No.
                  LIB189-009-Q1-E1-G7
Seq. ID
Method
                  BLASTX
                  q68029
NCBI GI
BLAST score
                  222
                  4.0e-18
E value
Match length
                  45
% identity
                  98
                  phosphoenolpyruvate carboxylase (EC 4.1.1.31) - maize
NCBI Description
                  >qi 22408 emb CAA33317 (X15239) PEP carboxylase [Zea mays]
                  >gi 228619_prf 1807332A phosphoenolpyruvate carboxylase
                   [Zea mays]
Seq. No.
                  291319
                  LIB189-010-Q1-E1-B9
Seq. ID
Method
                  BLASTX
                  g2826842
NCBI GI
BLAST score
                  230
                  4.0e-19
E value
                  68
Match length
```

(AJ002236) loxc homologue [Lycopersicon pimpinellifolium]



```
291320
Seq. No.
Seq. ID
                  LIB189-010-Q1-E1-C11
Method
                  BLASTX
NCBI GI
                  g2494417
BLAST score
                  271
                  7.0e-24
E value
                  78
Match length
                  67
% identity
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC
NCBI Description
                  (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >qi 1364071 pir S57717 fructose-1, 6-bisphosphatase (EC
                  3.1.3.11) - sugarcane hybrid H65-7052
                  >gi 895909 emb CAA61409.1 (X89006) fructose-1,
                  6-bisphosphatase [Saccharum hybrid cultivar H65-7052]
                  291321
Seq. No.
Seq. ID
                  LIB189-010-Q1-E1-D3
                  BLASTN
Method
                  g3821780
NCBI GI
BLAST score
                  37
E value
                  3.0e-11
                  37
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  291322
Seq. No.
Seq. ID
                  LIB189-010-Q1-E1-E7
                  BLASTN
Method
NCBI GI
                  g3821780
BLAST score
                  37
E value
                  3.0e-11
Match length
                  37
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  291323
                  LIB189-010-Q1-E1-G7
Seg. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  37
E value
                   3.0e-11
Match length
                   49
% identity
                   67
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  291324
Seq. ID
                  LIB189-010-Q1-E1-H2
Method
                  BLASTX
NCBI GI
                   g485742
```

Method BLASTX
NCBI GI g485742
BLAST score 181
E value 2.0e-13
Match length 43
% identity 86

NCBI Description (L32791) pyrophosphatase [Beta vulgaris]

Seq. No. 291325



164

90

Match length

% identity

```
LIB189-011-Q1-E1-A11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2130082
                  330
BLAST score
                  9.0e-31
E value
Match length
                  136
% identity
                  46
                  protein kinase Xa21 (EC 2.7.1.-) - rice >gi 1122443
NCBI Description
                   (U37133) receptor kinase-like protein [Oryza sativa]
                  >qi 2586085 (U72723) receptor kinase-like protein [Oryza
                   longistaminata] >gi_1586408_prf 2203451A receptor
                   kinase-like protein [Oryza sativa]
                   291326
Seq. No.
                  LIB189-011-Q1-E1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g118104
BLAST score
                   569
E value
                   6.0e-59
                   123
Match length
                   89
% identity
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                   >gi 68408 pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                   maize >gi 168461 (M55021) cyclophilin [Zea mays]
                   >gi 82914\overline{8} emb CAA48638_ (X68678) cyclophilin [Zea mays]
Seq. No.
                   291327
                   LIB189-011-Q1-E1-C3
Seq. ID
                   BLASTN
Method
                   g22549
NCBI GI
                   35
BLAST score
                   4.0e-10
E value
Match length
                   67
                   88
% identity
NCBI Description Maize gene for a 27kDa storage protein, zein
Seq. No.
                   291328
                   LIB189-011-Q1-E1-C4
Seq. ID
                   BLASTN
Method
                   q4416300
NCBI GI
BLAST score
                   44
E value
                   2.0e-15
Match length
                   48
                   98
% identity
                   Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                   region, complete sequence
Seq. No.
                   291329
                   LIB189-011-Q1-E1-C9
Seq. ID
Method
                   BLASTN
                   g22549
NCBI GI
BLAST score
                   96
                   2.0e-46
E value
```

NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. ID Method

NCBI GI



```
291330
Seq. No.
Seq. ID
                  LIB189-011-Q1-E1-D3
Method
                  BLASTN
NCBI GI
                  g4206307
BLAST score
                  46
                  1.0e-16
E value
                  266
Match length
                  79
% identity
NCBI Description Zea mays retrotransposon Cinful-2
                  291331
Seq. No.
Seq. ID
                  LIB189-011-Q1-E1-E12
Method
                  BLASTX
NCBI GI
                  g2832651
BLAST score
                  171
E value
                  1.0e-12
Match length
                  41
% identity
                  (AL021710) RNA helicase - like protein [Arabidopsis
NCBI Description
                  thaliana]
                  291332
Seq. No.
Seq. ID
                  LIB189-011-Q1-E1-G6
Method
                  BLASTX
NCBI GI
                  g4432837
BLAST score
                  160
                  7.0e-11
E value
                  49
Match length
% identity
NCBI Description (AC006283) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  291333
Seq. ID
                  LIB189-011-Q1-E1-H1
Method
                  BLASTX
NCBI GI
                  g3868853
BLAST score
                  145
                  4.0e-09
E value
Match length
                  33
% identity
                  73
NCBI Description (AB013853) GPI-anchored protein [Vigna radiata]
Seq. No.
                  291334
                  LIB189-011-Q1-E1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1946372
BLAST score
                  226
                  1.0e-18
E value
Match length
                  70
% identity
                   63
                  (U93215) yeast hypothetical protein YDB1_SCHPO isolog
NCBI Description
                   [Arabidopsis thaliana]
                  291335
Seq. No.
```

40532

LIB189-011-Q1-E1-H4

BLASTX

g2829751



BLAST score 188 E value 3.0e-14 Match length 102 % identity 38

NCBI Description MACROPHAGE MIGRATION INHIBITORY FACTOR HOMOLOG (BMMIF) >gi_1850559 (U88035) macrophage migration inhibitory factor [Brugia malayi] >gi 2190976 (AF002699) macrophage migration

inhibitory factor [Brugia malayi]

Seq. No. 291336

Seq. ID LIB189-011-Q1-E1-H6

Method BLASTX
NCBI GI g2326947
BLAST score 310
E value 1.0e-28
Match length 76
% identity 80

NCBI Description (Z50801) Chlorophyll a/b-binding protein CP29 precursor

[Zea mays]

Seq. No. 291337

Seq. ID LIB189-012-Q1-E1-A6

Method BLASTX
NCBI GI g168701
BLAST score 143
E value 3.0e-09
Match length 65
% identity 51

NCBI Description (M60837) zein [Zea mays]

Seq. No. 291338

Seq. ID LIB189-012-Q1-E1-A7

Method BLASTX
NCBI GI g120941
BLAST score 185
E value 7.0e-14
Match length 49
% identity 65

NCBI Description GAR1 PROTEIN >gi_83030_pir__S19634 nucleolar protein GAR1 -

yeast (Saccharomyces cerevisiae) >gi_3728 emb_CAA45162_ (X63617) GAR1 [Saccharomyces cerevisiae] >gi_487935 (U00060) Garlp: Small nucleolar RNA protein required for

pre-rRNA splicing [Saccharomyces cerevisiae]

Seq. No. 291339

Seq. ID LIB189-012-Q1-E1-D6

Method BLASTX
NCBI GI g2723471
BLAST score 217
E value 7.0e-18
Match length 83
% identity 55

NCBI Description (D87819) sucrose transporter [Oryza sativa]

Seq. No. 291340

Seq. ID LIB189-012-Q1-E1-G2

Method BLASTX

```
g2213607
NCBI GI
                  188
BLAST score
                  2.0e-14
E value
Match 1 th
                  99
                  51
% ident. .
NCBI De: iption (AC000103) F21J9.1 [Arabidopsis thaliana]
                  291341
Seq. No.
                  LIB189-012-Q1-E1-H12
Seq. ID
                  BLASTN
Method
NCBI GI
                  q949979
BLAST score
                  37
                  2.0e-11
E value
                  37
Match length
                  100
% identity
NCBI Description Z.mays Glossy2 locus DNA
                  291342
Seq. No.
Seq. ID
                  LIB189-012-Q1-E1-H6
                  BLASTX
Method
                  g3878134
NCBI GI
                  147
BLAST score
                  1.0e-09
E value
                  59
Match length
                  42
% identity
NCBI Description (Z68218) K01H12.1 [Caenorhabditis elegans]
                  291343
Seq. No.
                  LIB189-013-Q1-E1-C3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q145404
BLAST score
                  346
                  9.0e-33
E value
Match length
                  119
% identity
NCBI Description (M77739) betaine aldehyde dehydrogenase [Escherichia coli]
Seq. No.
                  291344
Seq. ID
                  LIB189-013-Q1-E1-G1
Method
                  BLASTN
NCBI GI
                  q2062705
BLAST score
                  36
E value
                  9.0e-11
Match length
                  36
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  291345
                  LIB189-013-Q1-E1-G10
Seq. ID
Method
                  BLASTX
```

NCBI GI g1345588 BLAST score 166 E value 4.0e-12 Match length 61 59 % identity

NCBI Description 14-3-3-LIKE PROTEIN GF14-12 >gi 998432 bbs 164524

GF14-12=GRF2 product/14-3-3 protein homolog [Zea mays,

NCBI Description

Seq. No.

291351



XL80, Peptide, 261 aa]

```
291346
Seq. No.
                  LIB189-013-Q1-E1-G2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g12408
                  327
BLAST score
                  0.0e + 00
E value
                  352
Match length
                   98
% identity
                  Maize chloroplast 3'part of rpoC2 gene, rps2 gene, atpI
NCBI Description
                  gene and 5'part of atpH gene
                  291347
Seq. No.
                  LIB189-013-Q1-E1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4505823
BLAST score
                   259
E value
                   4.0e-28
                   125
Match length
% identity
                   50
                  pirin >gi_1907076_emb_CAA69194_ (Y07867) pirin [Homo
NCBI Description
                   sapiens] >gi_1907078_emb_CAA69195 (Y07868) pirin [Homo
                   sapiens]
                   291348
Seq. No.
Seq. ID
                   LIB189-014-Q1-E1-A11
Method
                   BLASTN
NCBI GI
                   q6598490
BLAST score
                   163
E value
                   1.0e-86
                   184
Match length
% identity
                   96
                   Arabidopsis thaliana chromosome II BAC F15K20 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   291349
Seq. No.
                   LIB189-014-Q1-E1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1666096
BLAST score
                   341
E value
                   4.0e-32
Match length
                   111
% identity
                   59
                  (Y09113) dioxygenase [Marah macrocarpus]
NCBI Description
Seq. No.
                   291350
                   LIB189-015-Q1-E1-E1
Seq. ID
Method
                   BLASTX
                   g1652848
NCBI GI
                   291
BLAST score
                   3.0e-26
E value
Match length
                   75
% identity
                   68
```

40535

(D90909) DNA photolyase [Synechocystis sp.]

Match length

% identity

128

62



```
LIB189-015-Q1-E1-E2
Seq. ID
Method
                  BLASTX
                  g3850075
NCBI GI
BLAST score
                  195
                  5.0e-15
E value
Match length
                  80
% identity
                  49
NCBI Description (Z98533) hypothetical protein [Schizosaccharomyces pombe]
                  291352
Seq. No.
Seq. ID
                  LIB189-015-Q1-E1-F3
Method
                  BLASTN
                  g168579
NCBI GI
BLAST score
                  221
                  1.0e-121
E value
                  309
Match length
% identity
                  93
NCBI Description Maize pyruvate, orthophosphate dikinase mRNA, complete cds
                  291353
Seq. No.
                  LIB189-015-Q1-E1-H5
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2062705
BLAST score
                  36
                  8.0e-11
E value
                  36
Match length
                  100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                   291354
Seq. No.
                  LIB189-015-Q1-E1-H7
Seq. ID
                  BLASTN
Method
NCBI GI
                   g3821780
BLAST score
                   36
E value
                   5.0e-11
                   36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   291355
Seq. No.
Seq. ID
                   LIB189-016-Q1-E1-A2
Method
                   BLASTX
NCBI GI
                   q4539660
BLAST score
                   231
E value
                   2.0e-19
Match length
                   71
% identity
                   59
NCBI Description (AF061282) polyprotein [Sorghum bicolor]
                   291356
Seq. No.
                   LIB189-016-Q1-E1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3776557
BLAST score
                   382
                   6.0e - 37
E value
```



(AC005388) Contains similarity to gi_2924495 hypothetical

protein Rv1920 from Mycobacterium tuberculosis genome gb AL022020. [Arabidopsis thaliana]

Seq. No. 291357

NCBI Description

Seq. ID LIB189-016-Q1-E1-C5

Method BLASTN
NCBI GI g2668737
BLAST score 55
E value 1.0e-22
Match length 113

Match length 113 % identity 99

NCBI Description Zea mays translation initiation factor 5A (TIF5A) mRNA,

complete cds

Seq. No. 291358

Seq. ID LIB189-016-Q1-E1-C8

Method BLASTX
NCBI GI g2190540
BLAST score 279
E value 8.0e-25
Match length 84

% identity 62
NCBI Description (AC001229) Similar to Arabidopsis TFL1 (gb_U77674).

[Arabidopsis thaliana]

Seq. No. 291359

Seq. ID LIB189-016-Q1-E1-H4

Method BLASTX
NCBI GI g3522937
BLAST score 195
E value 5.0e-15
Match length 50
% identity 60

NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]

Seq. No. 291360

Seq. ID LIB189-016-Q1-E1-H8

Method BLASTX
NCBI GI g4539457
BLAST score 411
E value 3.0e-40
Match length 81
% identity 88

NCBI Description (AL049500) heat shock transcription factor-like protein

[Arabidopsis thaliana]

Seq. No. 291361

Seq. ID LIB189-017-Q1-E1-A8

Method BLASTX
NCBI GI g3738208
BLAST score 147
E value 3.0e-14
Match length 89
% identity 47

NCBI Description (AL031853) strong similarity to human Rev interacting

protein Rip-1 [Schizosaccharomyces pombe]



```
291362
Seq. No.
Seq. ID
                  LIB189-017-Q1-E1-B2
Method
                  BLASTX
NCBI GI
                  q2244955
BLAST score
                  295
                  9.0e-27
E value
                  112
Match length
% identity
                  (Z97340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  291363
Seq. No.
Seq. ID
                  LIB189-017-Q1-E1-D7
Method
                  BLASTX
NCBI GI
                  q113466
BLAST score
                  537
E value
                  4.0e-55
Match length
                  122
                  88
% identity
                  ADP, ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE
NCBI Description
                  NUCLEOTIDE TRANSLOCATOR) (ANT) >gi 72020 pir XWNC ADP, ATP
                   carrier protein - Neurospora crassa >gi 2977 emb CAA25104
                   (X00363) ADP/ATP carrier protein [Neurospora crassa]
                  291364
Seq. No.
Seq. ID
                  LIB189-017-Q1-E1-F10
Method
                  BLASTX
NCBI GI
                  q2961355
BLAST score
                   360
E value
                   2.0e-34
                  114
Match length
                   59
% identity
NCBI Description (AL022140) glucosidase like protein [Arabidopsis thaliana]
                   291365
Seq. No.
                   LIB189-017-Q1-E1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1778147
BLAST score
                   268
E value
                   1.0e-23
Match length
                   95
% identity
                   66
                  (U66403) phosphate/phosphoenolpyruvate translocator
NCBI Description
                   precursor [Zea mays]
                   291366
Seq. No.
                   LIB189-017-Q1-E1-F4
Seq. ID
Method
                   BLASTX
                   g2829888
NCBI GI
BLAST score
                   175
                   2.0e-18
E value
                   108
Match length
% identity
                   43
```

Seq. No. 291367

NCBI Description

Seq. ID LIB189-017-Q1-E1-H10

40538

(AC002396) Hypothetical protein [Arabidopsis thaliana]



```
Method
NCBI GI
                  g2739219
BLAST score
                  245
E value
                  8.0e-21
Match length
                  51
% identity
                   98
                  (AJ001161) rpS28 [Hordeum vulgare]
NCBI Description
Seq. No.
                  291368
Seq. ID
                  LIB189-017-Q1-E1-H5
Method
                  BLASTN
NCBI GI
                  g829147
BLAST score
                  95
E value
                   4.0e-46
Match length
                  111
% identity
                   96
NCBI Description
                  Z.mays gene for cyclophilin
Seq. No.
                  291369 - 30
Seq. ID
                  LIB189-017-Q1-E1-H8
Method
                  BLASTX
NCBI GI
                  g1173104
BLAST score
                  244
E value
                   1.0e-20
Match length
                  101
                   43
% identity
NCBI Description
                  RIBONUCLEASE 2 PRECURSOR >gi 289210 (M98336) ribonuclease
                   [Arabidopsis thaliana] >gi 2642160 (AC003000) ribonuclease,
                   RNS2 [Arabidopsis thaliana]
Seq. No.
                   291370
Seq. ID
                  LIB189-018-Q1-E1-A3
Method
                  BLASTX
NCBI GI
                   q4582459
BLAST score
                   154
                   1.0e-10
E value
Match length
                   41
% identity
                  73
                   (AC007071) putative RanBP7/importin protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   291371
Seq. ID
                  LIB189-018-Q1-E1-A4
                  BLASTX
Method
                   q4582459
NCBI GI
BLAST score
                   355
E value
                   7.0e-34
Match length
                   111
% identity
                   (AC007071) putative RanBP7/importin protein [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. No. 291372

Seq. ID LIB189-018-Q1-E1-A6

Method BLASTN NCBI GI g22312 BLAST score 47



E value 2.0e-17 Match length 171 % identity 82

NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA =

abscisic acid)

Seq. No. 291373

Seq. ID LIB189-018-Q1-E1-B6

Method BLASTX
NCBI GI g134039
BLAST score 345
E value 1.0e-32
Match length 81
% identity 83

NCBI Description SMALL NUCLEAR RIBONUCLEOPROTEIN SM D1 (SNRNP CORE PROTEIN

D1) (SM-D1) (SM-D AUTOANTIGEN) >gi_88610_pir_ A27668 Sm-D ribonucleoprotein autoantigen - human >gi_338265 (J03798) small nuclear riboprotein Sm-D [Homo sapiens] >gi_1256741

(M58558) Sm-D autoantigen [Mus musculus]

Seq. No. 291374

Seq. ID LIB189-018-Q1-E1-C8

Method BLASTN
NCBI GI g22176
BLAST score 56
E value 1.0e-22
Match length 84
% identity 46

NCBI Description Z.mays P gene

Seq. No. 291375

Seq. ID LIB189-018-Q1-E1-D8

Method BLASTX
NCBI GI g3386611
BLAST score 318
E value 2.0e-29
Match length 121
% identity 50

NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 291376

Seq. ID LIB189-018-Q1-E1-E10

Method BLASTN
NCBI GI g11957
BLAST score 58
E value 6.0e-24
Match length 130
% identity 86

NCBI Description Rice complete chloroplast genome

Seq. No. 291377

Seq. ID LIB189-018-Q1-E1-E4

Method BLASTX
NCBI GI g419803
BLAST score 279
E value 3.0e-33
Match length 106



% identity zein protein - maize >gi 168705 (M72708) zein protein [Zea NCBI Description

mays]

Seq. No.

Seq. ID

LIB189-018-Q1-E1-F4

Method NCBI GI BLASTX q399942 290

291378

BLAST score E value

6.0e-31

Match length % identity

86 86

NCBI Description

CHLOROPLAST STROMA 70 KD HEAT SHOCK-RELATED PROTEIN

PRECURSOR >gi 421881_pir__S32818 heat shock protein, 70K, chloroplast - garden pea >gi 169023 (L03299) 70 kDa heat shock protein [Pisum sativum] >qi 871515 emb CAA49147_ (X69213) Psst70 (stress 70 protein) [Pisum sativum]

Seq. No.

291379

Seq. ID

LIB189-018-Q1-E1-F9

Method NCBI GI BLASTX q3650379

BLAST score

466

E value Match length 9.0e-47 114 75

% identity NCBI Description

(AL031740) 60s ribosomal protein 110a. [Schizosaccharomyces

pombe]

Seq. No.

291380

Seq. ID

LIB189-018-Q1-E1-H10 BLASTX

Method NCBI GI BLAST score

q1084952 162

E value Match length % identity

4.0e-11 127

31

NCBI Description

hypothetical protein YPR031w - yeast (Saccharomyces cerevisiae) >gi_809596_emb_CAA89285 (Z49274) unknown [Saccharomyces cerevisiae] >gi_1314105_emb_CAA95027

(Z71255) unknown [Saccharomyces cerevisiae]

Seq. No.

291381

Seq. ID

LIB189-019-Q1-E1-B4

Method NCBI GI BLASTX q4582783

BLAST score E value

511

Match length

6.0e-52

% identity

131

68

NCBI Description

(AJ006752) starch synthase, isoform V [Vigna unguiculata]

Seq. No.

291382

Seq. ID

LIB189-019-Q1-E1-E7

Method NCBI GI

BLASTN

BLAST score

g1698669 263



E value 1.0e-146 Match length 286 % identity 99

NCBI Description Zea mays S-like RNase (kin1) mRNA, complete cds

Seq. No. 291383

Seq. ID LIB189-019-Q1-E1-F8

Method BLASTN
NCBI GI 9799029
BLAST score 167
E value 5.0e-89
Match length 193
% identity 98

NCBI Description Z.mays BET1 mRNA

Seq. No. 291384

Seq. ID LIB189-020-Q1-E1-E7

Method BLASTN
NCBI GI g168700
BLAST score 88
E value 7.0e-42
Match length 199
% identity 86

NCBI Description Z.mays zein mRNA, complete cds

Seq. No. 291385

Seq. ID LIB189-020-Q1-E1-F2

Method BLASTN
NCBI GI g2062705
BLAST score 35
E value 2.0e-10
Match length 39
% identity 97

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 291386

Seq. ID LIB189-020-Q1-E1-F5

Method BLASTN
NCBI GI g468055
BLAST score 67
E value 3.0e-29
Match length 83
% identity 95

NCBI Description Zea mays B73 QM protein mRNA, complete cds

Seq. No. 291387

Seq. ID LIB189-021-Q1-E1-B9

Method BLASTN
NCBI GI g3821780
BLAST score 34
E value 2.0e-09
Match length 34
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 291388

Seq. ID LIB189-021-Q1-E1-E10



```
BLASTX
Method
                  q3913640
NCBI GI
BLAST score
                  319
E value
                  2.0e-29
Match length
                  69
                  91
% identity
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC
NCBI Description
                  (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi_3041775_dbj_BAA25422_ (AB007193)
                  fructose-1,6-bisphosphatase [Oryza sativa]
Seq. No.
                  291389
                  LIB189-021-Q1-E1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1170937
BLAST score
                  282
E value
                  1.0e-25
Match length
                  58
                   98
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb_CAA81481 (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
Seq. No.
                   291390
Seq. ID
                  LIB189-021-Q1-E1-F6
Method
                   BLASTN
NCBI 6
                   g3821780
BLAST
                   35
         re
                   4.0e-10
E valı
Match
         qth
                   35
% ider
                   100
         У
                  Xenopus laevis cDNA clone 27A6-1
NCBI !
         ription
                   291391
Seq. 1
                   LIB189-021-Q1-E1-G1
Seq. :
Method
                   BLASTX
                   q3882081
NCBI (
                   702
BLAST
         re
                   3.0e-74
E val
                   148
Match
         ıgth
                   38
% ide
         .у
                   (AJ012552) polyubiquitin [Vicia faba]
         :ription
NCBI
                   291392
Seq.
                   LIB189-021-Q1-E1-G10
Seq.
                   BLASTX
Metho
                   g3850588
NCBI (
                   194
BLAST
         re
                   2.0e-15
E valı
Match
         ıgth
                   70
% ide
                   57
         ΣУ
                   (AC005278) Contains similarity to gb AB011110 KIAA0538
NCBI |
         ription
                   protein from Homo sapiens brain and to phospholipid-binding
```

from this gene. [Arabidopsis thaliana]

domain C2 PF 00168. ESTs gb_AA585988 and gb_T04384 come



```
Seq. No.
                  291393
Seq. ID
                  LIB189-022-Q1-E1-A6
Method
                  BLASTX
NCBI GI
                  g4468802
BLAST score
                  309
E value
                  3.0e-28
Match length
                  106
                  55
% identity
NCBI Description
                  (AL035601) cytochrome p450-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  291394
Seq. ID
                  LIB189-022-Q1-E1-D5
Method
                  BLASTX
NCBI GI
                  q3885882
BLAST score
                  279
E value
                  6.0e-25
Match length
                  80
                  69
% identity
NCBI Description (AF093629) inorganic pyrophosphatase [Oryza sativa]
Seq. No.
                  291395
                  LIB189-022-Q1-E1-E11
Seq. ID
Method
                  BLASTX
                  q1805261
NCBI GI
BLAST score
                  676
E value
                  3.0e-71
Match length
                  141
% identity
                  (U75347) fatty acid synthase, alpha subunit [Emericella
NCBI Description
                  nidulans]
Seq. No.
                  291396
                  LIB189-022-Q1-E1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4416301
BLAST score
                  483
E value
                  8.0e-49
Match length
                  102
% identity
                  89
NCBI Description (AF105716) gag protein [Zea mays]
Seq. No.
                  291397
                  LIB189-022-Q1-E1-F10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1498385
BLAST score
                  33
                  3.0e-09
E value
Match length
                  77
                  86
% identity
NCBI Description Zea mays actin (Maz87) gene, partial cds
                  291398
```

Seq. No.

LIB189-022-Q1-E1-G1 Seq. ID

Method BLASTX NCBI GI g2191163 BLAST score 256



```
E value
Match length
                  89
                  72
% identity
                  (AF007270) contains similarity to beta transducins
NCBI Description
                  [Arabidopsis thaliana]
                  291399
Seq. No.
Seq. ID
                  LIB189-022-Q1-E1-H12
Method
                  BLASTX
NCBI GI
                  q2306981
BLAST score
                  169
                  2.0e-15
E value
                  68
Match length
% identity
                  68
NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]
Seq. No.
                  291400
Seq. ID
                  LIB189-023-Q1-E1-A6
Method
                  BLASTX
NCBI GI
                  g468516
BLAST score
                  325
                  3.0e-30
E value
Match length
                  102
                  69
% identity
NCBI Description
                  (X55724) zein [Zea mays]
                  291401
Seq. No.
Seq. ID
                  LIB189-023-Q1-E1-A8
Method
                  BLASTX
NCBI GI
                  g266578
BLAST score
                  214
                  2.0e-17
E value
Match length
                  56
% identity
                  METALLOTHIONEIN-LIKE PROTEIN 1 >gi 100898 pir S17560
NCBI Description
                  metallothionein-like protein - maize >gi 236730 bbs 57629
                  (S57628) metallothionein homologue [Zea mays, Peptide, 76
                  aa] [Zea mays] >gi 559536 emb CAA57676 (X82186)
                  metallothionein- like protein [Zea mays]
                  >gi 228095 prf 1717215A metallothionein-like protein [Zea
                  mays]
Seq. No.
                  291402
Seq. ID
                  LIB189-023-Q1-E1-C2
Method
                  BLASTX
NCBI GI
                  g2129518
BLAST score
                  166
E value
                  1.0e-11
Match length
                  84
% identity
                  5'-adenylylphosphosulfate reductase (EC 2.8.2.-) APR2 -
NCBI Description
                  Arabidopsis thaliana >gi_1336168 (U56921)
                  5'-adenylylphosphosulfate reductase [Arabidopsis thaliana]
```

Seq. No. 291403

Seq. ID LIB189-023-Q1-E1-F9

Method BLASTX



NCBI GI g1785621 BLAST score 353 E value 1.0e-33 Match length 92 % identity 71

NCBI Description (Z84202) AtPK2324 [Arabidopsis thaliana] >gi_2465927

(AF024650) receptor-like serine/threonine kinase

[Arabidopsis thaliana] >gi_4249408 (AC006072) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 291404

Seq. ID LIB189-023-Q1-E1-G1

Method BLASTX
NCBI GI g115771
BLAST score 312
E value 1.0e-28
Match length 115
% identity 58

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >gi 82682 pir S04453 chlorophyll

a/b-binding protein precursor - maize

>gi 22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No. 291405

Seq. ID LIB189-023-Q1-E1-G11

Method BLASTX
NCBI GI g1825645
BLAST score 173
E value 2.0e-12
Match length 62
% identity 56

NCBI Description (U88173) weak similarity to Arabidopsis thaliana

ubiquitin-like protein 8 [Caenorhabditis elegans]

Seq. No. 291406

Seq. ID LIB189-023-Q1-E1-G4

Method BLASTN
NCBI GI g3821780
BLAST score 37
E value 2.0e-11
Match length 37
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 291407

Seq. ID LIB189-024-Q1-E1-A12

Method BLASTN
NCBI GI g22396
BLAST score 87
E value 3.0e-41
Match length 286
% identity 84

NCBI Description Z.mays gene for phosphoenolpyruvate carboxylase (EC

4.1.1.31)

Seq. No. 291408



Seq. ID LIB189-024-Q1-E1-A3

Method BLASTX
NCBI GI g3659974
BLAST score 176
E value 8.0e-13
Match length 62
% identity 50

NCBI Description Chain H, Cytochrome Bcl Complex From Chicken

>gi_3660383_pdb_3BCC_H Chain H, Stigmatellin And Antimycin

Bound Cytochrome Bc1 Complex From Chicken

Seq. No. 291409

Seq. ID LIB189-024-Q1-E1-A9

Method BLASTX
NCBI GI g3860008
BLAST score 235
E value 5.0e-20
Match length 87
% identity 52

NCBI Description (AF091085) unknown [Homo sapiens]

Seq. No. 291410

Seq. ID LIB189-024-Q1-E1-B12

Method BLASTN
NCBI GI g11957
BLAST score 34
E value 1.0e-09
Match length 102
% identity 42

NCBI Description Rice complete chloroplast genome

Seq. No. 291411

Seq. ID LIB189-024-Q1-E1-C1

Method BLASTX
NCBI GI g1778147
BLAST score 353
E value 1.0e-33
Match length 73
% identity 97

NCBI Description (U66403) phosphate/phosphoenolpyruvate translocator

precursor [Zea mays]

Seq. No. 291412

Seq. ID LIB189-024-Q1-E1-C6

Method BLASTX
NCBI GI g1352469
BLAST score 375
E value 5.0e-36
Match length 71
% identity 99

NCBI Description BETA-FRUCTOFURANOSIDASE, CELL WALL ISOZYME PRECURSOR

(SUCROSE-6-PHOSPHATE HYDROLASE) (INVERTASE) >gi_736359 (U17695) invertase [Zea mays] >gi_1582380_prf__2118364A

cell wall invertase [Zea mays]

Seq. No. 291413

Seq. ID LIB189-024-Q1-E1-E4



Method NCBI GI q68029 BLAST score 150 3.0e-10 E value Match length 46 % identity phosphoenolpyruvate carboxylase (EC 4.1.1.31) - maize NCBI Description >qi 22408 emb CAA33317 (X15239) PEP carboxylase [Zea mays] >qi 228619 prf 1807332A phosphoenolpyruvate carboxylase [Zea mays] 291414 Seq. No. Seq. ID LIB189-024-Q1-E1-F12 Method BLASTN g169818 NCBI GI BLAST score 52 E value 1.0e-20 Match length 171 % identity 84 NCBI Description Rice 25S ribosomal RNA gene 291415 Seq. No. Seq. ID LIB189-024-Q1-E1-G11 BLASTX Method g3747111 NCBI GI BLAST score 233 2.0e-19 E value 73 Match length % identity NCBI Description (AF095641) MTN3 homolog [Arabidopsis thaliana] 291416 Seq. No. Seq. ID LIB189-024-Q1-E1-H9 Method BLASTX NCBI GI g4557445 BLAST score 174 E value 2.0e-12 Match length 114 % identity 13 RCC1-like G exchanging factor RLG >gi 3789799 (AF060219) NCBI Description RCC1-like G exchanging factor RLG [Homo sapiens] Seq. No. 291417 LIB189-025-Q1-E1-A2 Seq. ID

Method BLASTX g82696 NCBI GI BLAST score 202 E value 2.0e-20 Match length 56 95 % identity

glycine-rich protein - maize >gi_22293_emb_CAA43431_ NCBI Description

(X61121) glycine-rich protein [Zea mays]

291418 Seq. No.

LIB189-025-Q1-E1-B11 Seq. ID

Method BLASTX NCBI GI g3738285

A. T.



```
BLAST score
  E value
                    1.0e-10
  Match length
                    70
                    49
  % identity
  NCBI Description
                    (AC005309) unknown protein [Arabidopsis thaliana]
                    291419
  Seq. No.
                    LIB189-025-Q1-E1-B9
  Seq. ID
  Method
                    BLASTN
  NCBI GI
                    q4206305
  BLAST score
                    36
                    9.0e-11
  E value
                    38
  Match length
  % identity
                    51
  NCBI Description Zea mays retrotransposon Cinful-1, complete sequence
  Seq. No.
                    291420
  Seq. ID
                    LIB189-025-Q1-E1-E5
  Method
                    BLASTX
NCBI GI
                   _ q2911364
                    226
  BLAST score
                    1.0e-18
  E value
  Match length
                    72
                    67
  % identity
  NCBI Description (AF041046) NADPH HC toxin reductase [Zea mays]
                    291421
  Seq. No.
                    LIB189-025-Q1-E1-E8
  Seq. ID
                    BLASTN
  Method
  NCBI GI
                    g2226328
  BLAST score
                    34
                    2.0e-09
  E value
  Match length
                     46
                    93
  % identity
                    Zea mays physical impedance induced protein (IIG1) mRNA,
  NCBI Description
                    complete cds
  Seq. No.
                    291422
                    LIB189-025-Q1-E1-G1
  Seq. ID
  Method
                    BLASTN
  NCBI GI
                    g2062705
  BLAST score
                     36
  E value
                     8.0e-11
  Match length
                     36
  % identity
                     100
                    Human butyrophilin (BTF5) mRNA, complete cds
  NCBI Description
  Seq. No.
                    291423
                    LIB189-025-Q1-E1-H1
  Seq. ID
  Method
                    BLASTX
                    g1709000
  NCBI GI
  BLAST score
                    573
  E value
                    2.0e-59
  Match length
                    118
                     92
  % identity
                    S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
  NCBI Description
                    ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
```





>gi_960357_dbj_BAA09895_ (D63835) S-adenosylmethionine synthetase [Hordeum vulgare]

Seq. No. 291424

Seq. ID LIB189-025-Q1-E1-H5

Method BLASTN
NCBI GI g2267594
BLAST score 36
E value 8.0e-11
Match length 168

Match length 168 % identity 80

NCBI Description Oryza sativa plastocyanin precursor, mRNA, complete cds

Seq. No. 291425

Seq. ID LIB189-026-Q1-E1-A2

Method BLASTX
NCBI GI g2668742
BLAST score 413
E value 9.0e-41

Match length 86 % identity 93

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 291426

Seq. ID LIB189-026-Q1-E1-A4

Method BLASTX
NCBI GI g266578
BLAST score 241
E value 2.0e-20
Match length 56

% identity 77

NCBI Description METALLOTHIONEIN-LIKE PROTEIN 1 >gi_100898_pir__S17560

metallothionein-like protein - maize >gi 236730 bbs 57629 (S57628) metallothionein homologue [Zea mays, Peptide, 76

aa] [Zea mays] >gi 559536 emb CAA57676 (X82186)

metallothionein- like protein [Zea mays]

>gi 228095 prf 1717215A metallothionein-like protein [Zea

mays]

Seq. No. 291427

Seq. ID LIB189-026-Q1-E1-C8

Method BLASTX
NCBI GI g2673920
BLAST score 196
E value 3.0e-15
Match length 87
% identity 48

NCBI Description (AC002561) similar to Drosophila couch potato protein

[Arabidopsis thaliana]

Seq. No. 291428

Seq. ID LIB189-026-Q1-E1-D1

Method BLASTX
NCBI GI g4158230
BLAST score 194
E value 2.0e-15
Match length 69



```
% identity
NCBI Description
                  (Y18625) amylogenin [Triticum aestivum]
                  291429
Seq. No.
Seq. ID
                  LIB189-026-Q1-E1-D3
Method
                  BLASTX
                  g2529680
NCBI GI
                  276
BLAST score
                  9.0e-25
E value
Match length
                  94
                  57
% identity
                  (AC002535) putative protein disulfide-isomerase precursor
NCBI Description
                  [Arabidopsis thaliana]
                  291430
Seq. No.
Seq. ID
                  LIB189-026-Q1-E1-D8
Method
                  BLASTX
NCBI GI
                  g2191136
BLAST score
                  271
                  3.0e-24
E value
                  66
Match length
                  71
% identity
                  (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                  coded for by A. thaliana cDNA T46230; coded for by A.
                  thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                  [Arabidopsis thaliana]
Seq. No.
                  291431
Seq. ID
                  LIB189-026-Q1-E1-F3
Method
                  BLASTX
                  q1946265
NCBI GI
BLAST score
                  431
E value
                  1.0e-42
Match length
                  102
% identity
                  79
NCBI Description (Y11414) myb [Oryza sativa]
Seq. No.
                  291432
Seq. ID
                  LIB189-026-Q1-E1-F4
Method
                  BLASTX
NCBI GI
                  g2739168
BLAST score
                  220
E value
                  6.0e-18
Match length
                  80
% identity
                  (AF032386) aldose-1-epimerase-like protein [Nicotiana
NCBI Description
                  tabacum]
Seq. No.
                  291433
                  LIB189-026-Q1-E1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2062705
```

NCBI GI g2062705
BLAST score 37
E value 2.0e-11
Match length 37
% identity 100

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

NCBI Description



```
291434
 Seq. No.
                    LIB189-026-Q1-E1-G3
 Seq. ID
                    BLASTX
 Method
                    g141617
 NCBI GI
                    306
 BLAST score
                     6.0e-28
 E value
 Match length
                    115
 % identity
                     55
                    ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
 NCBI Description
                    >gi 100941 pir S12140 zein Zc1 - maize
                     >gi_100945_pir__B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
                     >gi^{-}16866^{\circ} (M^{-}6460) 16^{-}kDa zein protein [Zea mays]
                     291435
 Seq. No.
                     LIB189-027-Q1-E1-A7
 Seq. ID
                     BLASTX
 Method
NCBI GI
                     g4481948
                     170
BLAST score
                     4.0e-12
 E value
 Match length
                     117
 % identity
                     39
                    (AL035637) hypothetcal protein [Schizosaccharomyces pombe]
 NCBI Description
 Seq. No.
                     291436
                     LIB189-027-Q1-E1-D3
 Seq. ID
                     BLASTX
 Method
                     q476418
 NCBI GI
 BLAST score
                     319
                     1.0e-29
 E value
                     73
 Match length
                     81
  % identity
 NCBI Description cytochrome c - maize
                     291437
  Seq. No.
                     LIB189-027-Q1-E1-E4
  Seq. ID
                     BLASTX
 Method
 NCBI GI
                     q3482967
 BLAST score
                     263
                     3.0e-23
 E value
                     87
 Match length
                     53
  % identity
                     (AL031369) Protein phosphatase 2C-like protein [Arabidopsis
  NCBI Description
                     thaliana] >gi 4559345 gb AAD23006.1_AC006585_1 (AC006585)
                     protein phosphatase 2C [Arabidopsis thaliana]
                     291438
  Seq. No.
  Seq. ID
                     LIB189-027-Q1-E1-G10
 Method
                     BLASTX
  NCBI GI
                     q141597
                     200
  BLAST score
  E value
                     7.0e-16
  Match length
                     62
  % identity
                     69
```

>gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)





>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]

```
[Zea mays]
                  291439
Seq. No.
                  LIB189-028-Q1-E1-A3
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1049252
BLAST score
                  118
                  5.0e-60
E value
                  174
Match length
                  92
% identity
NCBI Description Zea mays vacuolar ATPase 69 kDa subunit mRNA, partial cds
Seq. No.
                  291440
                  LIB189-028-Q1-E1-A4
Seq. ID
                  BLASTX
Method
                  g2497486
NCBI GI
BLAST score
                  426
                  5.0e-42
E value
Match length
                  127
                  57
% identity
                  URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP
NCBI Description
                  KINASE) >gi 2121275 (AF000147) UMP/CMP kinase [Arabidopsis
                  thaliana]
                  291441
Seq. No.
                  LIB189-028-Q1-E1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4115363
                  222
BLAST score
                  4.0e-18
E value
Match length
                  132
% identity
                  (AC005957) putative disease resistance protein [Arabidopsis
NCBI Description
                  thaliana]
                  291442
Seq. No.
Seq. ID
                  LIB189-028-Q1-E1-B3
Method
                  BLASTX
NCBI GI
                  q2119187
                  195
BLAST score
E value
                  1.0e-15
Match length
                  45
% identity
                   96
                  transmembrane protein, glucose starvation-induced - maize
NCBI Description
                   >qi 575731 emb CAA57955 (X82633) transmembrane protein
                   [Zea mays]
Seq. No.
                   291443
                  LIB189-028-Q1-E1-C2
Seq. ID
                  BLASTX
Method
```

NCBI GI g2668742

BLAST score 422 E value 1.0e-41 Match length 90 % identity 91

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]



```
Seq. No.
                  291444
                  LIB189-028-Q1-E1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2618723
BLAST score
                  152
E value
                  5.0e-10
Match length
                  36
                  81
% identity
                  (U49073) IAA17 [Arabidopsis thaliana] >gi 2921756
NCBI Description
                  (AF040631) IAA17/AXR3 protein [Arabidopsis thaliana]
                  >gi 4389514 gb AAB70451 (AC000104) Identical to
                  Arabidopsis gb AF040632 and gb_U49073 IAA17/AXR3 gene. ESTs
                  gb_H36782 and gb_F14074 come from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  291445
                  LIB189-028-Q1-E1-D5
Seq. ID
Method
                  BLASTX
                  g4454468
NCBI GI
BLAST score
                  305
                  3.0e - 32
E value
Match length
                  132
                  58
% identity
                  (AC006234) putative NADH dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  291446
Seq. ID
                  LIB189-028-Q1-E1-F12
Method
                  BLASTX
NCBI GI
                  q2213558
                  242
BLAST score
E value
                  2.0e-20
Match length
                  121
% identity
NCBI Description (Z97052) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                  291447
Seq. ID
                  LIB189-028-Q1-E1-F3
Method
                  BLASTX
NCBI GI
                  q4033838
BLAST score
                  313
E value
                  8.0e-29
Match length
                  132
% identity
                  47
NCBI Description (Y18550) sigma-like factor [Arabidopsis thaliana]
Seq. No.
                  291448
                  LIB189-028-Q1-E1-G8
Seq. ID
```

Method BLASTX
NCBI GI g2465529
BLAST score 438
E value 2.0e-43
Match length 110
% identity 76

NCBI Description (AF000355) phosphate transporter [Medicago truncatula]



```
291449
Seq. No.
                  LIB189-029-Q1-E1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4416303
                  Ĩ76
BLAST score
                  2.0e-23
E value
Match length
                  113
% identity
                  58
NCBI Description (AF105716) gag protein [Zea mays]
                  291450
Seq. No.
                  LIB189-029-Q1-E1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q135103
BLAST score
                  153
                  1.0e-10
E value
                  52
Match length
                  54
% identity
                  MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE [CONTAINS:
NCBI Description
                  GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE);
                  PROLYL-TRNA SYNTHETASE (PROLINE--TRNA LIGASE)]
                  >gi 103253 pir S18644 multifunctional amino acid--tRNA
                  ligase (EC 6.1.1.-) - fruit fly (Drosophila melanogaster)
                  >qi 157564 (M74104) transfer RNA-Glu-Pro aminoacyl
                  synthetase [Drosophila melanogaster] >gi_1871360 (U59923)
                  glutamyl-prolyl-tRNA synthetase [Drosophila melanogaster]
                  291451
Seq. No.
Seq. ID
                  LIB189-029-Q1-E1-D10
                  BLASTX
Method
                  g72307
NCBI GI
BLAST score
                  163
                  3.0e-11
E value
Match length
                  92
                  42
% identity
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi 168686
                  (J01246) 26.99 kd zein protein [Zea mays]
                  291452
Seq. No.
Seq. ID
                  LIB189-029-Q1-E1-F1
Method
                  BLASTX
NCBI GI
                  g1170714
BLAST score
                  325
E value
                  2.0e-30
Match length
                  83
                  67
% identity
```

SHAGGY RELATED PROTEIN KINASE ASK-GAMMA NCBI Description

> >gi 541850 pir S41597 protein kinase ASK-gamma (EC 2.7.1.-) - Arabidopsis thaliana >gi_456509_emb_CAA53180_ (X75431) ASK-gamma (Arabidopsis shaggy-related kinase) [Arabidopsis thaliana] >gi_2059329_emb_CAA73247_ (Y12710)

shaggy-like kinase gamma [Arabidopsis thaliana]

Seq. No. 291453

LIB189-029-Q1-E1-F6 Seq. ID

Method BLASTX NCBI GI g4580727



```
BLAST score
                  2.0e-51
E value
Match length
                  113
                  81
% identity
                  (AF137371) phosphate transporter precursor [Drosophila
NCBI Description
                  melanogaster]
                  291454
Seq. No.
                  LIB189-029-Q1-E1-G6
Seq. ID
Method
                  BLASTN
                  g2062705
```

Method BLASTN
NCBI GI g2062705
BLAST score 38
E value 4.0e-12
Match length 38
% identity 100

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

 Seq. No.
 291455

 Seq. ID
 LIB189-029-Q1-E1-H10

 Method
 BLASTN

 NCBI GI
 g3821780

 BLAST score
 35

 E value
 2.0e-10

E value 2.0eMatch length 35
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 291456

Seq. ID LIB189-029-Q1-E1-H12

Method BLASTN
NCBI GI g1840117
BLAST score 51
E value 1.0e-19
Match length 126
% identity 94

NCBI Description Zea mays PIF-12 transposable element in r-1 (r-p) locus,

complete sequence

Seq. No. 291457

Seq. ID LIB189-030-Q1-E1-A10

Method BLASTX
NCBI GI g1077386
BLAST score 171
E value 1.0e-23
Match length 110
% identity 50

NCBI Description hypothetical protein YLR345w - yeast (Saccharomyces

cerevisiae) >gi_609382 (U19028) Ylr345wp [Saccharomyces

cerevisiae]

Seq. No. 291458

Seq. ID LIB189-030-Q1-E1-A11

Method BLASTX
NCBI GI 9455858
BLAST score 402
E value 2.0e-39
Match length 112

% identity

38

NCBI Description (U92974) unknown [Lactococcus lactis]



```
% identity
                  (AC007138) putative polygalacturonidase [Arabidopsis
NCBI Description
                  thaliana]
                  291459
Seq. No.
Seq. ID
                  LIB189-030-Q1-E1-D5
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  198
                  2.0e-15
E value
                  87
Match length
                  46
% identity
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                  291460
Seq. No.
                  LIB189-030-Q1-E1-D7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  291461
Seq. No.
Seq. ID
                  LIB189-030-Q1-E1-E3
                  BLASTX
Method
NCBI GI
                  g3288594
BLAST score
                  172
                  3.0e-12
E value
Match length
                  64
% identity
                  59
NCBI Description (AJ006340) 26S proteasome subunit p112 [Rattus norvegicus]
                  291462
Seq. No.
Seq. ID
                  LIB189-030-Q1-E1-G1
                  BLASTX
Method
NCBI GI
                  g1706260
BLAST score
                  272
                  3.0e-26
E value
Match length
                  116
% identity
                  59
NCBI Description
                  CYSTEINE PROTEINASE 1 PRECURSOR >qi 2118131 pir S59597
                  cysteine proteinase 1 precursor - maize
                  >gi 643597 dbj BAA08244 (D45402) cysteine proteinase [Zea
                  mays]
Seq. No.
                  291463
Seq. ID
                  LIB189-030-Q1-E1-G9
Method
                  BLASTX
NCBI GI
                  g2565150
BLAST score
                  142
E value
                  9.0e-09
Match length
                  93
```

BLAST score

Match length % identity

E value

272 4.0e-24

102

54



```
291464
Seq. No.
Seq. ID
                  LIB189-031-Q1-E1-B2
                  BLASTX
Method
NCBI GI
                  g3395443
                  314
BLAST score
                  7.0e-29
E value
Match length
                  113
% identity
                  55
                  (AC004683) putative ammonium transporter, 3' partial
NCBI Description
                  [Arabidopsis thaliana]
                  291465
Seq. No.
                  LIB189-031-Q1-E1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1710580
                  381
BLAST score
                  9.0e-37
E value
Match length
                  129
% identity
                  60
                  60S RIBOSOMAL PROTEIN L9 B (YL11) (RP25)
NCBI Description
                  >gi_1078363_pir__S53915 ribosomal protein L9.e.B, cytosolic
                  - yeast (Saccharomyces cerevisiae) >gi_791121_emb_CAA60195_
                   (X86470) putative second copy of ribosomal protein gene
                  YL9A, SWISS PROT:RL9 YEAST [Saccharomyces cerevisiae]
                  >gi 994820 (U12141) ribosomal protein YL9 [Saccharomyces
                  cerevisiae] >gi 1301947 emb CAA95940 (Z71343) ORF YNL067w
                  [Saccharomyces cerevisiae]
Seq. No.
                  291466
Seq. ID
                  LIB189-031-Q1-E1-E2
                  BLASTX
Method
NCBI GI
                  q1658315
BLAST score
                  141
                  9.0e-09
E value
                  29
Match length
                  86
% identity
NCBI Description (Y08988) osr40g3 [Oryza sativa]
                  291467
Seq. No.
Seq. ID
                  LIB189-031-Q1-E1-F4
                  BLASTX
Method
NCBI GI
                  g2262170
BLAST score
                  157
E value
                  7.0e-11
                  80
Match length
% identity
                  (AC002329) predicted glycosyl hydrolase [Arabidopsis
NCBI Description
                  thaliana]
                   291468
Seq. No.
                   LIB189-031-Q1-E1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2160144
```



(AC000375) Strong similarity to Arabidopsis oligopeptide transporter (gb_X77503). [Arabidopsis thaliana]

291469 Seq. No.

NCBI Description

Seq. ID LIB189-031-Q1-E1-H12

Method BLASTX NCBI GI g115608 264 BLAST score 8.0e-30 E value 103 Match length 74 % identity

PHOSPHOENOLPYRUVATE CARBOXYLASE 1 (PEPCASE) NCBI Description

>gi 22563_emb_CAA33316_ (X15238) phosphoenolpyruvate

carboxylase (AA 1 - 970) [Zea mays]

291470 Seq. No.

Seq. ID LIB189-032-Q1-E1-B11

BLASTX Method NCBI GI q3023852 BLAST score 464 1.0e-46 E value 118 Match length % identity 70

GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE NCBI Description

PROTEIN (CROSS-PATHWAY CONTROL WD-REPEAT PROTEIN CPC-2) >gi 1362527_pir__S57839 CPC2 protein - Neurospora crassa >gi 971566 emb CAA57460 (X81875) CPC2 protein [Neurospora

crassa]

291471 Seq. No.

LIB189-032-Q1-E1-C3 Seq. ID

BLASTX Method NCBI GI q2191138 BLAST score 276 2.0e-24 E value 75 Match length

% identity

(AF007269) A IG002N01.18 gene product [Arabidopsis NCBI Description

thaliana]

Seq. No. 291472

LIB189-032-Q1-E1-D7 Seq. ID

Method BLASTN NCBI GI q3821780 BLAST score 35 4.0e-10 E value Match length 35 % identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

291473 Seq. No.

LIB189-032-Q1-E1-E4 Seq. ID

Method BLASTX g115608 NCBI GI 507 BLAST score 1.0e-51 E value Match length 109



% identity

PHOSPHOENOLPYRUVATE CARBOXYLASE 1 (PEPCASE) NCBI Description

>gi 22563 emb CAA33316 (X15238) phosphoenolpyruvate

carboxylase (AA 1 - 970) [Zea mays]

Seq. No. 291474

Seq. ID LIB189-032-Q1-E1-E9

Method BLASTX NCBI GI g3738301 BLAST score 150 6.0e-10 E value Match length 51 53 % identity

(AC005309) putative zinc-finger protein [Arabidopsis NCBI Description thaliana] >gi_4249397 (AC006072) putative zinc-finger

protein (B-box zinc finger domain) [Arabidopsis thaliana]

Seq. No. 291475

Seq. ID LIB189-033-Q1-E1-A8

 ${\tt BLASTN}$ Method g3290005 NCBI GI BLAST score 81 5.0e-38 E value 172 Match length 87 % identity

Zea mays pathogenesis related protein-5 (PR-5) mRNA, NCBI Description

complete cds

291476 Seq. No.

Seq. ID LIB189-033-Q1-E1-B8

Method BLASTX NCBI GI g4056486 BLAST score 162 E value 3.0e-11 Match length 89 39 % identity

(AC005896) hypothetical protein [Arabidopsis thaliana] NCBI Description

291477 Seq. No.

Seq. ID LIB189-033-Q1-E1-D1

BLASTX Method g3135543 NCBI GI BLAST score 242 E value 2.0e-40 128 Match length % identity

(AF062393) aquaporin [Oryza sativa] NCBI Description

Seq. No. 291478

Seq. ID LIB189-033-Q1-E1-D11

Method BLASTX NCBI GI g2244807 BLAST score 147 E value 2.0e-09 Match length 88 % identity 38

(Z97336) hypothetical protein [Arabidopsis thaliana] NCBI Description



```
291479
Seq. No.
                  LIB189-033-Q1-E1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4454016
BLAST score
                  147
                  1.0e-09
E value
                  54
Match length
                  56
% identity
                  (AL035396) UMP/CMP kinase like protein [Arabidopsis
NCBI Description
                  thaliana]
                  291480
Seq. No.
Seq. ID
                  LIB189-034-Q1-E1-A3
                  BLASTN
Method
NCBI GI
                  g643596
BLAST score
                  65
E value
                  2.0e-28
                  116
Match length
                  90
% identity
NCBI Description Corn mRNA for cysteine proteinase, clone CCP, complete cds
                  291481
Seq. No.
                  LIB189-034-Q1-E1-B9
Seq. ID
                  BLASTX
Method
                  g132147
NCBI GI
BLAST score
                  523
                  2.0e-53
E value
                  110
Match length
% identity
                  86
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi 68089_pir__RKZMS
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - maize >gi_22474_emb_CAA29784_ (X06535)
                   ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor
                   [Zea mays] >gi_217964_dbj_BAA00120_ (D00170) ribulose
                   1,5-bisphosphate carboxylase small subunit [Zea mays]
                   >gi_359512_prf__1312317A ribulosebisphosphate carboxylase
                   [Zea mays]
Seq. No.
                   291482
                   LIB189-034-Q1-E1-C2
Seq. ID
Method
                   BLASTX
                   q4468913
NCBI GI
                   279
BLAST score
                   9.0e-25
E value
                   130
Match length
% identity
                   45
NCBI Description (AJ131720) alpha integrin binding protein 80 [Homo sapiens]
```

Seq. No.

291483

LIB189-034-Q1-E1-C5 Seq. ID

BLASTN Method g902200 NCBI GI 182 BLAST score 6.0e-98 E value Match length 317



```
% identity
NCBI Description
                  Z.mays complete chloroplast genome
Seq. No.
                  291484
Seq. ID
                  LIB189-034-Q1-E1-C7
Method
                  BLASTX
NCBI GI
                  g1352461
BLAST score
                  368
                  5.0e-46
E value
Match length
                  130
% identity
                  79
NCBI Description IN2-2 PROTEIN
                  291485
Seq. No.
                  LIB189-034-Q1-E1-C9
Seq. ID
Method
                  BLASTX
                  g1835731
NCBI GI
BLAST score
                  321
                  1.0e-29
E value
                  89
Match length
% identity
                  66
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                  291486
Seq. No.
                  LIB189-034-Q1-E1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827716
BLAST score
                  397
                  1.0e-38
E value
Match length
                  111
% identity
NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.
                  291487
Seq. ID
                  LIB189-034-01-E1-D8
Method
                  BLASTX
NCBI GI
                  g4176544
BLAST score
                  372
E value
                  1.0e-35
Match length
                  136
% identity
                  54
NCBI Description
                  (AL035259) putative utp--glucose-1-phosphate
                  uridylyltransferase [Schizosaccharomyces pombe]
Seq. No.
                  291488
                  LIB189-034-Q1-E1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3318613
```

BLAST score 250 E value 1.0e-21 Match length 90 % identity 58

NCBI Description (AB016064) mitochondrial phosphate transporter [Zea mays]

Seq. No. 291489

LIB189-034-Q1-E1-G9 Seq. ID

Method BLASTX



```
NCBI GI
                   q3482914
BLAST score
                   271
E value
                   8.0e-24
                  117
Match length
                   52
% identity
NCBI Description
                  (AC003970) Similar to nodulins and lipase [Arabidopsis
                  thaliana]
                  291490
Seq. No.
Seq. ID
                  LIB189-034-Q1-E1-H3
                  BLASTX
                   g3044214
```

Method NCBI GI BLAST score 155 3.0e-10 E value 133 Match length 32 % identity

(AF057044) acyl-CoA oxidase [Arabidopsis thaliana] NCBI Description

291491 Seq. No. Seq. ID LIB3059-001-Q1-K1-B8 Method BLASTN NCBI GI g22326 BLAST score 113 5.0e~57 E value 165 Match length 92

NCBI Description Z.mays gene for Hageman factor inhibitor

Seq. No. 291492 Seq. ID LIB3059-001-Q1-K1-D5 Method BLASTX NCBI GI g224514 BLAST score 254 3.0e-22 E value

Match length 61 % identity 84

% identity

NCBI Description zein M8 [Zea mays]

Seq. No. 291493

Seq. ID LIB3059-001-Q1-K1-G10

Method BLASTX NCBI GI g121345 BLAST score 257 E value 1.0e-22 Match length 59 % identity 86

NCBI Description GLUTAMINE SYNTHETASE PR-2 (ISOZYME ALPHA)

(GLUTAMATE--AMMONIA LIGASE) >qi 68593 pir AJFBQA

glutamate--ammonia ligase (EC 6.3.1.2) alpha, cytosolic kidney bean >gi 21013 emb CAA27632 (X04002) glutamine synthetase subunit (aa 1-356) [Phaseolus vulgaris] >gi 225068 prf 1208270B synthetase R2,Gln [Phaseolus

vulgaris]

Seq. No. 291494

LIB3059-001-Q1-K1-G12 Seq. ID

Method BLASTN



```
NCBI GI
BLAST score
                  70
E value
                  2.0e-31
                  102
Match length
% identity
NCBI Description G.max mRNA from stress-induced gene (SAM22)
                  291495
Seq. No.
                  LIB3059-001-Q1-K1-G6
Seq. ID
                  BLASTN
Method
NCBI GI
                  q22222
BLAST score
                  51
                  3.0e-20
E value
                  107
Match length
                  88
% identity
NCBI Description Z.mays ZSF4C4 gene for zein
                  291496
Seq. No.
Seq. ID
                  LIB3059-001-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  g224513
BLAST score
                  271
                  3.0e-24
E value
                  62
Match length
% identity
                  85
NCBI Description zein M6 [Zea mays]
                  291497
Seq. No.
                  LIB3059-001-Q1-K2-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2832681
BLAST score
                  165
E value
                  2.0e-11
Match length
                  69
% identity
                  49
NCBI Description (AL021712) putative protein [Arabidopsis thaliana]
Seq. No.
                  291498
                  LIB3059-001-Q1-K2-B6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22549
BLAST score
                  269
                  1.0e-150
E value
Match length
                  365
% identity
                  93
NCBI Description Maize gene for a 27kDa storage protein, zein
Seq. No.
                  291499
                  LIB3059-001-Q1-K2-D10
Seq. ID
                  BLASTX
Method
                  g141610
NCBI GI
BLAST score
                  405
E value
                  2.0e-39
                  143
Match length
% identity
                   63
```

NCBI Description ZEIN-ALPHA PRECURSOR (CLONE Z4)



```
Seq. No.
                  LIB3059-001-Q1-K2-D4
Seq. ID
Method
                  BLASTN
                  g168704
NCBI GI
                  127
BLAST score
E value
                  3.0e-65
Match length
                  187
                  92
% identity
NCBI Description Zea mays zein protein gene, complete cds
                  291501
Seq. No.
                  LIB3059-001-Q1-K2-E4
Seq. ID
                  BLASTX
Method
                  g1168940
NCBI GI
                  403
BLAST score
                  2.0e-39
E value
                  104
Match length
                  72
% identity
                  CHORISMATE MUTASE PRECURSOR (CM-1) >gi_629509_pir__S38958
NCBI Description
                  chorismate mutase precursor - Arabidopsis thaliana
                  >qi 429153 emb CAA81286 (Z26519) chorismate mutase
                  precursor [Arabidopsis thaliana]
                  291502
Seq. No.
                  LIB3059-001-Q1-K2-G10
Seq. ID
                  BLASTX
Method
                  g141617
NCBI GI
BLAST score
                  317
                  3.0e-29
E value
                  74
Match length
                  82
% identity
                  ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                  >gi 100941 pir__S12140 zein Zc1 - maize
                  >gi_100945_pir__B29017 zein 2 - maize
                  >gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                  >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
                  291503
Seq. No.
                  LIB3059-001-Q1-K2-G5
Seq. ID
                  BLASTX
Method
                   q4090257
NCBI GI
BLAST score
                   307
E value
                   4.0e-28
Match length
                   60
% identity
                  (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
NCBI Description
                   291504
Seq. No.
                   LIB3059-001-Q1-K2-H7
Seq. ID
                   BLASTX
Method
```

NCBI GI g1841462 BLAST score 190 E value 2.0e-14 Match length 84 % identity 52

(Y10991) Elongation factor 2 [Nicotiana tabacum] NCBI Description

Method

NCBI GI

BLAST score

BLASTX

310

q4185308



```
Seq. No.
                  291505
Seq. ID
                  LIB3059-002-Q1-K2-A5
Method
                  BLASTX
                  g3914423
NCBI GI
BLAST score
                  222
                  2.0e-18
E value
Match length
                  61
% identity
                  74
NCBI Description PROFILIN 4 >gi_2642324 (AF032370) profilin [Zea mays]
                  291506
Seq. No.
Seq. ID
                  LIB3059-002-Q1-K2-C10
                  BLASTN
Method
NCBI GI
                  q899609
BLAST score
                  58
                  3.0e-24
E value
Match length
                  120
                  87
% identity
                  Zea mays acidic ribosomal protein P2 (RPA-2A1) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  291507
                  LIB3059-002-Q1-K2-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1184774
BLAST score
                   350
E value
                   3.0e-33
Match length
                  83
% identity
                   84
                  (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC3 [Zea mays]
Seq. No.
                   291508
Seq. ID
                  LIB3059-003-Q1-K1-C8
                  BLASTX
Method
NCBI GI
                   g3046815
                   394
BLAST score
                   3.0e-38
E value
                   104
Match length
% identity
                   66
NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana]
                   291509
Seq. No.
Seq. ID
                   LIB3059-003-Q1-K1-D11
Method
                   BLASTX
NCBI GI
                   g141610
BLAST score
                   235
                   7.0e-20
E value
                   99
Match length
% identity
                   58
NCBI Description ZEIN-ALPHA PRECURSOR (CLONE Z4)
                   291510
Seq. No.
Seq. ID
                   LIB3059-003-Q1-K1-D9
```

E value

Match length

% identity

4.0e-21

124

45



```
3.0e-40
E value
Match length
                  111
% identity
                  (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
NCBI Description
                  291511
Seq. No.
Seq. ID
                  LIB3059-003-Q1-K1-E3
                  {\tt BLASTX}
Method
NCBI GI
                  g3738285
                  181
BLAST score
                  4.0e-15
E value
                  96
Match length
% identity
                  49
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                  291512
Seq. No.
                  LIB3059-003-Q1-K1-E4
Seq. ID
                  BLASTX
Method
                  g3860247
NCBI GI
BLAST score
                  321
                  1.0e-29
E value
                  83
Match length
                  71
% identity
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                  291513
Seq. No.
                  LIB3059-003-Q1-K1-F3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1718238
                   459
BLAST score
                  7.0e-46
E value
Match length
                  135
% identity
                   64
                   (U59313) (1,4)-beta-xylan endohydrolase, isoenzyme X-II
NCBI Description
                   [Hordeum vulgare]
                   291514
Seq. No.
Seq. ID
                   LIB3059-003-Q1-K1-G11
                   BLASTX
Method
                   q141601
NCBI GI
BLAST score
                   189
                   7.0e-15
E value
Match length
                   55
% identity
                   69
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
NCBI Description
                   >gi 82657 pir__S03417 19K zein precursor (clone gZ19AB11) -
                   maize >gi_22543_emb_CAA29340_ (X05911) 19 kd alpha zein (AA
                   1 - 234) [Zea mays]
                   291515
Seq. No.
                   LIB3059-003-Q1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4371292
BLAST score
                   248
```

```
(AC006260) unknown protein [Arabidopsis thaliana]
NCBI Description
                  291516
Seq. No.
Seq. ID
                  LIB3059-003-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g1174448
BLAST score
                  187
                  3.0e-18
E value
Match length
                  98
                  51
% identity
                  TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR
NCBI Description
                  (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT)
                  (SSR-ALPHA) >gi 547391 (L32016) alpha-subunit; putative
                  [Arabidopsis thaliana]
                  291517
```

Seq. No. Seq. ID LIB3059-003-Q1-K1-H2 Method BLASTX NCBI GI g2130035 273 BLAST score E value 4.0e-24 130 Match length 52 % identity

glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) small NCBI Description

chain A - barley >gi 1143500 emb CAA88449 (Z48562) ADP-glucose pyrophosphorylase small subunit [Hordeum

vulgare]

Seq. No. 291518 Seq. ID

LIB3059-004-Q1-K1-A2

BLASTX Method NCBI GI g419803 BLAST score 150 5.0e-10 E value 69 Match length % identity 45

zein protein - maize >gi 168705 (M72708) zein protein [Zea NCBI Description

mays]

291519 Seq. No.

Seq. ID LIB3059-004-Q1-K1-B3

Method BLASTX NCBI GI q16073 BLAST score 200 E value 2.0e-24 Match length 71 % identity 87

NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 291520

LIB3059-004-Q1-K1-C2 Seq. ID

Method BLASTN NCBI GI g22531 BLAST score 71 8.0e-32 E value Match length 131 % identity 89

NCBI Description

thaliana]



```
NCBI Description
                  Zea mays mRNA encoding a zein (clone pZ22.1)
                  >gi_270688_gb_I03336_ Sequence 10 from Patent US 4885357
                  >gi 270741 gb I03273 Sequence 2 from Patent US
Seq. No.
                  291521
Seq. ID
                  LIB3059-004-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  q3033398
BLAST score
                  200
                  9.0e-16
E value
Match length
                  96
% identity
                  43
NCBI Description
                  (AC004238) putative phosphoribosylaminoimidazolecarboxamide
                  formyltransferase [Arabidopsis thaliana]
Seq. No.
                  291522
Seq. ID
                  LIB3059-004-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g3650036
BLAST score
                  216
E value
                  2.0e-17
Match length
                  129
% identity
                  41
NCBI Description
                  (AC005396) putative transposase [Arabidopsis thaliana]
Seq. No.
                  291523
Seq. ID
                  LIB3059-004-Q1-K1-D2
Method
                  BLASTN
NCBI GI
                  g902583
BLAST score
                  47
E value
                  1.0e-17
Match length
                  75
% identity
                  91
NCBI Description Zea mays clone MubG1 ubiquitin gene, complete cds
Seq. No.
                  291524
Seq. ID
                  LIB3059-004-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  g141603
BLAST score
                  500
E value
                  1.0e-50
Match length
                  109
% identity
                  94
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
                  >qi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
                  >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
Seq. No.
                  291525
Seq. ID
                  LIB3059-004-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g3928084
BLAST score
                  410
E value
                  4.0e-40
Match length
                  137
% identity
                  65
```

40569

(AC005770) retrotransposon-like protein [Arabidopsis

Seq. No.

Seq. ID Method

291531

BLASTX

LIB3059-005-Q1-K1-A2



```
Seq. No.
                  291526
Seq. ID
                  LIB3059-004-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                  g168699
BLAST score
                  357
                  6.0e-34
E value
Match length
                  111
                  69
% identity
NCBI Description (M60836) zein [Zea mays]
                  291527
Seq. No.
                  LIB3059-004-Q1-K1-G10
Seq. ID
Method
                  BLASTX
                  q4582457
NCBI GI
BLAST score
                  572
E value
                  3.0e-59
Match length
                  116
% identity
                  82
                  (AC007071) putative zinc finger protein [Arabidopsis
NCBI Description
                  thaliana]
                  291528
Seq. No.
Seq. ID
                  LIB3059-004-Q1-K1-G5
Method
                  BLASTN
NCBI GI
                  g4105122
BLAST score
                  66
                  1.0e-28
E value
Match length
                  101
% identity
                  91
NCBI Description Zea mays cell wall invertase (incw3) gene, complete cds
Seq. No.
                  291529
Seq. ID
                  LIB3059-004-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g141603
BLAST score
                  276
E value
                  2.0e-24
Match length
                  76
% identity
                  76
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
                  >qi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
                  >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
Seq. No.
                  291530
                  LIB3059-005-Q1-K1-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  9.0e-11
Match length
                  48
% identity
                  67
NCBI Description Xenopus laevis cDNA clone 27A6-1
```



```
NCBI GI
                  q2494650
BLAST score
                  167
E value
                  8.0e-12
Match-length
                  88
% idencity
                  44
NCBI Description
                  GLYCEROL-3-PHOSPHATE DEHYDROGENASE MITOCHONDRIAL PRECURSOR
                  (GPD-M) (GPDH-M) >gi 1408263 (U60987) FAD-linked
                  glycerol-3-phosphate dehydrogenase [Mus musculus]
Seq. No.
                  291532
Seq. ID
                  LIB3059-005-Q1-K1-B3
Method
                  BLASTN
NCBI GI
                  q540534
BLAST score
                  38
E value
                  2.0e-12
Match length
                  86
% identity
                  86
NCBI Description Rice mRNA for q group of receptor for activated C-kinase,
                  complete cds
                  291533
Seq. No.
Seq. ID
                  LIB3059-005-Q1-K1-B6
Method-
                  BLASTX
NCBI GI
                  g3881976
BLAST score
                  280
E value
                  4.0e-25
Match length
                  99
% identity
                  52
NCBI Description (AJ012409) hypothetical protein [Homo sapiens]
Seq. No.
                  291534
Seq. ID
                  LIB3059-005-Q1-K1-C3
Method
                  BLASTN
NCBI GI
                  g22326
BLAST score
                  218
E value
                  1.0e-119
Match length
                  218
% identity
                  100
NCBI Description Z.mays gene for Hageman factor inhibitor
Seq. No.
                  291535
Seq. ID
                  LIB3059-005-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  q2511695
BLAST score
                  453
E value
                  3.0e-45
Match length
                  121
% identity
                  68
```

NCBI Description (Z99955) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No. 291536

Seq. ID LIB3059-005-Q1-K1-D8

Method BLASTX NCBI GI q4185308 BLAST score 503 E value 5.0e-51 Match length 140

Seq. ID



```
% identity
   NCBI Description
                     (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
                     291537
   Seq. No.
   Seq. ID
                     LIB3059-005-Q1-K1-E4
   Method
                     BLASTX
   NCBI GI
                     q82696
   BLAST score
                     262
E value
                     9.0e-23
   Match length
                     72
   % identity
                     71
   NCBI Description
                     glycine-rich protein - maize >gi 22293 emb CAA43431
                     (X61121) glycine-rich protein [Zea mays]
   Seq. No.
                     291538
   Seq. ID
                     LIB3059-005-Q1-K1-F4
   Method
                     BLASTX
   NCBI GI
                     g2832243
   BLAST score
                     186
   E value
                     4.0e-14
                     69
   Match length
   % identity
                     59
   NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
   Seq. No.
                     291539
   Seq. ID
                     LIB3059-006-Q1-K1-B1
   Method
                     BLASTX
   NCBI GI
                     g1321627
   BLAST score
                     266
                     5.0e-29
   E value
   Match length
                     91
   % identity
                     75
   NCBI Description
                     (D83656) thylakoid-bound ascorbate peroxidase [Cucurbita
                     sp.]
   Seq. No.
                     291540
   Seq. ID
                     LIB3059-006-Q1-K1-B7
   Method
                     BLASTX
   NCBI GI
                     q4467124
   BLAST score
                     165
   E value
                     2.0e-11
   Match length
                     129
   % identity
   NCBI Description
                     (AL035538) hypothetical protein [Arabidopsis thaliana]
   Seq. No.
                     291541
                     LIB3059-006-Q1-K1-E11
   Seq. ID
   Method
                     BLASTN
   NCBI GI
                     g22524
   BLAST score
                     41
   E value
                     4.0e-14
   Match length
                     161
   % identity
                     81
   NCBI Description
                     Zea mays mRNA encoding a zein (clone ZG31A)
                     291542
   Seq. No.
```

40572

LIB3059-006-Q1-K1-F1



```
Method
NCBI GI
                  q2984709
BLAST score
                  201
                  3.0e-16
E value
Match length
                  69
% identity
                  59
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                  291543
Seq. No.
Seq. ID
                  LIB3059-006-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g141603
BLAST score
                  526
                  9.0e-54
E value
Match length
                  136
% identity
                  81
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
                  >gi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
                  >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
                  291544
Seq. No.
Seq. ID
                  LIB3059-006-Q1-K1-F8
Method
                  BLASTN
NCBI GI
                  q20266
BLAST score
                  56
                  3.0e-23
E value
Match length
                  80
% identity
                  93
NCBI Description
                  O.sativa mRNA for lipoxygenase L-2
                  >gi_2171696_dbj_E03480_E03480 cDNA encoding rice
                  lipoxygenase L-\overline{3}
Seq. No.
                  291545
Seq. ID
                  LIB3059-006-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g168699
BLAST score
                  243
E value
                  8.0e-34
Match length
                  120
% identity
                  72
NCBI Description
                  (M60836) zein [Zea mays]
Seq. No.
                  291546
Seq. ID
                  LIB3059-006-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  q3395938
BLAST score
                  177
E value
                  3.0e-16
Match length
                  90
% identity
                  53
                  (AF076924) polypyrimidine tract-binding protein homolog
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 291547

LIB3059-006-Q1-K1-G8 Seq. ID

Method BLASTX NCBI GI g118104



BLAST score 397 E value 4.0e-56 Match length 145 % identity 79

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)

>gi 68408 pir CSZM peptidylprolyl isomerase (EC 5.2.1.8) -

maize >gi 168461 (M55021) cyclophilin [Zea mays]

>gi_829148 emb CAA48638 (X68678) cyclophilin [Zea mays]

Seq. No. 291548

Seq. ID LIB3059-007-Q1-K1-A1

Method BLASTX
NCBI GI g100846
BLAST score 263
E value 7.0e-23
Match length 76
% identity 72

NCBI Description 22K zein precursor (clone gZ22.8H3) - maize

>gi_22179_emb_CAA43399_ (X61085) 22 kD alpha-zein [Zea

mays]

Seq. No. 291549

Seq. ID LIB3059-007-Q1-K1-A5

Method BLASTN
NCBI GI g1061304
BLAST score 148
E value 1.0e-77
Match length 275
% identity 91

NCBI Description Z.mays ZSF4C5 gene for zein

Seq. No. 291550

Seq. ID LIB3059-007-Q1-K1-A6

Method BLASTX
NCBI GI g3337356
BLAST score 353
E value 2.0e-33
Match length 81
% identity 88

NCBI Description (AC004481) putative protein transport protein SEC61 alpha

subunit [Arabidopsis thaliana]

Seq. No. 291551

Seq. ID LIB3059-007-Q1-K1-B1

Method BLASTX
NCBI GI g1806140
BLAST score 189
E value 3.0e-14
Match length 71
% identity 61

NCBI Description (X97314) cdc2MsC [Medicago sativa]

Seq. No. 291552

Seq. ID LIB3059-007-Q1-K1-B3

Method BLASTN NCBI GI g22292

% identity

NCBI Description

81



```
BLAST score
                  4.0e-23
E value
Match length
                  92
                  91
% identity
NCBI Description Z.mays mRNA for glycine-rich protein
Seq. No.
                  291553
Seq. ID
                  LIB3059-007-Q1-K1-C4
Method
                  BLASTN
                  g168681
NCBI GI
BLAST score
                  140
E value
                  5.0e-73
                  235
Match length
                  91
% identity
                  Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                  >gi 270686 gb I03333 Sequence 8 from Patent US
Seq. No.
                  291554
Seq. ID
                  LIB3059-007-Q1-K1-C7
                  {\tt BLASTX}
Method
                  g2827663
NCBI GI
BLAST score
                  212
E value
                  5.0e-17
Match length
                  124
% identity
NCBI Description
                  (AL021637) membrane-associated salt-inducible-like protein
                   [Arabidopsis thaliana]
Seq. No.
                  291555
Seq. ID
                  LIB3059-007-Q1-K1-D4
                  BLASTX
Method
NCBI GI
                  g4337027
BLAST score
                  186
                  8.0e-14
E value
Match length
                  65
% identity
                  58
NCBI Description
                  (AF123254) MFP2 [Arabidopsis thaliana]
Seq. No.
                  291556
Seq. ID
                  LIB3059-007-Q1-K1-D7
Method
                  BLASTN
                  q22544
NCBI GI
BLAST score
                  121
E value
                  8.0e-62
Match length
                  153
% identity
                  95
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
                  291557
Seq. No.
                  LIB3059-007-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1304266
BLAST score
                  320
E value
                  1.0e-29
Match length
                  79
```

40575

(D64051) HALF-1 [Triticum aestivum]



NCBI Description Z.mays GapC4 gene

Seq. No.

291563

```
291558
Seq. No.
                  LIB3059-007-Q1-K1-E2
Seq. ID
                  BLASTX
Method
                  g141608
NCBI GI
BLAST score
                  167
E value
                  1.0e-11
                  63
Match length
                  56
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943 pir_ S15655
NCBI Description
                  zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
                  zein [Zea mays]
                  291559
Seq. No.
                  LIB3059-007-Q1-K1-F3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g141603
BLAST score
                  169
                  4.0e-20
E value
                  81
Match length
                  75
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                  >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
                  291560
Seq. No.
Seq. ID
                  LIB3059-007-Q1-K1-G10
                  BLASTN
Method
                  g168677
NCBI GI
                  37
BLAST score
                  1.0e-11
E value
Match length
                  73
                  88
% identity
NCBI Description Maize 19 kDa zein mRNA, clone cZ19C1, complete cds
                  291561
Seq. No.
Seq. ID
                  LIB3059-007-Q1-K1-G3
Method
                  BLASTN
NCBI GI
                  g1184775
BLAST score
                  54
E value
                   1.0e-21
Match length
                   170
% identity
                   83
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC4
                   (gpc4) mRNA, complete cds
                   291562
Seq. No.
Seq. ID
                  LIB3059-007-Q1-K1-G7
Method
                  BLASTN
                   g312180
NCBI GI
BLAST score
                   146
                   2.0e-76
E value
Match length
                   192
% identity
                   92
```



```
LIB3059-007-Q1-K1-H8
Seq. ID
                  BLASTX
Method
                  g100940
NCBI GI
                  291
BLAST score
E value
                  4.0e-26
Match length
                  84
% identity
                  74
NCBI Description zein zA1 - maize
                  291564
Seq. No.
Seq. ID
                  LIB3059-008-Q1-K1-B12
                  BLASTN
Method
NCBI GI
                  g2062705
BLAST score
                  36
                  9.0e-11
E value
Match length
                  36
% identity
                  100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  291565
Seq. No.
Seq. ID
                  LIB3059-008-Q1-K1-C10
                  BLASTX
Method
NCBI GI
                  q4185308
BLAST score
                  320
                  1.0e-29
E value
                  100
Match length
                  36
% identity
NCBI Description (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
                  291566
Seq. No.
Seq. ID
                  LIB3059-008-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  q629861
                  328
BLAST score
                  9.0e-31
E value
                  101
Match length
                  72
% identity
NCBI Description zein Zd1, 19K - maize >gi 535020_emb_CAA47639_ (X67203)
                  zein Zd1 (19 kDa zein) [Zea mays]
                  291567
Seq. No.
Seq. ID
                  LIB3059-008-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                   q1519251
BLAST score
                   143
                   2.0e-09
E value
                   44
Match length
                   73
% identity
NCBI Description (U65957) GF14-c protein [Oryza sativa]
                   291568
Seq. No.
Seq. ID
                   LIB3059-008-Q1-K1-D4
Method
                   BLASTX
NCBI GI
                   g82660
BLAST score
                   269
```

x.

40577

8.0e-24

93

E value

Match length



% identity 62

NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)

>gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 291569
Seq. ID LIB3059-008-Q1-K1-E8

Method BLASTX
NCBI GI g1707924
BLAST score 550
E value 1.0e-56
Match length 124
% identity 86

NCBI Description GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT 1

PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE

PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) (SHRUNKEN-2) >gi_1947182 (M81603) shrunken-2 [Zea mays] >gi_444329_prf__1906378A ADP glucose

pyrophosphorylase [Zea mays]

Seq. No. 291570

Seq. ID LIB3059-008-Q1-K1-F6

Method BLASTN
NCBI GI g2832242
BLAST score 72
E value 2.0e-32
Match length 300
% identity 59

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 291571

Seq. ID LIB3059-008-Q1-K1-G5

Method BLASTN
NCBI GI g168698
BLAST score 114
E value 2.0e-57
Match length 234
% identity 88

NCBI Description Z.mays zein mRNA, complete cds

Seq. No. 291572

Seq. ID LIB3059-008-Q1-K1-G9

Method BLASTN
NCBI GI g22544
BLAST score 218
E value 1.0e-119
Match length 302
% identity 96

NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)

Seq. No. 291573

Seq. ID LIB3059-008-Q1-K1-H1

Method BLASTX
NCBI GI g3152613
BLAST score 163
E value 1.0e-11
Match length 79
% identity 39





```
(AC004482) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  291574
Seq. No.
                  LIB3059-009-Q1-K1-A12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2662341
BLAST score
                  157
E value
                  9.0e-11
                  75
Match length
                  49
% identity
                  (D63580) EF-1 alpha [Oryza sativa]
NCBI Description
                  >gi 2662345 dbj_BAA23659_ (D63582) EF-1 alpha [Oryza
                  satīva] >gi 2662347 dbj BAA23660 (D63583) EF-1 alpha
                  [Oryza sativa]
                  291575
Seq. No.
                  LIB3059-009-Q1-K1-B4
Seq. ID
                  BLASTX
Method
                  g2832243
NCBI GI
                  408
BLAST score
                   4.0e-40
E value
Match length
                  109
                  78
% identity
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
                  291576
Seq. No.
                  LIB3059-009-Q1-K1-D2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2244759
BLAST score
                  361
                   2.0e-34
E value
                  85
Match length
                   78
% identity
NCBI Description (Z97335) selenium-binding protein [Arabidopsis thaliana]
                   291577
Seq. No.
Seq. ID
                  LIB3059-009-Q1-K1-E5
                  BLASTX
Method
NCBI GI
                   g232282
BLAST score
                   285
E value
                   2.0e-25
                   73
Match length
                   70
% identity
                  22.0 KD CLASS IV HEAT SHOCK PROTEIN PRECURSOR
NCBI Description
                   >gi_477760_pir__B48113 heat shock protein HSP22.0 - soybean
                   >gi 18661 emb CAA44882 (X63198) heat shock protein
                   [Glycine max]
Seq. No.
                   291578
                   LIB3059-010-Q1-K1-C7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q141601
BLAST score
                   168
E value
                   4.0e-12
Match length
                   62
                   53
% identity
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
```



>gi_82657_pir__S03417 19K zein precursor (clone gZ19AB11) maize >gi_22543_emb_CAA29340_ (X05911) 19 kd alpha zein (AA
1 - 234) [Zea mays]

```
291579
Seq. No.
Seq. ID
                  LIB3059-010-Q1-K1-D1
                  BLASTN
Method
                  q535019
NCBI GI
                  162
BLAST score
                  6.0e-86
E value
                  274
Match length
                  46
% identity
                  Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)
NCBI Description
                  291580
Seq. No.
                  LIB3059-010-Q1-K1-D4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g168695
BLAST score
                  253
                  1.0e-21
E value
                  111
Match length
                   35
% identity
                  (M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A
NCBI Description
                  zein gamma [Zea mays]
                  291581
Seq. No.
Seq. ID
                  LIB3059-010-Q1-K1-E10
                  BLASTN
Method
                   g2665839
NCBI GI
BLAST score
                   170
                   7.0e-91
E value
Match length
                   194
                   97
% identity
                   Zea mays putative histone deacetylase RPD3 mRNA, complete
NCBI Description
                   291582
Seq. No.
Seq. ID
                   LIB3059-010-Q1-K1-E11
                   BLASTX
Method
NCBI GI
                   q419803
BLAST score
                   219
                   6.0e-18
E value
Match length
                   90
% identity
                   48
                   zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                   mays]
                   291583
Seq. No.
                   LIB3059-010-Q1-K1-F7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g168677
BLAST score
                   84
E value
                   1.0e-39
Match length
                   92
% identity
                   98
NCBI Description Maize 19 kDa zein mRNA, clone cZ19C1, complete cds
```

NCBI GI

E value

BLAST score

q3914685

1.0e-17

195



```
Seq. No.
                   291584
Seq. ID
                  LIB3059-010-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  g22216
BLAST score
                  380
                   1.0e-36
E value
                  104
Match length
% identity
                   77
NCBI Description (X55722) 22kD zein [Zea mays]
                   291585
Seq. No.
                  LIB3059-010-Q1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1173027
                   222
BLAST score
                   2.0e-18
E value
                   76
Match length
% identity
                   59
                  60S RIBOSOMAL PROTEIN L31 >gi_915313 (U23784) ribosomal
NCBI Description
                   protein L31 [Nicotiana glutinosa]
Seq. No.
                   291586
                   LIB3059-011-Q1-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2832247
BLAST score
                   296
E value
                   8.0e-27
Match length
                   115
% identity
                   57
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]
                   291587
Seq. No.
                   LIB3059-011-Q1-K1-B5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3688162
                   337
BLAST score
                   1.0e-31
E value
                   90
Match length
                   76
% identity
NCBI Description (AJ009672) centrin [Arabidopsis thaliana]
                   291588
Seq. No.
                   LIB3059-011-Q1-K1-C12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2062705
BLAST score
                   37
                   2.0e-11
E value
                   37
Match length
                   100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                   291589
Seq. No.
Seq. ID
                   LIB3059-011-Q1-K1-D2
Method
                   BLASTX
```



```
Match length
                  51
% identity
                  60S RIBOSOMAL PROTEIN L17 >gi_2668748 (AF034948) ribosomal
NCBI Description
                  protein L17 [Zea mays]
                  291590
Seq. No.
                  LIB3059-011-Q1-K1-D8
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2828011
                  121
BLAST score
                  9.0e-62
E value
                  168
Match length
                  98
% identity
                  Zea mays starch synthase I precursor (Ss1) mRNA, nuclear
NCBI Description
                  gene encoding plastid protein, complete cds
                  291591
Seq. No.
Seq. ID
                  LIB3059-011-Q1-K1-E8
                  BLASTX
Method
NCBI GI
                  g3024738
                  276
BLAST score
                  2.0e-24
E value
                  145
Match length
                  45
% identity
                  TYPE II DNA TOPOISOMERASE VI SUBUNIT A
NCBI Description
                  >gi_1926404_emb_CAA71605_ (Y10582) type II DNA
                  topoisomerase subunit A [Sulfolobus shibatae]
                  291592
Seq. No.
                  LIB3059-011-Q1-K1-G9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3135751
BLAST score
                  533
E value
                  1.0e-54
                  125
Match length
                  85
% identity
                  (AJ006095) 26S protease regulatory subunit 6 [Cicer
NCBI Description
                  arietinum]
                  291593
Seq. No.
                  LIB3059-011-Q1-K1-H6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q224508
BLAST score
                  394
                   3.0e-38
E value
Match length
                  105
                   83
% identity
NCBI Description zein A20 [Zea mays]
                   291594
```

Seq. No.

LIB3059-012-Q1-K1-C6 Seq. ID

BLASTX Method q2245138 NCBI GI BLAST score 509 E value 9.0e-52 138 Match length 68 % identity



```
(Z97344) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  291595
Seq. No.
Seq. ID
                  LIB3059-012-Q1-K1-C8
                  BLASTX
Method
NCBI GI
                  g419803
BLAST score
                  235
                  8.0e-20
E value
                  104
Match length
                  55
% identity
                  zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                  mays]
                  291596
Seq. No.
                  LIB3059-012-Q1-K1-E9
Seq. ID
                  BLASTX
Method
                  g3834322
NCBI GI
BLAST score
                  166
                  1.0e-11
E value
Match length
                  83
% identity
                  54
                  (AC005679) EST gb R30300 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  291597
Seq. No.
Seq. ID
                  LIB3059-012-Q1-K1-F8
                  BLASTX
Method
NCBI GI
                  g508545
                  275
BLAST score
                  2.0e-24
E value
                  121
Match length
                  50
% identity
NCBI Description (L34340) zein [Zea mays]
                  291598
Seq. No.
Seq. ID
                  LIB3059-013-Q1-K1-A2
Method
                  BLASTN
NCBI GI
                  g22292
BLAST score
                  . 75
                   5.0e-34
E value
                  87
Match length
                   97
% identity
NCBI Description Z.mays mRNA for glycine-rich protein
Seq. No.
                   291599
                  LIB3059-013-Q1-K1-A3
Seq. ID
Method
                  BLASTN
                  q3342820
NCBI GI
BLAST score
                  170
                   7.0e-91
E value
                  199
Match length
                   96
% identity
                  Zea mays eukaryotic translation initiation factor small
NCBI Description
```

Seq. No. 291600

Seq. ID LIB3059-013-Q1-K1-A6

40583

subunit (eIF-4E) mRNA, complete cds

NCBI GI

BLAST score

g2865177

153



```
Method
                  BLASTX
NCBI GI
                  q2244933
BLAST score
                  179
E value
                  3.0e-13
Match length
                  45
% identity
                  73
NCBI Description
                  (Z97339) similar to hypothetical protein YPL211w - yeast
                  [Arabidopsis thaliana]
Seq. No.
                  291601
Seq. ID
                  LIB3059-013-Q1-K1-B11
Method
                  BLASTN
NCBI GI
                  g22445
BLAST score
                  127
E value
                  3.0e-65
Match length
                  206
% identity
                  91
NCBI Description Zea mays ZMPMS1 gene for 19 kDa zein protein
                  291602
Seq. No.
Seq. ID
                  LIB3059-013-Q1-K1-B4
Method
                  BLASTX
                  q1184776
NCBI GI
BLAST score
                  298
E value
                  2.0e-29
Match length
                  71
% identity
                  94
NCBI Description
                  (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
                  GAPC4 [Zea mays]
Seq. No.
                  291603
Seq. ID
                  LIB3059-013-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  q629861
BLAST score
                  255
E value
                  5.0e-22
Match length
                  118
% identity
                  48
NCBI Description
                  zein Zd1, 19K - maize >gi 535020 emb CAA47639 (X67203)
                  zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                  291604
Seq. ID
                  LIB3059-013-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  g3212879
BLAST score
                  261
E value
                  1.0e-22
Match length
                  80
% identity
                  60
NCBI Description
                  (AC004005) putative ribosomal protein L7 [Arabidopsis
                  thaliana]
                  291605
Seq. No.
Seq. ID
                  LIB3059-013-Q1-K1-D2
Method
                  BLASTX
```



```
4.0e-10
E value
Match length
                  59
% identity
                  46
                  (AB010946) AtRer1B [Arabidopsis thaliana]
NCBI Description
                  291606
Seq. No.
                  LIB3059-013-Q1-K1-D8
Seq. ID
Method
                  BLASTX
                  g629767
NCBI GI
                  198
BLAST score
                  2.0e-15
E value
                  70
Match length
                  59
% identity
                  11S globulin - oat >gi_472867_emb_CAA52764_ (X74741) 11S
NCBI Description
                  globulin [Avena sativa]
                  291607
Seq. No.
                  LIB3059-013-Q1-K1-E2
Seq. ID
Method
                  BLASTX
                   g419803
NCBI GI
                  304
BLAST score
                   8.0e-28
E value
                   111
Match length
                   55
% identity
                  zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                  mays]
                   291608
Seq. No.
                   LIB3059-013-Q1-K1-E7
Seq. ID
Method
                   BLASTN
                   g2668739
NCBI GI
                   109
BLAST score
                   1.0e-54
E value
                   173
Match length
% identity
                   91
NCBI Description Zea mays translation initiation factor GOS2 (TIF) mRNA,
                   complete cds
                   291609
Seq. No.
                   LIB3059-013-Q1-K1-G11
Seq. ID
                   BLASTX
Method
                   g2982434
NCBI GI
                   163
BLAST score
E value
                   2.0e-11
Match length
                   92
                   34
% identity
NCBI Description (AL022224) putative protein [Arabidopsis thaliana]
                   291610
Seq. No.
                   LIB3059-013-Q1-K1-H5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g629861
                   236
BLAST score
E value
                   4.0e-20
Match length
                   71
                   82
% identity
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
```



zein Zd1 (19 kDa zein) [Zea mays]

```
291611
Seq. No.
Seq. ID
                  LIB3059-013-Q1-K1-H9
                  BLASTN
Method
NCBI GI
                  g3821780
BLAST score
                  36
                  1.0e-10
E value
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  291612
Seq. No.
Seq. ID
                  LIB3059-014-Q1-K1-B7
                  BLASTN
Method
                  g3892651
NCBI GI
BLAST score
                  353
                  0.0e+00
E value
                  379
Match length
                   98
% identity
                  Z.mays mRNA for putative MADS-domain transcription factor,
NCBI Description
                   ZMM8
                  291613
Seq. No.
Seq. ID
                  LIB3059-014-Q1-K1-C12
                  BLASTX
Method
                   g113360
NCBI GI
BLAST score
                  247
                   2.0e-25
E value
                   109
Match length
% identity
                   61
                  ALCOHOL DEHYDROGENASE 1 >gi 100652 pir JQ0474 alcohol
NCBI Description
                   dehydrogenase (EC 1.1.1.1) 1 - rice >gi 20165 emb CAA34363
                   (X16296) alcohol dehydrogenase 1 [Oryza sativa]
                   291614
Seq. No.
                   LIB3059-014-Q1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q82696
BLAST score
                   180
E value
                   1.0e-13
Match length
                   56
% identity
                   66
                   glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
Seq. No.
                   291615
                   LIB3059-014-Q1-K1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2781345
                   430
BLAST score
                   2.0e-42
E value
Match length
                   127
% identity
                   70
```

Seq. No. 291616

NCBI Description

(AC003113) F2401.2 [Arabidopsis thaliana]

```
LIB3059-014-Q1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3522946
BLAST score
                  333
E value
                  3.0e-31
Match length
                  101
% identity
                  57
NCBI Description
                  (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
                  291617
Seq. No.
                  LIB3059-014-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2674203
BLAST score
                  187
E value
                   4.0e-14
Match length
                   63
                   67
% identity
                   (AF036328) CLP protease regulatory subunit CLPX
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   291618
Seq. ID
                   LIB3059-014-Q1-K1-G12
Method
                   BLASTX
NCBI GI
                   g1652892
BLAST score
                   265
E value
                   4.0e-23
Match length
                   81
% identity
                   59
NCBI Description (D90909) ABC transporter [Synechocystis sp.]
                   291619
Seq. No.
                   LIB3059-014-Q1-K1-G5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
                   8.0e-11
E value
Match length
                   36
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   291620
Seq. No.
Seq. ID
                   LIB3059-015-Q1-K1-B1
                   BLASTX
Method
NCBI GI
                   q4335758
BLAST score
                   182
                   2.0e-13
E value
                   52
Match length
                   69
% identity
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]
                   291621
Seq. No.
                   LIB3059-015-Q1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g984525
BLAST score
                   170
```

5.0e-12

74

E value

Match length

Seq. No.

Seq. ID Method



```
% identity
                  (U31541) DZS18 [Zea mays]
NCBI Description
Seq. No.
                  291622
                  LIB3059-015-Q1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455256
BLAST score
                   402
E value
                   3.0e-39
Match length
                   95
% identity
                   73
                   (AL035523) protein-methionine-S-oxide reductase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   291623
                  LIB3059-015-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3757521
BLAST score
                   182
                   2.0e-13
E value
Match length
                   81
% identity
                   41
                  (AC005167) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   291624
                   LIB3059-015-Q1-K1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4454459
                   202
BLAST score
E value
                   1.0e-15
                   49
Match length
                   80
% identity
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                   291625
Seq. No.
Seq. ID
                   LIB3059-015-Q1-K1-E9
                   BLASTX
Method
NCBI GI
                   g1171577
BLAST score
                   221
                   5.0e-18
E value
Match length
                   119
                   43
% identity
                  (X95343) hypersensitivity-related gene [Nicotiana tabacum]
NCBI Description
Seq. No.
                   291626
Seq. ID
                   LIB3059-015-Q1-K1-F1
Method
                   BLASTX
                   q3201618
NCBI GI
BLAST score
                   191
                   4.0e-15
E value
                   66
Match length
% identity
                  (AC004669) Sop2p-like protein [Arabidopsis thaliana]
NCBI Description
```

BLASTX

LIB3059-015-Q1-K1-F8

291627



```
q4158230
NCBI GI
BLAST score
                  331
E value
                  4.0e-31
                  92
Match length
                  73
% identity
NCBI Description (Y18625) amylogenin [Triticum aestivum]
Seq. No.
                  291628
                  LIB3059-015-Q1-K1-G5
Seq. ID
Method
                  BLASTN
                  g168698
NCBI GI
                  56
BLAST score
                   4.0e-23
E value
Match length
                  104
% identity
                   88
NCBI Description Z.mays zein mRNA, complete cds
                   291629
Seq. No.
Seq. ID
                  LIB3059-015-Q1-K1-G8
Method
                  BLASTN
NCBI GI
                   q3821780
BLAST score
                   36
E value
                   1.0e-10
Match length
                   36
% identity
                   100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   291630
Seq. No.
                   LIB3059-016-Q1-K1-B3
Seq. ID
Method
                   BLASTN
                   g168702
NCBI GI
BLAST score
                   44
                   1.0e-15
E value
Match length
                   174
% identity
                   88
NCBI Description Corn 22 kDa zein protein gene, complete cds
                   291631
Seq. No.
Seq. ID
                   LIB3059-016-Q1-K1-C11
                   BLASTX
Method
                   g1710236
NCBI GI
BLAST score
                   252
                   1.0e-21
E value
Match length
                   73
% identity
                   60
NCBI Description (U79270) unknown [Homo sapiens]
                   291632
Seq. No.
Seq. ID
                   LIB3059-016-Q1-K1-C9
                   BLASTX
Method
                   g3334474
NCBI GI
BLAST score
                   290
                   2.0e-26
E value
Match length
                   85
% identity
                   74
NCBI Description OLEOSIN ZM-I (OLEOSIN 16 KD) (LIPID BODY-ASSOCIATED MAJOR
```

PROTEIN) (LIPID BODY-ASSOCIATED PROTEIN L3)
40589





>gi 1076817 pir S52029 oleosin 16 - maize >gi_687245

(U13701) 16 kDa oleosin [Zea mays] 291633 Seq. No. LIB3059-016-Q1-K1-D3 Seq. ID BLASTX Method NCBI GI g3395441 BLAST score 181 2.0e-13 E value 54 Match length % identity NCBI Description (AC004683) unknown protein [Arabidopsis thaliana] Seq. No. 291634 LIB3059-016-Q1-K1-G1 Seq. ID BLASTX Method g2829910 NCBI GI 184 BLAST score 1.0e-13 E value 128 Match length 38 % identity (AC002291) Unknown protein, contains regulator of NCBI Description chromosome condensation motifs [Arabidopsis thaliana] 291635 Seq. No. LIB3059-016-Q1-K1-H6 Seq. ID BLASTX Method g4091117 NCBI GI 278 BLAST score 1.0e-24 E value 90 Match length 59 % identity

NCBI Description (AF047428) nucleic acid binding protein [Oryza sativa]

Seq. No. LIB3059-017-Q1-K1-A11 Seq. ID BLASTX Method NCBI GI g141599 190 BLAST score 1.0e-14 E value 65 Match length % identity 65

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19A2)

>gi_72316_pir__ZIZMA2 19K zein precursor (clone cZ19A2) maize (fragment) >gi_168670 (M12142) 19 kDa zein protein

[Zea mays]

291636

291637 Seq. No.

LIB3059-017-Q1-K1-C11 Seq. ID

BLASTX Method NCBI GI g3970823 BLAST score 647 E value 5.0e-68 Match length 121 % identity

NCBI Description (X17555) pyruvate decarboxylase [Zea mays]

NCBI GI

E value

BLAST score

g3747050

391 6.0e-38



```
291638
Seq. No.
                  LIB3059-017-Q1-K1-C12
Seq. ID
Method
                  BLASTX
                  g1362009
NCBI GI
                   430
BLAST score
                   2.0e-42
E value
                   92
Match length
                   52
% identity
                  ubiquitin-like protein 7 - Arabidopsis thaliana
NCBI Description
                   291639
Seq. No.
                   LIB3059-017-Q1-K1-D9
Seq. ID
                   BLASTN
Method
NCBI GI
                   q2832242
                   59
BLAST score
                   1.0e-24
E value
                   180
Match length
% identity
                   73
                   Zea mays 22-kDa alpha zein gene cluster, complete sequence
NCBI Description
                   291640
Seq. No.
                   LIB3059-017-Q1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g168697
BLAST score
                   216
                   1.0e-17
E value
                   90
Match length
                   28
% identity
                   (M60835) zein [Zea mays]
NCBI Description
                   291641
Seq. No.
                   LIB3059-017-Q1-K1-E7
Seq. ID
                   BLASTX
Method
                   g2832246
NCBI GI
BLAST score
                   184
                   1.0e-13
E value
                   49
Match length
                   80
% identity
                  (AF031569) 22-kDa alpha zein 8 [Zea mays]
NCBI Description
                   291642
Seq. No.
Seq. ID
                   LIB3059-017-Q1-K1-G5
                   BLASTX
Method
NCBI GI
                   q2982259
                   140
BLAST score
                   4.0e-09
E value
                   50
Match length
                   52
% identity
                   (AF051212) probable 60s ribosomal protein L13a [Picea
NCBI Description
                   mariana]
                   291643
Seq. No.
                   LIB3059-017-Q1-K1-G7
Seq. ID
Method
                   BLASTX
```

NCBI Description



```
Match length
                   93
% identity
                   (AF093540) ribosomal protein L26 [Zea mays]
NCBI Description
                   291644
Seq. No.
                   LIB3059-017-Q1-K1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4580389
BLAST score
                   200
E value
                   1.0e-15
                   69
Match length
 % identity
                   52
                   (AC007171) unknown protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                   291645
                   LIB3059-017-Q1-K1-H9
 Seq. ID
                   BLASTN

    Method

 NCBI GI
                    g168704
 BLAST score
                    177
                    4.0e-95
 E value
                    213
Match length
                    97
 % identity
                   Zea mays zein protein gene, complete cds
 NCBI Description
                    291646
 Seq. No.
                    LIB3059-018-Q1-K1-A11
 Seq. ID
 Method
                    BLASTX
                    g141600
 NCBI GI
                    181
 BLAST score
 E value
                    2.0e-13
                    103
 Match length
                    43
 % identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
 NCBI Description
                    >gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) -
                    maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]
                    291647
 Seq. No.
                    LIB3059-018-Q1-K1-B10
 Seq. ID
                    BLASTN
 Method
                    g902583
 NCBI GI
                    147
 BLAST score
                    4.0e-77
 E value
                    223
 Match length
                    53
 % identity
 NCBI Description Zea mays clone MubGl ubiquitin gene, complete cds
 Seq. No.
                    291648
                    LIB3059-018-Q1-K1-C5
 Seq. ID
                    BLASTX
 Method
                    g421960
 NCBI GI
                    183
 BLAST score
                    1.0e-13
 E value
                    42
 Match length
 % identity
                    86
```

(M72892) spliceosomal protein [Solanum tuberosum]

small nuclear ribonucleoprotein U2B'' - potato >gi_169589



```
291649
Seq. No.
                  LIB3059-018-Q1-K1-C6
Seq. ID
                  BLASTN
Method
                  g22516
NCBI GI
                  124
BLAST score
                  3.0e-63
E value
                  156
Match length
                  95
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                  291650
Seq. No.
                  LIB3059-018-Q1-K1-C9
Seq. ID
                  BLASTN
Method
                   q6012171
NCBI GI
                   35
BLAST score
                   3.0e-10
E value
                   71
Match length
                   87
% identity
                  Hordeum vulgare mRNA for vacuolar membrane
NCBI Description
                   proton-translocating inorganic pyrophosphat
Seq. No.
                   291651
                   LIB3059-018-Q1-K1-D2
Seq. ID
                   BLASTX
Method
                   g1053059
NCBI GI
                   193
BLAST score
                   3.0e-15
E value
                   44
Match length
                   84
% identity
NCBI Description (U38423) histone H3 [Triticum aestivum]
                   291652
Seq. No.
                   LIB3059-018-Q1-K1-D6
Seq. ID
                   BLASTN
Method
                   g168696
NCBI GI
                   44
BLAST score
                   1.0e-15
E value
                   116
Match length
                   87
% identity
NCBI Description Z.mays zein mRNA, 3' end
                   291653
Seq. No.
Seq. ID
                   LIB3059-018-Q1-K1-D9
Method
                   BLASTX
                   a168701
NCBI GI
                   217
BLAST score
                   1.0e-17
E value
                   107
Match length
 % identity
                   48
NCBI Description
                   (M60837) zein [Zea mays]
                   291654
 Seq. No.
                   LIB3059-018-Q1-K1-E3
```

Seq. ID

Method BLASTX g3461848 NCBI GI 168 BLAST score 2.0e-12 E value

```
- SECTION SECT
```

```
56
Match length
                   61
% identity
                   (AC005315) putative ATPase [Arabidopsis thaliana]
NCBI Description
                   291655
Seq. No.
                   LIB3059-018-Q1-K1-F6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g168699
                   314
BLAST score
                   6.0e-29
E value
                   96
Match length
                   67
% identity
NCBI Description (M60836) zein [Zea mays]
                   291656
Seq. No.
                   LIB3059-018-Q1-K1-G9
Seq. ID
                   BLASTN
Method
                   g2062705
NCBI GI
BLAST score
                   36
                   6.0e-11
E value
                   36
Match length
                   100
% identity
                   Human butyrophilin (BTF5) mRNA, complete cds
NCBI Description
                   291657
Seq. No.
                   LIB3059-018-Q1-K1-H1
Seq. ID
                   BLASTX
Method
                   g1184774
NCBI GI
                   159
BLAST score
                   4.0e-11
E value
                   87
Match length
                   47
% identity
                   (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC3 [Zea mays]
                   291658
Seq. No.
                   LIB3059-019-Q1-K1-A3
Seq. ID
                   BLASTX
Method
                   g1352316
NCBI GI
                   339
BLAST score
                   8.0e-32
E value
                   99
Match length
                   71
% identity
                   DR1 PROTEIN HOMOLOG >gi_633026_dbj_BAA07288_ (D38110) Dr1
NCBI Description
                   [Arabidopsis thaliana]
                   291659
Seq. No.
                   LIB3059-019-Q1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2832243
BLAST score
                   385
                   3.0e-37
E value
                   123
Match length
```

Seq. No. 291660

% identity

NCBI Description

(AF031569) 22-kDa alpha zein 4 [Zea mays]



LIB3059-019-Q1-K1-C4

Seq. ID

```
BLASTX
Method
                  g3163946
NCBI GI
BLAST score
                  593
E value
                  1.0e-61
                  113
Match length
% identity
                  98
NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]
                  291661
Seq. No.
                  LIB3059-019-Q1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141597
BLAST score
                  251
E value
                  6.0e-37
                  127
Match length
                   65
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                  >qi 72314 pir ZIZM3 19K zein precursor (clone A30) - maize
                  >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
                   [Zea mays]
                  291662
Seq. No.
                  LIB3059-019-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q141617
                   491
BLAST score
E value
                   1.0e-49
Match length
                  119
                   80
% identity
                  ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                   >gi_100941_pir__S12140 zein Zc1 - maize
                   >gi_100945_pir__B29017 zein 2 - maize
                   >qi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                   >qi^{-}16866\overline{6} (M\overline{1}6460) 16-kDa zein protein [Zea mays]
                   291663
Seq. No.
                   LIB3059-019-Q1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g72307
BLAST score
                   458
E value
                   8.0e-46
Match length
                   122
% identity
                   79
                   22K zein precursor (clone pZ22.3) - maize >gi 168686
NCBI Description
                   (J01246) 26.99 kd zein protein [Zea mays]
                   291664
Seq. No.
Seq. ID
                   LIB3059-019-Q1-K1-F6
Method
                   BLASTX
NCBI GI
                   q464705
BLAST score
                   146
E value
                   3.0e-09
Match length
                   77
% identity
                   48
                   40S RIBOSOMAL PROTEIN S13 >gi 419802 pir S30146 ribosomal
NCBI Description
                   protein S13.e - maize >gi 288059 emb CAA44311 (X62455)
```

BLAST score

Match length

E value

351 3.0e-33

141





cytoplasmatic ribosomal protein S13 [Zea mays]

Seq. No. 291665 LIB3059-019-Q1-K1-G1 Seq. ID Method BLASTX NCBI GI g3294467 BLAST score 281 E value 2.0e-35 Match length 131 61 % identity NCBI Description (U89341) phosphoglucomutase 1 [Zea mays] 291666 Seq. No. LIB3059-019-Q1-K1-G5 Seq. ID Method BLASTX NCBI GI g3150404 BLAST score 475 E value 9.0e-48 Match length 142 % identity 65 (AC004165) putative mitochondrial carrier protein NCBI Description [Arabidopsis thaliana] Seq. No. 291667 LIB3059-020-Q1-K1-B2 Seq. ID Method BLASTX NCBI GI g141613 BLAST score 173 2.0e-12 E value Match length 78 % identity 51 ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1) NCBI Description >gi_72305_pir__ZIZM21 22K zein precursor (clone pZ22.1) maize >gi 22532 emb CAA24725 (V01478) zein [Zea mays] Seq. No. 291668 LIB3059-020-Q1-K1-C2 Seq. ID BLASTX Method g113621 NCBI GI 687 BLAST score 1.0e-72 E value 131 Match length 100 % identity NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A cytoplasmic aldolase [Zea mays] 291669 Seq. No. LIB3059-020-Q1-K1-C4 Seq. ID BLASTX Method NCBI GI g3337367

```
The second section is
```

```
% identity
                  (AC004481) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  291670
Seq. No.
                  LIB3059-020-Q1-K1-C6
Seq. ID
                  BLASTN
Method
                  g168696
NCBI GI
BLAST score
                  40
E value
                   4.0e-13
Match length
                   40
                   100
% identity
NCBI Description Z.mays zein mRNA, 3' end
                   291671
Seq. No.
                  LIB3059-020-Q1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g468516
BLAST score
                   399
E value
                   8.0e-39
Match length
                   112
                   75
% identity
NCBI Description (X55724) zein [Zea mays]
Seq. No.
                   291672
                   LIB3059-020-Q1-K1-D7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3935167
BLAST score
                   143
                   5.0e-10
E value
Match length
                   60
                   65
% identity
                  (AC004557) F17L21.10 [Arabidopsis thaliana]
NCBI Description
                   291673
Seq. No.
                   LIB3059-020-Q1-K1-E9
Seq. ID
                   BLASTX
Method
                   g168703
NCBI GI
                   238
BLAST score
                   5.0e-20
E value
                   64
Match length
                   80
% identity
                   (M86591) 22 kDa zein protein [Zea mays]
NCBI Description
                   291674
Seq. No.
Seq. ID
                   LIB3059-020-Q1-K1-G3
                   BLASTX
Method
                   q2618689
NCBI GI
                   674
BLAST score
                   4.0e-71
E value
Match length
                   146
                   86
% identity
                   (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
                   291675
Seq. No.
Seq. ID
                   LIB3059-020-Q1-K1-H10
```

BLASTX

q168699

Method

NCBI GI



```
BLAST score
                  452
E value
                  4.0e-45
Match length
                  96
% identity
                  97
NCBI Description
                 (M60836) zein [Zea mays]
Seq. No.
                  291676
Seq. ID
                  LIB3059-020-Q1-K1-H12
Method
                  BLASTN
NCBI GI
                  g4185305
BLAST score
                  55
E value
                  4.0e-22
Match length
                  60
% identity
                  56
                 Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                  (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes
                  291677
Seq. No.
Seq. ID
                  LIB3059-021-Q1-K1-A6
Method
                  BLASTX
                  q4176420
NCBI GI
                  213
BLAST score
E value
                  3.0e-20
Match length
                  78
% identity
                  62
NCBI Description (AB008097) cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                  291678
                  LIB3059-021-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q141600
BLAST score
                  201
E value
                  7.0e-16
Match length
                  68
                  65
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
                  >gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) -
                  maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]
Seq. No.
                  291679
Seg. ID
                  LIB3059-021-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g141613
BLAST score
                  308
E value
                  3.0e-28
Match length
                  104
                  65
% identity
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
NCBI Description
                  >gi 72305 pir ZIZM21 22K zein precursor (clone pZ22.1) -
                  maize >gi_22532 emb_CAA24725 (V01478) zein [Zea mays]
```

Seq. No. 291680

Seq. ID LIB3059-021-Q1-K1-E12

Method BLASTX NCBI GI g1705733



```
BLAST score
                   9.0e-39
E value
                   112
Match length
% identity
                   CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM 1 (CDPK 1)
NCBI Description
                   >gi_542156_pir__JC1515 calcium-dependent protein kinase (EC
2.7.1.-) - rice >gi_435466_dbj_BAA02698_ (D13436)
                   calcium-dependent protein kinase [Oryza sativa]
                   291681
Seq. No.
                   LIB3059-021-Q1-K1-F1
Seq. ID
                   BLASTN
Method
                   q1778148
NCBI GI
                   204
BLAST score
                   1.0e-111
E value
                   220
Match length
                   98
% identity
                   Zea mays plastid phosphate/phosphoenolpyruvate translocator
NCBI Description
                   precursor (MZPPT4) mRNA, complete cds
                   291682
Seq. No.
                   LIB3059-021-Q1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3548810
                   155
BLAST score
E value
                   1.0e-10
                   91
Match length
% identity
                    (AC005313) putative chloroplast nucleoid DNA binding
NCBI Description
                   protein [Arabidopsis thaliana]
                    291683
Seq. No.
                   LIB3059-021-Q1-K1-H1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2832643
BLAST score
                    217
                    2.0e-17
E value
                    80
Match length
% identity
                   (AL021710) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    291684
Seq. No.
                    LIB3059-022-Q1-K1-A1
Seq. ID
                    BLASTN
Method
                    g22292
NCBI GI
                    42
BLAST score
                    8.0e-15
E value
                    142
Match length
                    83
% identity
NCBI Description Z.mays mRNA for glycine-rich protein
                    291685
Seq. No.
                    LIB3059-022-Q1-K1-B2
 Seq. ID
                    BLASTN
Method
NCBI GI
                    q22326
```

1.0e-13

BLAST score

E value

84 Match length 88 % identity Z.mays gene for Hageman factor inhibitor NCBI Description

291686 Seq. No.

LIB3059-022-Q1-K1-B8 Seq. ID

BLASTX Method NCBI GI g136063 147 BLAST score 2.0e-12 E value 68 Match length

65 % identity

TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) NCBI Description

>gi_68426_pir__ISZMT triose-phosphate isomerase (EC 5.3.1.1) - maize >gi_168647 (L00371) triosephosphate isomerase 1 [Zea mays] >gi_217974_dbj_BAA00009_ (D00012)

triosephosphate isomerase [Zea mays]

Seq. No. 291687

LIB3059-022-Q1-K1-C6 Seq. ID

Method BLASTN NCBI GI g22445 86 BLAST score 1.0e-40 E value Match length 231 92 % identity

Zea mays ZMPMS1 gene for 19 kDa zein protein NCBI Description

291688 Seq. No.

LIB3059-022-Q1-K1-D1 Seq. ID

BLASTX Method g1737492 NCBI GI 229 BLAST score 3.0e-25 E value 105 Match length

66 % identity

(U81318) poly(A)-binding protein [Triticum aestivum] NCBI Description

291689 Seq. No.

LIB3059-022-Q1-K1-D4 Seq. ID

BLASTX Method g72307 NCBI GI 255 BLAST score 4.0e-22 E value 107 Match length 60 % identity

22K zein precursor (clone pZ22.3) - maize >gi_168686 NCBI Description

(J01246) 26.99 kd zein protein [Zea mays]

291690 Seq. No.

LIB3059-022-Q1-K1-D5 Seq. ID

BLASTX Method q3927825 NCBI GI BLAST score 187 E value 7.0e-29 108 Match length 73 % identity

(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No. 291691

NCBI Description

Seq. ID LIB3059-022-Q1-K1-E5

Method BLASTX
NCBI GI g141615
BLAST score 184
E value 1.0e-18
Match length 81
% identity 77

NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)

>gi 22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]

Seq. No. 291692

Seq. ID LIB3059-022-Q1-K1-E9

Method BLASTN
NCBI GI g168677
BLAST score 69
E value 2.0e-30
Match length 97
% identity 93

NCBI Description Maize 19 kDa zein mRNA, clone cZ19C1, complete cds

Seq. No. 291693

Seq. ID LIB3059-022-Q1-K1-F2

Method BLASTX
NCBI GI g168701
BLAST score 258
E value 2.0e-22
Match length 94
% identity 62

NCBI Description (M60837) zein [Zea mays]

Seq. No. 291694

Seq. ID LIB3059-022-Q1-K1-F6

Method BLASTX
NCBI GI g419803
BLAST score 306
E value 4.0e-28
Match length 88
% identity 67

NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea

mays]

Seq. No. 291695

Seq. ID LIB3059-022-Q1-K1-G1

Method BLASTX
NCBI GI g451193
BLAST score 179
E value 3.0e-13
Match length 62
% identity 61

NCBI Description (L28008) wali7 [Triticum aestivum]

>gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]

Seq. No. 291696

NCBI GI

BLAST score

g4056487

543



```
LIB3059-022-Q1-K1-G3
Seq. ID
                  BLASTX
Method
                  g4558564
NCBI GI
                  174
BLAST score
                  1.0e-12
E value
                  101
Match length
                   39
% identity
                   (AC007138) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                  291697
Seq. No.
                  LIB3059-022-Q1-K1-G5
Seq. ID
                  BLASTN
Method
NCBI GI
                   q2665839
                   33
BLAST score
                   2.0e-09
E value
                   61
Match length
                   89
% identity
                   Zea mays putative histone deacetylase RPD3 mRNA, complete
NCBI Description
Seq. No.
                   291698
                   LIB3059-022-Q1-K1-H3
Seq. ID
Method
                   BLASTX
                   g224970
NCBI GI
                   219
BLAST score
                   6.0e-18
E value
                   49
Match length
                   90
% identity
                  heat shock protein hsp70 [Zea mays]
NCBI Description
                   291699
Seq. No.
                   LIB3059-023-Q1-K1-A12
Seq. ID
                   {\tt BLASTX}
Method
NCBI GI
                   q419803
                   154
BLAST score
                   2.0e-10
E value
                   53
Match length
                   60
% identity
                   zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                   mays]
                   291700
Seq. No.
                   LIB3059-023-Q1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2253411
                   252
BLAST score
                   1.0e-21
E value
Match length
                   99
% identity
                   43
                  (AF007219) PP2A inhibitor [Tetraodon fluviatilis]
NCBI Description
                   291701
Seq. No.
Seq. ID
                   LIB3059-023-Q1-K1-G5
Method
                   BLASTX
```

```
9.0e-56
E value
Match length
                  128
                  83
% identity
                  (AC005896) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  291702
Seq. No.
                  LIB3059-023-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141604
                  379
BLAST score
                  1.0e-36
E value
                  106
Match length.
                  75
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)
NCBI Description
                  >gi 72310 pir ZIZM91 19K zein precursor (clone cZ19C1) -
                  maize >gi_168678 (M12146) 19 kDa zein protein [Zea mays]
                   291703
Seq. No.
                  LIB3059-023-Q1-K1-H4
Seq. ID
                  BLASTX
Method
                   g168699
NCBI GI
BLAST score
                   624
                   3.0e-65
E value
                   142
Match length
                   92
% identity
                  (M60836) zein [Zea mays]
NCBI Description
                   291704
Seq. No.
                   LIB3059-024-Q1-K1-A3
Seq. ID
                   BLASTX
Method
                   g629861
NCBI GI
                   174
BLAST score
                   7.0e-13
E value
                   63
Match length
% identity
                   59
                   zein Zd1, 19K - maize >gi 535020 emb CAA47639 (X67203)
NCBI Description
                   zein Zd1 (19 kDa zein) [Zea mays]
                   291705
Seq. No.
                   LIB3059-024-Q1-K1-B2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g266398
BLAST score
                   451
E value
                   5.0e-45
Match length
                   102
                   77
% identity
                   TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR
NCBI Description
                   INHIBITOR) (CHFI) >gi_68849 pir TIZM1 trypsin/factor XIIa
                   inhibitor precursor - maize >gi 22327_emb_CAA37998_
                   (X54064) corn Hageman factor inhibitor [Zea mays]
                   291706
Seq. No.
                   LIB3059-024-Q1-K1-B9
```

Seq. ID

Method BLASTN NCBI GI q168681 BLAST score 45 2.0e-16 E value



```
53
Match length
                   96
% identity
                  Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                  >gi_270686_gb_I03333_ Sequence 8 from Patent US
                   291707
Seq. No.
                  LIB3059-024-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g141614
                   175
BLAST score
                   2.0e-19
E value
                   102
Match length
                   65
% identity
                   ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)
NCBI Description
                   >gi_82662_pir_B22831 22K zein precursor (clone M1) - maize
                   >gi 22527 emb CAA24722 (V01475) reading frame zein [Zea
                   mays] >gi224\overline{5}10 prf\overline{1}107201D zein M1 [Zea mays]
                   291708
Seq. No.
                   LIB3059-024-Q1-K1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g135060
                   347
BLAST score
                   9.0e-33
E value
Match length
                   68
                   97
% identity
                   SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
NCBI Description
                   (SHRUNKEN-1) >gi_66570_pir _YUZMS sucrose synthase (EC
                   2.4.1.13) - maize >gi_22486 emb_CAA26247 (X02400) sucrose
                   synthase [Zea mays] >gi_22488_emb_CAA26229_ (X02382)
                   sucrose synthase [Zea mays]
Seq. No.
                   291709
                   LIB3059-024-Q1-K1-F4
Seq. ID
                   BLASTX
Method
                   g126066
NCBI GI
                   449
BLAST score
                   9.0e-45
E value
Match length
                   126
% identity
                   L-LACTATE DEHYDROGENASE (LDH) >gi_82704_pir__S22492
NCBI Description
                   L-lactate dehydrogenase (EC 1.1.1.27) chain Ldh1 - maize
                   >gi 22353 emb_CAA77808_ (Z11754) lactate dehydrogenase [Zea
                   mays]
                   291710
Seq. No.
Seq. ID
                   LIB3059-024-Q1-K1-F8
                   BLASTX
Method
NCBI GI
                   g2118425
                   241
BLAST score
                   2.0e-20
E value
                   73
Match length
                   64
 % identity
                   subtilisin/chymotrypsin inhibitor - maize
NCBI Description
                   >gi_475253_emb_CAA55588_ (X78988) proteinase inhibitor [Zea
                   mays] >gi \overline{47592}2 emb CA\overline{A}49593 (X69972) proteinase
```

inhibitor [Zea mays] >gi_559538_emb_CAA57677_ (X82187)

Seq. No.

291716



substilin /chymotrypsin-like inhibitor [Zea mays]

```
Seq. No.
                  291711
                  LIB3059-024-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1947086
BLAST score
                  163
E value
                   3.0e-11
Match length
                   40
% identity
                   65
                   (U88368) inositol(1,3,4,5)tetrakisphosphate receptor [Sus
NCBI Description
                   scrofa]
Seq. No.
                   291712
                   LIB3059-025-Q1-K1-A5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g168704
BLAST score
                   80
E value
                   4.0e-37
Match length
                   105
                   95
% identity
                  Zea mays zein protein gene, complete cds
NCBI Description
Seq. No.
                   291713
                   LIB3059-025-Q1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1421730
                   176
BLAST score
                   6.0e-13
E value
                   57
Match length
                   58
% identity
                  (U43082) RF2 [Zea mays]
NCBI Description
Seq. No.
                   291714
                   LIB3059-025-Q1-K1-B3
Seq. ID
                   BLASTX
Method
                   q4220524
NCBI GI
                   143
BLAST score
                   8.0e-09
E value
                   71
Match length
                   41
% identity
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
                   291715
Seq. No.
                   LIB3059-025-Q1-K1-C5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q266398
                   350
BLAST score
                   3.0e-33
E value
                   97
Match length
% identity
                   66
                   TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR
NCBI Description
                   INHIBITOR) (CHFI) >gi_68849_pir__TIZM1 trypsin/factor XIIa
                   inhibitor precursor - maize >gi 22327 emb_CAA37998_
                   (X54064) corn Hageman factor inhibitor [Zea mays]
```

Method

NCBI GI

BLAST score

BLASTX q2499488

165



```
LIB3059-025-Q1-K1-F11
Seq. ID
                   BLASTN
Method
                   g22516
NCBI GI
                   51
BLAST score
                   1.0e-19
E value
                   119
Match length
                   86
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                   291717
Seq. No.
                   LIB3059-025-Q1-K1-G5
Seq. ID
                   BLASTX
Method
                   q508545
NCBI GI
BLAST score
                   417
                   6.0e-41
E value
                   124
Match length
                   70
% identity
NCBI Description (L34340) zein [Zea mays]
                   291718
Seq. No.
                   LIB3059-026-Q1-K1-A9
Seq. ID
Method
                   BLASTX
NCBI GI
                    q2662343
                    212
BLAST score
E value
                    3.0e-18
                    105
Match length
                    56
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                    291719
Seq. No.
                    LIB3059-026-Q1-K1-B12
Seq. ID
                    BLASTX
Method
                    g3024018
NCBI GI
                    460
BLAST score
E value
                    5.0e-46
                    128
Match length
                    73
% identity
                    INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
NCBI Description
                    >gi_1546919_emb_CAA69225_ (Y07920) translation initiation
factor 5A [Zea mays] >gi_2668738 (AF034943) translation
                    initiation factor 5A [Zea mays]
                    291720
Seq. No.
Seq. ID
                    LIB3059-026-Q1-K1-B9
Method
                    BLASTX
                    q16073
NCBI GI
                    146
BLAST score
                    1.0e-09
E value
                    62
Match length
                    63
% identity
                   (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
                    291721
Seq. No.
Seq. ID
                    LIB3059-026-Q1-K1-C11
```



```
2.0e-11
E value
Match length
                  80
% identity
                  44
                  PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
NCBI Description
                  ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                   (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                   (PPI-PFK) >gi 483547_emb_CAA83682_ (Z32849)
                  pyrophosphate-dependent phosphofructokinase alpha subunit
                  [Ricinus communis]
Seq. No.
                  291722
                  LIB3059-026-Q1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q629861
BLAST score
                  262
                  5.0e-23
E value
Match length
                  64
                  81
% identity
                  zein Zd1, 19K - maize >gi 535020_emb_CAA47639_ (X67203)
NCBI Description
                  zein Zd1 (19 kDa zein) [Zea mays]
                  291723
Seq. No.
                  LIB3059-026-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q122007
BLAST score
                  196
E value
                   3.0e-15
Match length
                   39
% identity
                   97
                  HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley
NCBI Description
                   >qi 20448 emb CAA37828 (X53831) H2A histone protein (AA 1
                   - 149) [Petroselinum crispum]
Seq. No.
                   291724
                  LIB3059-026-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g141610
                   303
BLAST score
                   1.0e-27
E value
Match length
                   106
                   64
% identity
NCBI Description ZEIN-ALPHA PRECURSOR (CLONE Z4)
                   291725
Seq. No.
Seq. ID
                   LIB3059-026-Q1-K1-D1
                   BLASTX
Method
NCBI GI
                   g1351904
BLAST score
                   315
E value
                   3.0e-29
Match length
                   96
                   67
% identity
                   ASPARTOKINASE 1 / HOMOSERINE DEHYDROGENASE 1 CHLOROPLAST
NCBI Description
```

ASPARTOKINASE 1 / HOMOSERINE DEHYDROGENASE 1 CHLOROPLAST PRECURSOR (AK-HSDH 1) (AKHSDH1) >gi 500851 (L33912)

aspartate kinase-homoserine dehydrogenase [Zea mays]

Seq. No. 291726

Seq. ID LIB3059-026-Q1-K1-D9



```
BLASTX
Method
NCBI GI
                   g141607
                   164
BLAST score
                   1.0e-11
E value
                   88
Match length
                   45
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE PZ19.1)
NCBI Description
                   >gi 22521_emb_CAA24718_ (V01471) zein [Zea mays] >gi_168672
                   (J01244) zein 19 kd protein (partial) [Zea mays]
                   291727
Seq. No.
                   LIB3059-026-Q1-K1-E11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q121472
                   392
BLAST score
                   4.0e-38
E value
                   94
Match length
% identity
                   81
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi 22289 emb CAA26149 (X02230) glutelin-2 precursor
                   [Zea mays] >gi \overline{22517} emb CAA\overline{37594} (X53514) zein Zc2 [Zea
                   mays] >gi_1684\overline{8}5 (M1\overline{6}066) gluteli\overline{n}-2 [Zea mays]
                   291728
Seq. No.
                   LIB3059-026-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   g3335351
NCBI GI
                   265
BLAST score
                   2.0e-23
E value
                   93
Match length
                   58
% identity
                   (AC004512) Similar to ERECTA receptor protein kinase
NCBI Description
                   gb D83257 from A. thaliana. ESTs gb T41629 and gb_AA586072
                   come from this gene. [Arabidopsis thaliana]
                   291729
Seq. No.
Seq. ID
                   LIB3059-026-Q1-K1-G1
                   BLASTX
Method
                   g2668742
NCBI GI
                   215
BLAST score
                   2.0e-17
E value
Match length
                   63
% identity
                   71
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]
                   291730
Seq. No.
                   LIB3059-026-Q1-K1-G11
Seq. ID
Method
                   BLASTX
                   g2224915
NCBI GI
                   325
BLAST score
```

(U95968) beta-expansin [Oryza sativa]

3.0e-30

108

57

E value Match length

% identity

NCBI Description



```
Seq. No.
Seq. ID
                  LIB3059-026-Q1-K1-G7
                  BLASTX
Method
                  g3136057
NCBI GI
                  210
BLAST score
                  7.0e-17
E value
Match length
                  71
% identity
                  51
NCBI Description (AL023592) actin-like protein [Schizosaccharomyces pombe]
                  291732
Seq. No.
                  LIB3059-026-Q1-K1-H11
Seq. ID
                  BLASTX
Method
                  g72307
NCBI GI
                  244
BLAST score
                   6.0e-21
E value
                  101
Match length
                   55
% identity
                  22K zein precursor (clone pZ22.3) - maize >gi_168686
NCBI Description
                   (J01246) 26.99 kd zein protein [Zea mays]
                   291733
Seq. No.
                   LIB3059-026-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                   g3953595
NCBI GI
                   196
BLAST score
                   3.0e-15
E value
                   75
Match length
                   53
% identity
NCBI Description (AB008486) response regulator 3 [Arabidopsis thaliana]
                   291734
Seq. No.
                   LIB3059-026-Q1-K1-H9
Seq. ID
                   BLASTX
Method
                   q168703
NCBI GI
                   177
BLAST score
                   5.0e-13
E value
                   50
Match length
                   72
% identity
NCBI Description (M86591) 22 kDa zein protein [Zea mays]
                   291735
Seq. No.
Seq. ID
                   LIB3059-027-Q1-K1-A11
Method
                   BLASTX
                   q4325324
NCBI GI
                   235
BLAST score
                   1.0e-19
E value
                   73
Match length
% identity
                   (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis
NCBI Description
                   thaliana]
                   291736
 Seq. No.
                   LIB3059-027-Q1-K1-C3
 Seq. ID
Method
                   BLASTX
```

g2149051

269

NCBI GI BLAST score



```
1.0e-23
E value
                  86
Match length
% identity
                  62
                  (U73810) small Ras-like GTP-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  291737
Seq. No.
Seq. ID
                  LIB3059-027-Q1-K1-D1
                  BLASTX
Method
                  q82696
NCBI GI
BLAST score
                  152
                  2.0e-12
E value
                  83
Match length
                  52
% identity
                  glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                  (X61121) glycine-rich protein [Zea mays]
                  291738
Seq. No.
                  LIB3059-027-Q1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3122753
BLAST score
                  222
                  3.0e-18
E value
Match length
                  82
                  55
% identity
                  60S RIBOSOMAL PROTEIN L44 >qi 2244789 emb CAB10211.1
NCBI Description
                  (Z97336) ribosomal protein [Arabidopsis thaliana]
                  291739
Seq. No.
Seq. ID
                  LIB3059-027-Q1-K1-F5
                  BLASTX
Method
                  g141599
NCBI GI
BLAST score
                  346
                  1.0e-32
E value
                  102
Match length
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19A2)
NCBI Description
                  >gi 72316 pir ZIZMA2 19K zein precursor (clone cZ19A2) -
                  maize (fragment) >gi 168670 (M12142) 19 kDa zein protein
                  [Zea mays]
Seq. No.
                  291740
Seq. ID
                  LIB3059-027-Q1-K1-G1
Method
                  BLASTN
NCBI GI
                  q4185305
BLAST score
                  43
E value
                  4.0e-15
Match length
                  227
% identity
                  80
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                   (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
```

protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No. 291741

Seq. ID LIB3059-027-Q1-K1-G7

Method BLASTN



```
g4416300
NCBI GI
BLAST score
                  184
                  5.0e-99
E value
Match length
                  289
% identity
                  46
NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster
                  region, complete sequence
Seq. No.
                  291742
Seq. ID
                  LIB3059-027-Q1-K1-H9
Method
                  BLASTN
NCBI GI
                  g2832242
BLAST score
                  123
                  1.0e-62
E value
Match length
                  327
                  10
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.
                  291743
Seq. ID
                  LIB3059-028-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  g22216
BLAST score
                  256
                  4.0e-22
E value
                  112
Match length
                  52
% identity
NCBI Description (X55722) 22kD zein [Zea mays]
Seq. No.
                  291744
Seq. ID
                  LIB3059-028-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  q168701
BLAST score
                  322
E value
                  6.0e-30
Match length
                  95
% identity
                  68
NCBI Description (M60837) zein [Zea mays]
                  291745
Seq. No.
Seq. ID
                  LIB3059-028-Q1-K1-D2
Method
                  BLASTX
                  g1565223
NCBI GI
BLAST score
                  196
E value
                  2.0e-16
Match length
                  82
                  59
% identity
NCBI Description (Y08301) MCM2-related protein [Arabidopsis thaliana]
                  291746
Seq. No.
Seq. ID
                  LIB3059-028-Q1-K1-G9
```

Method BLASTX

NCBI GI q122087 BLAST score 508 E value 1.0e-51 Match length 121 % identity 85

NCBI Description HISTONE H3 >gi 81849 pir S04520 histone H3 (clone pH3c-1)



- alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964 (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi_19609_emb_CAA31965 (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451 (X00937) H3 histone [Triticum aestivum] >gi_488565 (U09459) histone H3.1 [Medicago sativa] >gi_2565419 (AF026803) histone H3 [Onobrychis viciifolia]

 Seq. No.
 291747

 Seq. ID
 LIB3059-028-Q1-K1-H8

 Method
 BLASTX

 NCBI GI
 g2293566

 BLAST score
 202

 E value
 6.0e-16

 Match length
 61

% identity 72
NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]

 Seq. No.
 291748

 Seq. ID
 LIB3059-029-Q1-K1-B11

 Method
 BLASTX

 NCBI GI
 g123378

 BLAST score
 220

 E value
 2.0e-18

 Match length
 52

Match length 52 % identity 85 NCBI Description DN

NCBI Description DNA-BINDING PROTEIN MNB1B (HMG1-LIKE PROTEIN)

>gi_100886_pir__S16670 high mobility group protein - maize
>gi_539062_pir__B47150 DNA-binding protein MNB1b - maize
>gi_22329_emb_CAA41220_ (X58282) high mobility group

protein [Zea mays]

Seq. No.

291749

Seq. ID LIB3059-029-Q1-K1-B2

Method BLASTX
NCBI GI g119150
BLAST score 329
E value 5.0e-36
Match length 105
% identity 76

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_82081_pir__S10507 translation elongation factor eEF-1
alpha chain - tomato >gi_19273_emb_CAA32618_ (X14449) EF

1-alpha (AA 1-448) [Lycopersicon esculentum]

>gi_295810_emb_CAA37212_ (X53043) elongation factor 1-alpha

[Lycopersicon esculentum]

Seq. No. 291750

Seq. ID LIB3059-029-Q1-K1-B3

Method BLASTX
NCBI GI g3309583
BLAST score 251
E value 1.0e-21
Match length 101
% identity 56

NCBI Description (AF073830) fructose-6-phosphate

2-kinase/fructose-2,6-bisphosphatase [Solanum tuberosum]



```
Seq. No.
                   291751
Seq. ID
                   LIB3059-029-Q1-K1-C4
Method
                   BLASTX
NCBI GI
                   q231654
BLAST score
                   164
E value
                   2.0e-11
                   79
Match length
                   46
% identity
                   BRITTLE-1 PROTEIN PRECURSOR >gi 82676 pir JQ1459 Bt1
NCBI Description
                   protein precursor - maize >gi 168426 (M79333) brittle-1
                   protein [Zea mays]
                   291752
Seq. No.
Seq. ID
                   LIB3059-029-Q1-K1-D9
Method
                   BLASTX
NCBI GI
                   g266398
BLAST score
                   414
E value
                   1.0e-40
Match length
                   96
% identity
                   76
NCBI Description
                   TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR
                   INHIBITOR) (CHFI) >gi_68849_pir__TIZM1 trypsin/factor XIIa
inhibitor precursor - maize >gi_22327_emb_CAA37998_
                   (X54064) corn Hageman factor inhibitor [Zea mays]
                   291753
Seq. No.
Seq. ID
                   LIB3059-029-Q1-K1-E2
Method
                   BLASTX
NCBI GI
                   q141605
BLAST score
                   269
E value
                   1.0e-23
Match length
                   74
% identity
                   72
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
                   >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                   maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
                   291754
Seq. No.
Seq. ID
                   LIB3059-029-Q1-K1-F6
Method
                   BLASTX
NCBI GI
                   g82696
BLAST score
                   141
                   9.0e-09
E value
                   59
Match length
                   53
% identity
NCBI Description glycine-rich protein - maize >gi 22293 emb CAA43431
                   (X61121) glycine-rich protein [Zea mays]
Seq. No.
                   291755
Seq. ID
                   LIB3059-029-Q1-K1-G1
Method
                   BLASTX
NCBI GI
                   q4432825
BLAST score
                   269
                   1.0e-23
E value
```

100

58

Match length % identity



Seq. No.

```
LIB3059-029-Q1-K1-G7
Seq. ID
Method
                  BLASTX
                  g3334474
NCBI GI
BLAST score
                  190
                  8.0e-15
E value
                  64
Match length
                  64
% identity
NCBI Description OLEOSIN ZM-I (OLEOSIN 16 KD) (LIPID BODY-ASSOCIATED MAJOR
                  PROTEIN) (LIPID BODY-ASSOCIATED PROTEIN L3)
                  >gi_1076817_pir__S52029 oleosin 16 - maize >gi_687245
                  (U13701) 16 kDa oleosin [Zea mays]
                  291757
Seq. No.
Seq. ID
                  LIB3059-029-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  g82696
BLAST score
                  202
E value
                  4.0e-21
                  73
Match length
                  78
% identity
NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_
                  (X61121) glycine-rich protein [Zea mays]
                  291758
Seq. No.
Seq. ID
                  LIB3059-029-Q1-K1-H7
                  BLASTX
Method
NCBI GI
                  g2832683
BLAST score
                  171
E value
                  2.0e-12
                  99
Match length
                  38
% identity
NCBI Description (AL021712) putative protein [Arabidopsis thaliana]
                  291759
Seq. No.
                  LIB3059-030-Q1-K1-A11
Seq. ID
                  BLASTN
Method
NCBI GI
                  q168681
BLAST score
                  72
E value
                  3.0e-32
Match length
                  148
% identity
                  87
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
                  >gi_270686_gb_I03333_ Sequence 8 from Patent US
Seq. No.
                  291760
                  LIB3059-030-Q1-K1-B12
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2811133
BLAST score
                  54
                  1.0e-21
E value
Match length
                  66
% identity
                  95
NCBI Description Zea mays starch synthase isoform zSTSII-1 (zSSIIa) mRNA,
```

NCBI Description (AC006593) putative SOP2p protein [Arabidopsis thaliana]

partial cds



```
291761
Seq. No.
                   LIB3059-030-Q1-K1-D2
Seq. ID
                   BLASTX
Method
                   g22216
NCBI GI
                   236
BLAST score
                   2.0e-29
E value
Match length
                   126
% identity
                   64
NCBI Description (X55722) 22kD zein [Zea mays]
                   291762
Seq. No.
                   LIB3059-030-Q1-K1-D4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g121472
BLAST score
                   144
                    4.0e-09
E value
Match length
                    107
                    38
% identity
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                    (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                    >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
                    [Zea mays] >gi_\overline{2}251\overline{7}_emb_CAA\overline{3}7594_ (X53\overline{5}14) zein Zc2 [Zea
                    mays] >gi_1684\overline{8}5 (M1\overline{6}066) gluteli\overline{n}-2 [Zea mays]
                    291763
Seq. No.
                    LIB3059-030-Q1-K1-E10
Seq. ID
                    BLASTN
Method
NCBI GI
                    g168425
                    187
BLAST score
                    1.0e-101
E value
                    227
Match length
                    96
% identity
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds
                    291764
 Seq. No.
                    LIB3059-030-Q1-K1-E5
 Seq. ID
                    BLASTX
Method
                    q4006829
NCBI GI
                    483
 BLAST score
                    1.0e-48
E value
                    139
Match length
                    71
 % identity
NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]
                    291765
 Seq. No.
                    LIB3059-030-Q1-K1-G5
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g141610
                    202
 BLAST score
                     9.0e-16
 E value
                     80
 Match length
 % identity
 NCBI Description ZEIN-ALPHA PRECURSOR (CLONE Z4)
```

291766

Seq. No.



```
LIB3059-030-Q1-K1-H10
Seq. ID
                  BLASTX
Method
                  q168693
NCBI GI
                  366
BLAST score
                  5.0e-35
E value
                  126
Match length
                   67
% identity
NCBI Description (M29627) zein [Zea mays]
                  291767
Seq. No.
                  LIB3059-031-Q1-K1-B10
Seq. ID
                  BLASTX
Method
                   g2246625
NCBI GI
                   331
BLAST score
                   7.0e-31
E value
                   91
Match length
                   69
% identity
NCBI Description (AF004947) protein kinase [Oryza sativa]
                   291768
Seq. No.
                   LIB3059-031-Q1-K1-B4
Seq. ID
                   BLASTN
Method
                   g22447
NCBI GI
                   35
BLAST score
                   2.0e-10
E value
                   39
Match length
                   97
% identity
NCBI Description Zea mays ZMPMS2 gene for 19 kDa zein protein
                   291769
Seq. No.
                   LIB3059-031-Q1-K1-B6
Seq. ID
                   {\tt BLASTX}
Method
                   q419803
NCBI GI
                   165
BLAST score
                   5.0e-12
E value
                   56
Match length
                   59
% identity
                   zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                   mays]
                   291770
Seq. No.
Seq. ID
                   LIB3059-031-Q1-K1-D5
                   BLASTN
Method
NCBI GI
                   g899609
BLAST score
                   76
                   7.0e-35
E value
                   156
Match length
                   87
 % identity
                   Zea mays acidic ribosomal protein P2 (RPA-2A1) mRNA,
 NCBI Description
                   complete cds
                   291771
 Seq. No.
                   LIB3059-031-Q1-K1-E1
 Seq. ID
                   BLASTN
 Method
 NCBI GI
                   q22528
```

73

3.0e-33

BLAST score

E value



```
Match length
                  87
% identity
NCBI Description Zea mays mRNA encoding a zein (clone A20)
                  291772
Seq. No.
                  LIB3059-031-Q1-K1-F11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g543867
                  250
BLAST score
                  1.0e-21
E value
                  56
Match length
                  93
% identity
NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
                  >gi_1076684_pir__A47493 H+-transporting ATP synthase (EC
                   3.6.1.34) gamma chain precursor - sweet potato
                   >gi 303626 dbj BAA03526_ (D14699) F1-ATPase gammma subunit
                   [Ipomoea batatas]
Seq. No.
                   291773
                  LIB3059-031-Q1-K1-F2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2244842
                   272
BLAST score
                   3.0e-24
E value
                   94
Match length
                   56
% identity
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
                   291774
Seq. No.
                   LIB3059-031-Q1-K1-F7
Seq. ID
                   BLASTX
Method
                   g1658313
NCBI GI
                   159
BLAST score
                   2.0e-11
E value
Match length
                   51
                   51
% identity
NCBI Description (Y08987) osr40g2 [Oryza sativa]
                   291775
Seq. No.
                   LIB3059-031-Q1-K1-G2
Seq. ID
                   BLASTN
Method
                   g22326
NCBI GI
                   44
BLAST score
                   7.0e-16
E value
Match length
                   108
                   85
% identity
                   Z.mays gene for Hageman factor inhibitor
NCBI Description
                   291776
Seq. No.
                   LIB3059-031-Q1-K1-G6
Seq. ID
                   BLASTN
Method
```

NCBI GI g168425 BLAST score 39

E value 5.0e-13 Match length 59

% identity 92

NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds



```
291777
Seq. No.
Seq. ID
                   LIB3059-031-Q1-K1-G9
Method
                   BLASTX
NCBI GI
                   g2832247
BLAST score
                   257
E value
                   3.0e-22
Match length
                   117
% identity
                   50
NCBI Description
                  (AF031569) 22-kDa alpha zein 10 [Zea mays]
Seq. No.
                   291778
Seq. ID
                   LIB3059-031-Q1-K1-H3
Method
                   BLASTX
NCBI GI
                   q82696
BLAST score
                   216
E value
                   8.0e-18
Match length
                   48
% identity
                   85
                   glycine-rich protein - maize >gi 22293 emb CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
                   291779
Seq. No.
Seq. ID
                   LIB3059-032-Q1-K1-A2
Method
                   BLASTN
NCBI GI
                   g3319775
BLAST score
                   80
E value
                   5.0e-37
Match length
                   84
% identity
                   99
                  Zea mays mRNA for cytosolic seryl-tRNA synthetase
NCBI Description
Seq. No.
                   291780
Seq. ID
                   LIB3059-032-Q1-K1-D8
Method
                   BLASTX
NCBI GI
                   g3881873
BLAST score
                   409
E value
                   5.0e-40
Match length
                   138
% identity
                   59
                   (Z83246) predicted using Genefinder; cDNA EST EMBL:M79771
NCBI Description
                   comes from this gene [Caenorhabditis elegans]
                   291781
Seq. No.
                   LIB3059-032-Q1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g141608
BLAST score
                   236
E value
                   9.0e-20
Match length
                   65
% identity
                   72
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >qi 100943 pir
NCBI Description
                   zein, 19K - maize >gi_22446_emb_CAA3765\overline{1}_ (X53\overline{5}82)\overline{1}9 kDa
```

zein [Zea mays]

LIB3059-032-Q1-K1-E9

291782

Seq. No. Seq. ID



```
BLASTN
Method
                   q3821780
NCBI GI
                   36
BLAST score
E value
                   9.0e-11
                   36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   291783
Seq. No.
                   LIB3059-032-Q1-K1-F3
Seq. ID
Method
                   BLASTX
                   q2832246
NCBI GI
BLAST score
                   175
                   5.0e-13
E value
Match length
                   65
                   57
% identity
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]
                   291784
Seq. No.
                   LIB3059-032-Q1-K1-F6
                                                                      , .
, ...
Seq. ID
Method
                   BLASTX
                   q224508
NCBI GI
                   226
BLAST score
                   2.0e-29
E value
                   95
Match length
                   79
% identity
NCBI Description zein A20 [Zea mays]
                    291785
Seq. No.
                   LIB3059-032-Q1-K1-G11
Seq. ID
                   BLASTX
Method
                    q2117937
NCBI GI
                    585
BLAST score
                    1.0e-60
E value
                    115
Match length
                    96
 % identity
                    UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
NCBI Description
                    barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose
                    pyrophosphorylase [Hordeum vulgare]
                    291786
 Seq. No.
                    LIB3059-032-Q1-K1-G3
 Seq. ID
                    BLASTX
Method
                    g141606
 NCBI GI
                    163
 BLAST score
                    7.0e-14
 E value
 Match length
                    77
 % identity
                    58
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1)
 NCBI Description
                    >gi_72309_pir__ZIZMD1 19K zein precursor (clone cZ19D1) -
                    maize > gi_1^2 168 \overline{68} 2 (M12144) 19 kDa zein protein [Zea mays]
                    291787
 Seq. No.
                    LIB3059-032-Q1-K1-H9
 Seq. ID
                    BLASTX
 Method
```

g1351974

460

NCBI GI

BLAST score

BLAST score

Match length

% identity

E value

246

125

41

6.0e-21



```
E value
                  4.0e-46
Match length
                  109
                  83
% identity
                  ADP-RIBOSYLATION FACTOR >gi_1076788_pir__S49325
NCBI Description
                  ADP-ribosylation factor - maize >gi_1076789_pir__S53486
                  ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_
                  (X80042) ADP-ribosylation factor [Zea mays]
Seq. No.
                  291788
Seq. ID
                  LIB3059-033-Q1-K1-A6
Method
                  BLASTN
NCBI GI
                  g22326
BLAST score
                  81
E value
                  7.0e-38
Match length
                  149
                  89
% identity
NCBI Description Z.mays gene for Hageman factor inhibitor
Seq. No.
                  291789
Seq. ID
                  LIB3059-033-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g4126809
BLAST score
                  227
E value
                  6.0e-19
Match length
                  70
                  70
% identity
NCBI Description (AB017042) glyoxalase I [Oryza sativa]
                  291790
Seq. No.
Seq. ID
                  LIB3059-033-Q1-K1-B9
                  BLASTX
Method
NCBI GI
                  g629862
BLAST score
                  186
                  5.0e-14
E value
Match length
                  97
% identity
                  48
NCBI Description
                  zein Zd1, 19K - maize >gi 535021 emb CAA47640 (X67203)
                  zein Zd1 (19 kDa zein) [Zea mays]
                  291791
Seq. No.
                  LIB3059-033-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832243
BLAST score
                  425
E value
                  6.0e-42
Match length
                  116
% identity
                  75
                  (AF031569) 22-kDa alpha zein 4 [Zea mays]
NCBI Description
                  291792
Seq. No.
Seq. ID
                  LIB3059-033-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  g3193290
```



(AF069298) contains similarity to a protein kinase domain NCBI Description (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin legA.hmm, score: 16.72) [Arabido

Seq. No. Seq. ID LIB3059-033-Q1-K1-F6

291793

Method BLASTX NCBI GI q4056502 BLAST score 244 1.0e-20 E value Match length 91 % identity 54

NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]

Seq. No. 291794

Seq. ID LIB3059-033-Q1-K1-H9

Method BLASTX NCBI GI g1173104 BLAST score 282 E value 3.0e-25 Match length 112 41 % identity

RIBONUCLEASE 2 PRECURSOR >gi_289210 (M98336) ribonuclease NCBI Description

[Arabidopsis thaliana] >gi_2642160 (AC003000) ribonuclease,

RNS2 [Arabidopsis thaliana]

291795 Seq. No.

Seq. ID LIB3059-034-Q1-K1-A12

Method BLASTX NCBI GI g22216 BLAST score 199 E value 2.0e-15 Match length 63 % identity 70

NCBI Description (X55722) 22kD zein [Zea mays]

291796 Seq. No.

LIB3059-034-Q1-K1-A2 Seq. ID

Method BLASTX NCBI GI g141597 BLAST score 311 E value 1.0e-28 Match length 128 % identity 55

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)

>gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]

[Zea mays]

Seq. No. 291797

Seq. ID LIB3059-034-Q1-K1-C11

Method BLASTN g22544 NCBI GI BLAST score 55 E value 3.0e-22

NCBI Description



```
187
Match length
                  84
% identity
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
                  291798
Seq. No.
                  LIB3059-034-Q1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4588001
BLAST score
                  219
E value
                  8.0e-18
Match length
                  110
                   37
% identity
                   (AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   291799
Seq. No.
                  LIB3059-034-Q1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2326372
BLAST score
                   364
E value
                   9.0e-35
Match length
                   91
% identity
                   71
                  (Y14404) putative arabinose kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   291800
                   LIB3059-034-Q1-K1-F10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g22537
BLAST score
                   146
                   1.0e-76
E value
                   194
Match length
                   74
% identity
NCBI Description Maize mRNA for zein polypeptide (clone M6)
                   291801
Seq. No.
                   LIB3059-035-Q1-K1-B4
Seq. ID
                   BLASTX
Method
                   g2507443
NCBI GI
                   420
BLAST score
                   2.0e-41
E value
                   133
Match length
                   62
% identity
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) (23
NCBI Description
                   KD CALLUS PROTEIN) (P23) >gi_1675196 (L47968) callus
                   protein P23 [Pisum sativum]
                   291802
Seq. No.
                   LIB3059-035-Q1-K1-E7
Seq. ID
                   BLASTX
Method
                   g1346301
NCBI GI
                   644
BLAST score
                   2.0e-67
E value
Match length
                   158
% identity
                   79
```

40622

3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE (HMG-COA

REDUCTASE) >gi 1071805_pir__S46314 hydroxymethylglutaryl



CoA reductase - rice >gi_455459 (L28995) 3-hydroxy-3-methylglutaryl coenzyme A reductase [Oryza sativa]

LIB3059-035-Q1-K1-F4 Seq. ID BLASTX Method g141598 NCBI GI BLAST score 388 1.0e-37 E value Match length 114 % identity 75

Seq. No.

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE ZG99) NCBI Description

>gi_72313_pir__ZIZM99 19K zein precursor (clone ZG99) maize >gi 22519 emb CAA24717_ (V01470) zein [Zea mays]

>gi 22534_emb_CAA24726_ (V01479) zein [Zea mays]

Seq. No. LIB3059-036-Q1-K1-A3 Seq. ID

Method BLASTX g168693 NCBI GI 231 BLAST score E value 4.0e-19 Match length 110 % identity

NCBI Description (M29627) zein [Zea mays]

Seq. No. 291805

LIB3059-036-Q1-K1-B9 Seq. ID

Method BLASTX NCBI GI g2244814 393 BLAST score 4.0e-38 E value Match length 141

% identity 51

NCBI Description (Z97336) protein kinase [Arabidopsis thaliana]

291806 Seq. No.

LIB3059-036-Q1-K1-C5 Seq. ID

BLASTX Method g629862 NCBI GI 145 BLAST score 9.0e-14 E value 125 Match length 40 % identity

zein Zd1, 19K - maize >gi_535021_emb_CAA47640_ (X67203) NCBI Description

zein Zd1 (19 kDa zein) [Zea mays]

291807 Seq. No.

LIB3059-037-Q1-K1-A3 Seq. ID

BLASTX Method q1905930 NCBI GI 556 BLAST score 3.0e-57 E value Match length 135 % identity

(U31994) MADS box protein [Oryza sativa] NCBI Description



```
291808
Seq. No.
                  LIB3059-037-Q1-K1-A9
Seq. ID
Method
                  BLASTX
                  g2618699
NCBI GI
                  187
BLAST score
                  5.0e-14
E value
                  111
Match length
                  34
% identity
                 (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
                  291809
Seq. No.
                  LIB3059-037-Q1-K1-B6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q100728
                  253
BLAST score
                   1.0e-21
E value
                  139
Match length
                   43
% identity
                  aspartate transaminase (EC 2.6.1.1) AAT3 precursor - proso
NCBI Description
                  millet >gi_1084464_pir__S53304 aspartate aminotransferase -
                  proso millet >gi_20601_emb_CAA45024_ (X63430) aspartate
                   aminotransferase [Panicum miliaceum]
                   >gi 435459_dbj_BAA04993_ (D25323) aspartate
                   aminotransferase [Panicum miliaceum]
                   291810
Seq. No.
                   LIB3059-037-Q1-K1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g141597
                   303
BLAST score
                   1.0e-27
E value
                   128
Match length
% identity
                   55
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi 72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi 22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
                   291811
Seq. No.
                   LIB3059-037-Q1-K1-E10
Seq. ID
                   BLASTX
Method
                   g2245037
NCBI GI
                   156
BLAST score
E value
                   1.0e-10
                   56
Match length
% identity
                   (Z97342) nuclear antigen homolog [Arabidopsis thaliana]
NCBI Description
                   291812
Seq. No.
                   LIB3059-037-Q1-K1-E7
Seq. ID
                   BLASTN
Method
                   q459267
NCBI GI
BLAST score
                   61
 E value
                   1.0e-25
                   101
Match length
```

91

% identity



```
NCBI Description Z.mays gene for HMG protein
                  291813
Seq. No.
                  LIB3059-037-Q1-K1-G11
Seq. ID
                  BLASTX
Method
                  g595768
NCBI GI
                  165
BLAST score
                  2.0e-11
E value
                  47
Match length
                  64
% identity
NCBI Description (U13866) non-functional lacZ alpha peptide [Cloning vector]
                  291814
Seq. No.
                  LIB3059-037-Q1-K1-G3
Seq. ID
                  BLASTX
Method
                   q730450
NCBI GI
                   369
BLAST score
                   2.0e-35
E value
                   129
Match length
                   62
% identity
                   60S RIBOSOMAL PROTEIN L13-2 (COLD INDUCED PROTEIN C24B)
NCBI Description
                   >gi_480649_pir__S37134 cold-induced protein BnC24B - rape
                   >qi 398922 emb CAA80343 (Z22620) cold induced protein
                   (BnC24B) [Brassica napus]
                   291815
Seq. No.
                   LIB3059-037-Q1-K1-G7
Seq. ID
                   BLASTX
Method
                   g141599
NCBI GI
                   404
BLAST score
E value
                   2.0e-39
                   114
Match length
                   74
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19A2)
NCBI Description
                   >gi_72316_pir__ZIZMA2 19K zein precursor (clone cZ19A2) -
                   maize (fragment) >gi_168670 (M12142) 19 kDa zein protein
                   [Zea mays]
                   291816
 Seq. No.
                   LIB3059-037-Q1-K1-H7
 Seq. ID
                   BLASTX
 Method
                   g3785979
 NCBI GI
                   237
 BLAST score
                   8.0e-20
 E value
 Match length
                   63
 % identity
                   (AC005560) putative serine protease [Arabidopsis thaliana]
 NCBI Description
                   291817
 Seq. No.
                   LIB3059-038-Q1-K1-A1
 Seq. ID
                   BLASTX
 Method
                    g417821
 NCBI GI
                    365
 BLAST score
                    4.0e-35
 E value
                    91
 Match length
                    75
 % identity
 NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
```

(STEAROYL-ACP DESATURASE) >gi_322725_pir_S31959 acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) flax >gi_22682_emb_CAA50298_ (X70962) acyl-[acyl-carrier protein] desaturase; stearoyl-[acyl-carrier protein] desaturase [Linum usitatissimum]

```
291818
Seq. No.
                  LIB3059-038-Q1-K1-A8
Seq. ID
Method
                  BLASTN
                  g22537
NCBI GI
BLAST score
                  85
                   4.0e-40
E value
                  173
Match length
                   62
% identity
NCBI Description Maize mRNA for zein polypeptide (clone M6)
                   291819
Seq. No.
                   LIB3059-038-Q1-K1-B3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g82660
                   494
BLAST score
                   5.0e-50
E value
Match length
                   119
% identity
                   84
                   19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                   >gi 809117_emb_CAA24720_ (V01473) zein [Zea mays]
Seq. No.
                   LIB3059-038-Q1-K1-B7
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3747049
BLAST score
                   79
                   2.0e-36
E value
                   199
Match length
% identity
                   86
                   Zea mays ribosomal protein L26 mRNA, partial cds
NCBI Description
                   291821
Seq. No.
                   LIB3059-038-Q1-K1-C8
Seq. ID
                   BLASTX
Method
                   g3421090
NCBI GI
                   187
BLAST score
                   4.0e-14
E value
                   63
Match length
 % identity
                   (AF043525) 20S proteasome subunit PAE2 [Arabidopsis
NCBI Description
                   thaliana]
                   291822
 Seq. No.
                   LIB3059-038-Q1-K1-D5
 Seq. ID
                   BLASTX
 Method
                   g419803
 NCBI GI
                   305
 BLAST score
                   7.0e-28
 E value
 Match length
                   125
 % identity
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea
```

Method

BLASTX



mays]

```
291823
Seq. No.
                  LIB3059-038-Q1-K1-D9
Seq. ID
                  BLASTN
Method
                  g16072
NCBI GI
                  131
BLAST score
E value
                   2.0e-67
                   409
Match length
% identity
                   83
NCBI Description Acetabularia mediterranea zein gene
                   291824
Seq. No.
                   LIB3059-038-Q1-K1-E10
Seq. ID
                   BLASTX
Method
                   g16073
NCBI GI
                   399
BLAST score
                   7.0e-39
E value
                   133
Match length
                   65
% identity
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
                   291825
Seq. No.
                   LIB3059-038-Q1-K1-E12
Seq. ID
Method
                   BLASTX
                   g2832247
NCBI GI
                   155
BLAST score
                   2.0e-10
E value
                   103
Match length
% identity
                   40
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]
                   291826
Seq. No.
                   LIB3059-038-Q1-K1-E4
Seq. ID
Method
                   BLASTX
                   g4377328
NCBI GI
                   202
BLAST score
                   9.0e-16
E value
                   112
Match length
                   40
% identity
                   (AE001680) Polyribonucleotide Nucleotidyltransferase
NCBI Description
                   [Chlamydia pneumoniae]
                   291827
Seq. No.
                   LIB3059-038-Q1-K1-E8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3329314
                   211
BLAST score
                   7.0e-17
E value
                   109
Match length
                   44
 % identity
                   (AE001357) Polyribonucleotide Nucleotidyltransferase
NCBI Description
                   [Chlamydia trachomatis]
 Seq. No.
                   291828
                   LIB3059-038-Q1-K1-F2
 Seq. ID
```

BLAST score

247

```
q141605
NCBI GI
                  418
BLAST score
                  4.0e-41
E value
                  126
Match length
                  71
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi 72312_pir ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
                  291829
Seq. No.
                  LIB3059-038-Q1-K1-G9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g463152
                  258
BLAST score
                  3.0e-22
E value
                  51
Match length
                  94
% identity
                  (L29505) zein [Zea mays] >gi_1094858 prf 2106415A Met-rich
NCBI Description
                  seed storage protein [Zea mays]
                  291830
Seq. No.
                  LIB3059-038-Q1-K1-H12
Seq. ID
                  BLASTN
Method
                  g535019
NCBI GI
                  128
BLAST score
                  7.0e-66
E value
                  168
Match length
                   47
% identity
NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)
                   291831
Seq. No.
                  LIB3059-039-Q1-K1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                   g141600
                   258
BLAST score
                   2.0e-22
E value
                   117
Match length
                   50
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
                   >gi 72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) -
                   maize >gi 168674 (M12143) 19 kDa zein protein [Zea mays]
                   291832
Seq. No.
Seq. ID
                   LIB3059-039-Q1-K1-B10
                   BLASTN
Method
                   q22516
NCBI GI
                   247
BLAST score
                   1.0e-136
E value
Match length
                   363
% identity
                   93
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                   291833
Seq. No.
                   LIB3059-039-Q1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g141609
```

Seq. ID

```
5.0e-21
E value
                   66
Match length
                   77
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS2) >gi_100944_pir__S15656
NCBI Description
                   zein, 19K - maize >gi 22448 emb CAA4154\overline{3} (X58\overline{7}00) \overline{1}9 kDa
                   zein [Zea mays]
                   291834
Seq. No.
                   LIB3059-039-Q1-K1-C1
Seq. ID
Method
                   BLASTX
                   q4558672
NCBI GI
                   224
BLAST score
                   2.0e-21
E value
Match length
                   101
% identity
                   (AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis
NCBI Description
                   thaliana]
                   291835
Seq. No.
                   LIB3059-039-Q1-K1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3122071
                   254
BLAST score
                   2.0e-22
E value
                   53
Match length
% identity
                   89
                   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                   >gi 2130148_pir S66339 translation elongation factor eEF-1
                   alpha chain - maize >gi_1321656_dbj_BAA08249_ (D45408)
                   alpha subunit of tlanslation elongation factor 1 [Zea mays]
                    291836
Seq. No.
                   LIB3059-039-Q1-K1-C9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g141614
                    233
BLAST score
                    8.0e-21
E value
                    87
Match length
                    64
% identity
                    ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)
NCBI Description
                    >gi_82662_pir__B22831 22K zein precursor (clone M1) - maize
                    >gi 22527 emb CAA24722 (V01475) reading frame zein [Zea
                    mays] >gi_224\overline{5}10_prf_ \overline{1}107201D zein M1 [Zea mays]
Seq. No.
                    291837
                    LIB3059-039-Q1-K1-F7
Seq. ID
                    BLASTX
Method
                    q141616
NCBI GI
BLAST score
                    356
                    8.0e-34
E value
                    123
Match length
                    61
 % identity
                    ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
 NCBI Description
                    >gi 168662 (M12147) 15 kDa zein protein [Zea mays]
                    291838
 Seq. No.
```

LIB3059-039-Q1-K1-F8



```
BLASTN
Method
                  g22326
NCBI GI
BLAST score
                  51
                  5.0e-20
E value
                  147
Match length
                  86
% identity
NCBI Description Z.mays gene for Hageman factor inhibitor
Seq. No.
                  291839
                  LIB3059-039-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141598
                  249
BLAST score
                  2.0e-21
E value
Match length
                  73
                  71
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE ZG99)
NCBI Description
                  >gi_72313_pir__ZIZM99 19K zein precursor (clone ZG99) -
                  maize >gi_22519_emb_CAA24717_ (V01470) zein [Zea mays]
                  >gi 22534_emb_CAA24726_ (V01479) zein [Zea mays]
                   291840
Seq. No.
                  LIB3059-040-Q1-K1-A9
Seq. ID
Method
                   BLASTX
                   q2129608
NCBI GI
BLAST score
                   487
                   3.0e-49
E value
Match length
                   114
                   82
% identity
NCBI Description GTP-binding protein, 68K - Arabidopsis thaliana >gi_807577
                   (L38614) GTP-binding protein [Arabidopsis thaliana]
                   291841
Seq. No.
                   LIB3059-040-Q1-K1-C1
Seq. ID
                   BLASTX
Method
                   g2832247
NCBI GI
                   144
BLAST score
                   2.0e-09
E value
                   88
Match length
                   36
 % identity
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]
                   291842
 Seq. No.
                   LIB3059-040-Q1-K1-F7
 Seq. ID
                   BLASTX
 Method
                   g121472
 NCBI GI
                   153
 BLAST score
                   2.0e-17
 E value
                   99
 Match length
 % identity
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
 NCBI Description
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi 72326 pir_ ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi 22289 emb CAA26149 (X02230) glutelin-2 precursor
                   [Zea mays] >gi 22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
```

mays] >gi_1684 $\overline{8}$ 5 (M1 $\overline{6}$ 066) glutelin-2 [Zea mays]

E value

Match length

6.0e-40

125



```
Seq. No.
                  291843
                  LIB3059-040-Q1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g168699
BLAST score
                  143
                  5.0e-11
E value
                  43
Match length
                  93
% identity
NCBI Description
                  (M60836) zein [Zea mays]
Seq. No.
                  291844
                  LIB3059-041-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q168691
BLAST score
                  194
E value
                   6.0e-15
Match length
                  56
                  70
% identity
NCBI Description
                  (M29628) zein [Zea mays]
Seq. No.
                  291845
Seq. ID
                  LIB3059-041-Q1-K1-D1
Method
                  BLASTN
NCBI GI
                  g168677
BLAST score
                  50
E value
                   4.0e-19
                  50
Match length
                  100
% identity
NCBI Description Maize 19 kDa zein mRNA, clone cZ19C1, complete cds
Seq. No.
                   291846
Seq. ID
                  LIB3059-041-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  q3420051
BLAST score
                  282
E value
                   4.0e-25
Match length
                  56
% identity
                  91
                  (AC004680) unknown protein [Arabidopsis thaliana]
NCBI Description
                  291847
Seq. No.
                  LIB3059-041-Q1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g468516
BLAST score
                   264
E value
                  9.0e-31
Match length
                  149
% identity
                   52
NCBI Description (X55724) zein [Zea mays]
                   291848
Seq. No.
Seq. ID
                  LIB3059-041-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g141603
BLAST score
                   408
```



```
68
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                   >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                   >gi 22529_emb_CAA24723_ (V01476) zein [Zea mays]
                   291849
Seq. No.
                   LIB3059-041-Q1-K1-G8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3510252
BLAST score
                   206
                   3.0e-16
E value
                   70
Match length
 % identity
                   (AC005310) putative RNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   291850
 Seq. No.
                   LIB3059-042-Q1-K1-A1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g729762
                   218
 BLAST score
                   4.0e-18
 E value
                   70
Match length
 % identity
                   66
                   17.0 KD CLASS II HEAT SHOCK PROTEIN (HSP 18)
 NCBI Description
                   >gi_477225_pir__A48425 heat shock protein HSP18 - maize
                   >gi 300079 bbs 130952 (S59777) HSP18=18 kda heat shock
                   protein [Zea mays, Oh43, clone cMHSP18-1, Peptide, 154 aa]
                   [Zea mays]
                   291851
 Seq. No.
                   LIB3059-042-Q1-K1-A11
 Seq. ID
                   BLASTX
 Method
                   g168699
 NCBI GI
                    314
 BLAST score
                    5.0e-29
 E value
                    76
 Match length
 % identity
 NCBI Description (M60836) zein [Zea mays]
                    291852
 Seq. No.
                    LIB3059-042-Q1-K1-A7
 Seq. ID
                    BLASTN
 Method
                    g473602
 NCBI GI
 BLAST score
                    182
                    7.0e-98
 E value
                    358
 Match length
                    88
 % identity
                   Zea mays W-22 histone H2A mRNA, complete cds
 NCBI Description
                    291853
 Seq. No.
                    LIB3059-042-Q1-K1-B12
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    q2668742
 BLAST score
                    276
                    9.0e-25
 E value
```

73

Match length



% identity

NCBI Description

```
% identity
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                  291854
Seq. No.
                  LIB3059-042-Q1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1814401
BLAST score
                  288
E value
                  8.0e-26
Match length
                  83
% identity
                  66
NCBI Description (U84888) phosphoglucomutase [Mesembryanthemum crystallinum]
Seq. No.
                  291855
                  LIB3059-042-Q1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334474
BLAST score
                  311
E value
                  6.0e-29
Match length
                  77
% identity
                  83
                  OLEOSIN ZM-I (OLEOSIN 16 KD) (LIPID BODY-ASSOCIATED MAJOR
NCBI Description
                  PROTEIN) (LIPID BODY-ASSOCIATED PROTEIN L3)
                  >gi 1076817 pir S52029 oleosin 16 - maize >gi 687245
                  (U13701) 16 kDa oleosin [Zea mays]
                  291856
Seq. No.
                  LIB3059-042-Q1-K1-D4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g58174
BLAST score
                  49
E value
                  5.0e-19
Match length
                  129
% identity
                  84
NCBI Description Cloning vector pGEM-5Zf(-)
Seq. No.
                  291857
                  LIB3059-042-Q1-K1-E11
Seq. ID
                  BLASTN
Method
                  g2198852
NCBI GI
BLAST score
                  70
E value
                  5.0e-31
Match length
                  114
% identity
                  90
NCBI Description
                  Zea mays cystathionine gamma-synthase (CGS1) gene, complete
Seq. No.
                  291858
Seq. ID
                  LIB3059-042-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g168699
BLAST score
                  419
                  3.0e-41
E value
Match length
                  105
```

(M60836) zein [Zea mays]



```
291859
Seq. No.
                  LIB3059-042-Q1-K1-E4
Seq. ID
                  BLASTX
Method
                  q3915070
NCBI GI
                  281
BLAST score
                  2.0e-30
E value
                  103
Match length
                  76
% identity
                  HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS)
NCBI Description
                  >gi_1841704_emb_CAB06653_ (Z85984) histidyl tRNA Synthetase
                   [Oryza sativa]
                  291860
Seq. No.
                  LIB3059-042-Q1-K1-F1
Seq. ID
                  BLASTN
Method
                  g531828
NCBI GI
                   36
BLAST score
                   6.0e-11
E value
                   96
Match length
                   84
% identity
NCBI Description Cloning vector pSport1, complete cds
                   291861
Seq. No.
                   LIB3059-042-Q1-K1-F2
Seq. ID
Method
                   BLASTX
                   g122007
NCBI GI
                   167
BLAST score
                   6.0e-12
E value
                   36
Match length
                   92
% identity
                   HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley
NCBI Description
                   >gi 20448 emb CAA37828 (X\overline{53}831) H2A histone protein (AA 1
                   - 149) [Petroselinum crispum]
                   291862
Seq. No.
                   LIB3059-042-Q1-K1-G11
Seq. ID
                   BLASTX
Method
                   g1184776
NCBI GI
BLAST score
                   630
                   6.0e-66
E value
                   135
Match length
% identity
                   (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC4 [Zea mays]
                   291863
Seq. No.
                   LIB3059-042-Q1-K1-G4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2494165
                   342
BLAST score
                   4.0e-32
E value
                   100
Match length
 % identity
                   DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP))
NCBI Description
```

thaliana]

>gi_2129574_pir__S71278 DNA ligase - Arabidopsis thaliana >gi_1359495_emb_CAA66599 (X97924) DNA ligase [Arabidopsis



```
Seq. No.
                  LIB3059-043-Q1-K1-A11
Seq. ID
Method
                  BLASTX
                  q3687389
NCBI GI
                  309
BLAST score
                  2.0e-28
E value
                  81
Match length
% identity
NCBI Description (Y16124) putative cullin protein [Lycopersicon esculentum]
                  291865
Seq. No.
                  LIB3059-043-Q1-K1-A3
Seq. ID
                  BLASTN
Method
NCBI GI
                   q4103634
                   68
BLAST score
                   5.0e-30
E value
                   160
Match length
% identity
NCBI Description Hordeum vulgare ABA-responsive protein mRNA, complete cds
                   291866
Seq. No.
                   LIB3059-043-Q1-K1-A4
Seq. ID
                   BLASTN
Method
                   q1037129
NCBI GI
                   265
BLAST score
E value
                   1.0e-147
                   361
Match length
                   93
% identity
                   (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                   Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                   291867
Seq. No.
                   LIB3059-043-Q1-K1-D7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q728744
                   200
BLAST score
                   1.0e-15
E value
                   86
Match length
                   51
 % identity
                   AUXIN-INDUCED PROTEIN PCNT115 >gi_100305_pir__S16390
NCBI Description
                   auxin-induced protein - common tobacco
                   >gi_19799_emb_CAA39708_ (X56267) auxin-induced protein
                   [Nicotiana tabacum]
 Seq. No.
                   291868
                   LIB3059-043-Q1-K1-F2
 Seq. ID
                   BLASTX
 Method
                   q4056468
 NCBI GI
                   146
 BLAST score
                   9.0e-10
 E value
                   72
 Match length
                    44
 % identity
                   (AC005990) Contains similarity to gb_X66426
 NCBI Description
                   polygalacturonase from Persea americana and is a member of
                   the signal peptidase family PF_00461 and polygalacturonase
```

family PF_00295. [Arabidopsis thaliana]

% identity

NCBI Description



```
291869
Seq. No.
                   LIB3059-043-Q1-K1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g168693
BLAST score
                   160
E value
                   6.0e-11
Match length
                   116
% identity
NCBI Description
                   (M29627) zein [Zea mays]
Seq. No.
                   291870
Seq. ID
                   LIB3059-043-Q1-K1-G12
Method
                   BLASTX
NCBI GI
                   g2104712
BLAST score
                   219
E value
                   6.0e-18
                   73
Match length
                   62
% identity
NCBI Description (U95180) endosperm specific protein [Zea mays]
Seq. No.
                   291871
                   LIB3059-043-Q1-K1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g168695
BLAST score
                   265
E value
                   3.0e-23
Match length
                   86
% identity
                   (M16218) gamma zein [Zea mays] >gi 225315 prf 1211356A
NCBI Description
                   zein gamma [Zea mays]
                   291872
Seq. No.
                   LIB3059-043-Q1-K1-H2
Seq. ID
Method
                   BLASTX
                   g121472
NCBI GI
BLAST score
                   159
                   9.0e-11
E value
Match length
                   45
% identity
                   67
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                    (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi 22289 emb CAA26149 (X02230) glutelin-2 precursor [Zea mays] >gi 22517 emb CAA37594 (X53514) zein Zc2 [Zea
                   mays] >gi_1684\overline{8}5 (M1\overline{6}066) glutelin-2 [Zea mays]
                   291873
Seq. No.
Seq. ID
                   LIB3059-043-Q1-K1-H4
                   BLASTX
Method
NCBI GI
                   g4115377
BLAST score
                   309
                   1.0e-28
E value
Match length
                   89
```

40636

(AC005967) unknown protein [Arabidopsis thaliana]



```
Seq. No.
                  291874
Seq. ID
                  LIB3059-044-Q1-K1-A12
Method
                  BLASTN
NCBI GI
                  g463151
BLAST score
                  45
E value
                  2.0e-16
Match length
                  81
% identity
                  89
NCBI Description Zea mays high sulfur zein gene, complete cds
Seq. No.
                  291875
Seq. ID
                  LIB3059-044-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  q3023535
BLAST score
                  500
E value
                  1.0e-50
Match length
                  123
% identity
                  74
                  MOLYBDOPTERIN BIOSYNTHESIS CNX2 PROTEIN (MOLYBDENUM
NCBI Description
                  COFACTOR BIOSYNTHESIS ENZYME CNX2) >gi_662871_emb_CAA88107_
                  (Z48047) Cnx2 [Arabidopsis thaliana]
Seq. No.
                  291876
Seq. ID
                  LIB3059-044-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  g141599
BLAST score
                  153
E value
                  5.0e-10
Match length
                  47
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19A2)
NCBI Description
                  >gi 72316 pir ZIZMA2 19K zein precursor (clone cZ19A2) -
                  maize (fragment) >gi 168670 (M12142) 19 kDa zein protein
                  [Zea mays]
                  291877
Seq. No.
                  LIB3059-044-Q1-K1-C3
Seq. ID
Method
                  BLASTX
                  g232029
NCBI GI
BLAST score
                  139
                  5.0e-09
E value
Match length
                  43
% identity
                  65
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi 100154 pir S21989 translation elongation factor eEF-1
                  alpha chain - carrot >gi_18339_emb_CAA42843_ (X60302)
                  elongation factor 1A [Daucus carota]
                  291878
Seq. No.
Seq. ID
                  LIB3059-044-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  g2558654
```

Method BLASTX
NCBI GI g2558654
BLAST score 430
E value 2.0e-42
Match length 128
% identity 65

NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]



```
291879
Seq. No.
                  LIB3059-044-Q1-K1-E8
Seq. ID
                  BLASTN
Method
                  q3821780
NCBI GI
BLAST score
                  36
                  1.0e-10
E value
                  48
Match length
                  67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  291880
Seq. No.
                  LIB3059-044-Q1-K1-E9
Seq. ID
                  BLASTX
Method
                  g629861
NCBI GI
                  483
BLAST score
                  3.0e-52
E value
                  135
Match length
                  78
% identity
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
                   zein Zd1 (19 kDa zein) [Zea mays]
                  291881
Seq. No.
                  LIB3059-044-Q1-K1-F12
Seq. ID
                  BLASTN
Method
                   g3511235
NCBI GI
                   78
BLAST score
                   8.0e-36
E value
                   106
Match length
                   93
% identity
                   Zea mays starch branching enzyme IIb (ae) gene, complete
NCBI Description
                   291882
Seq. No.
                   LIB3059-044-Q1-K1-G10
Seq. ID
                   BLASTX
Method
                   q3763845
NCBI GI
BLAST score
                   378
                   2.0e-36
E value
                   82
Match length
 % identity
                   (AB018375) early nodulin [Oryza sativa]
NCBI Description
                   >gi 3763847 dbj BAA33814_ (AB018376) early nodulin [Oryza
                   sativa]
                   291883
 Seq. No.
                   LIB3059-044-Q1-K1-G2
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g1707924
 BLAST score
                   328
                   7.0e-31
 E value
                   84
 Match length
                   77
 % identity
                   GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT 1
 NCBI Description
                   PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE
                   PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE
```

ADENYL TRANSFERASE) (SHRUNKEN-2) >gi 1947182 (M81603)

BLAST score

E value Match length 43 4.0e-15

143



shrunken-2 [Zea mays] >gi_444329_prf__1906378A ADP glucose pyrophosphorylase [Zea mays]

```
291884
Seq. No.
                  LIB3059-044-Q1-K1-H1
Seq. ID
                  BLASTX
Method
                  g141603
NCBI GI
BLAST score
                  462
                  3.0e-46
E value
                  120
Match length
                  82
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >gi_72311 pir__ZIZM2 19K zein precursor (clone A20) - maize
                  >gi 22529_emb_CAA24723_ (V01476) zein [Zea mays]
                  291885
Seq. No.
                  LIB3059-044-Q1-K1-H4
Seq. ID
                  BLASTX
Method
                  g72307
NCBI GI
                  261
BLAST score
                  7.0e-23
E value
                  72
Match length
                  78
% identity
                  22K zein precursor (clone pZ22.3) - maize >gi 168686
NCBI Description
                   (J01246) 26.99 kd zein protein [Zea mays]
                   291886
Seq. No.
                  LIB3059-045-Q1-K1-A11
Seq. ID
                  BLASTX
Method
                   g82652
NCBI GI
                   340
BLAST score
                   6.0e-32
E value
                   85
Match length
% identity
                   1,4-alpha-glucan branching enzyme (EC 2.4.1.18) - maize
NCBI Description
                   (fragment) >gi_217960_dbj BAA01854_ (D11081) branching
                   enzyme-I precursor [Zea mays]
                   291887
Seq. No.
                   LIB3059-045-Q1-K1-A6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g141605
BLAST score
                   454
                   2.0e-45
E value
                   99
Match length
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                   >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                   maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
                   291888
Seq. No.
                   LIB3059-045-Q1-K1-A9
Seq. ID
                   BLASTN
Method
NCBI GI
                   g22324
```



```
% identity
NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)
Seq. No.
                  291889
                  LIB3059-045-Q1-K1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g168663
BLAST score
                  57
E value
                  1.0e-23
Match length
                  71
                  96
% identity
NCBI Description Maize sulfur-rich zein protein of Mr 15,000, complete cds
Seq. No.
                  291890
                  LIB3059-045-Q1-K1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22324
BLAST score
                  126
E value
                  1.0e-64
Match length
                  126
% identity
                  100
NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)
                  291891
Seq. No.
Seq. ID
                  LIB3059-045-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  q168697
BLAST score
                  325
E value
                  3.0e-30
Match length
                  80
% identity
                  86
NCBI Description
                  (M60835) zein [Zea mays]
                  291892
Seq. No.
                  LIB3059-045-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g468516
BLAST score
                  163
                  9.0e-24
E value
Match length
                  130
% identity
                  60
NCBI Description
                  (X55724) zein [Zea mays]
Seq. No.
                  291893
                  LIB3059-045-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141608
BLAST score
                  226
```

8.0e-19 E value 87 Match length 59 % identity

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943 pir S15655

zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa

zein [Zea mays]

Seq. No. 291894

Seq. ID LIB3059-045-Q1-K1-E12

E value

6.0e-11



```
BLASTX
Method
                  g141605
NCBI GI
                  360
BLAST score
                  3.0e - 34
E value
                  127
Match length
                  64
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi 72312 pir_ ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
                  291895
Seq. No.
                  LIB3059-045-Q1-K1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4415917
                   239
BLAST score
                   4.0e-20
E value
                   129
Match length
                   43
% identity
                   (AC006282) putative protein containing zinc finger domain
NCBI Description
                   [Arabidopsis thaliana]
                   291896
Seq. No.
                   LIB3059-045-Q1-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2653558
                   179
BLAST score
                   8.0e-27
E value
                   100
Match length
                   71
% identity
                  (D50679) ferredoxin-sulfite reductase precursor [Zea mays]
NCBI Description
                   291897
Seq. No.
                   LIB3059-045-Q1-K1-G7
Seq. ID
                   BLASTN
Method
                   g248338
NCBI GI
                   70
BLAST score
                   3.0e-31
E value
                   210
Match length
% identity
                   83
NCBI Description polyubiquitin [maize, Genomic, 3439 nt]
                   291898
Seq. No.
                   LIB3059-046-Q1-K1-A1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4008156
                   205
BLAST score
                   3.0e-16
E value
                   79
Match length
 % identity
                   (AB008845) NADH dependent Glutamate Synthase [Oryza sativa]
NCBI Description
                   291899
Seq. No.
                   LIB3059-046-Q1-K1-A4
 Seq. ID
Method
                   BLASTX
NCBI GI
                   q4335735
BLAST score
                   160
```



```
109
Match length
                  36
% identity
                 (AC006248) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  291900
Seq. No.
                  LIB3059-046-Q1-K1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g121472
                  383
BLAST score
                  5.0e-37
E value
                  130
Match length
                  54
% identity
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                  >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                  maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
                   [Zea\ mays] > gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
                  mays] >gi 168485 (M16066) glutelin-2 [Zea mays]
                   291901
Seq. No.
                  LIB3059-046-Q1-K1-F10
Seq. ID
                  BLASTX
Method
                   g3264605
NCBI GI
                   258
BLAST score
                   3.0e-22
E value
                   76
Match length
                   71
% identity
NCBI Description (AF061508) ribosomal protein L25 [Zea mays]
                   291902
Seq. No.
                   LIB3059-046-Q1-K1-F12
Seq. ID
                   BLASTX
Method
                   q141603
NCBI GI
                   234
BLAST score
                   4.0e-35
E value
                   107
Match length
                   79
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                   >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                   >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
                   291903
 Seq. No.
 Seq. ID
                   LIB3059-046-Q1-K1-F4
 Method
                   BLASTN
                   q22544
 NCBI GI
                   199
 BLAST score
                   1.0e-108
 E value
                   207
 Match length
 % identity
                   99
                   Maize mRNA (clone A30) for zein (a plant storage protein)
 NCBI Description
                   291904
 Seq. No.
                   LIB3059-047-Q1-K1-B1
 Seq. ID
 Method
                   BLASTX
```

q141617

3.0e-28

309

NCBI GI

E value

BLAST score



```
105
Match length
                   60
% identity
                   ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                   >gi_100941_pir__S12140 zein Zc1 - maize
                   >gi 100945_pir B29017 zein 2 - maize
                   >gi 22515 emb \overline{CAA}37595 (X53515) zein Zc1 [Zea mays]
                   >gi^{-}16866^{\overline{6}} (M^{\overline{1}}6460) 16^{-}kDa zein protein [Zea mays]
                   291905
Seq. No.
                   LIB3059-047-Q1-K1-B8
Seq. ID
                   BLASTX
Method
                   g629861
NCBI GI
                   329
BLAST score
                   1.0e-30
E value
                   116
Match length
                   58
% identity
                   zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
NCBI Description
                   zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                   291906
                   LIB3059-047-Q1-K1-C9
Seq. ID
Method
                   BLASTN
                   g218177
NCBI GI
                   34
BLAST score
                   9.0e-10
E value
                   88
Match length
                   84
% identity
                   Rice mRNA for ribosomal protein L35 (NH77 gene), partial
NCBI Description
                    sequence >gi_3106972_dbj_D42703_D42703 Rice callus cDNA,
                   NH077
                    291907
Seq. No.
                   LIB3059-047-Q1-K1-D11
Seq. ID
                    BLASTX
Method
                    g22216
NCBI GI
                    417
BLAST score
                    5.0e-41
E value
                    103
Match length
                    84
% identity
                   (X55722) 22kD zein [Zea mays]
NCBI Description
                    291908
Seq. No.
                    LIB3059-047-Q1-K1-D2
Seq. ID
                    BLASTX
Method
                    q141608
NCBI GI
                    332
BLAST score
                    5.0e-31
E value
                    111
Match length
                    65
 % identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_
 NCBI Description
                    zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
                    zein [Zea mays]
                    291909
 Seq. No.
                    LIB3059-047-Q1-K1-D9
 Seq. ID
```

BLASTX

q82696

Method NCBI GI

```
BLAST score
                  1.0e-26
E value
                  93
Match length
                  62
% identity
NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_
                   (X61121) glycine-rich protein [Zea mays]
Seq. No.
                  291910
                  LIB3059-047-Q1-K1-E7
Seq. ID
                  BLASTX
Method
                  g4490311
NCBI GI
                  142
BLAST score
                   1.0e-08
E value
                   96
Match length
                   31
% identity
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
                   291911
Seq. No.
                   LIB3059-047-Q1-K1-E9
Seq. ID
                   BLASTX
Method
                   g1154954
NCBI GI
                   306
BLAST score
                   2.0e-34
E value
                   118
Match length
                   72
% identity
                  (X94693) histone H2A [Triticum aestivum]
NCBI Description
                   291912
Seq. No.
                   LIB3059-047-Q1-K1-F1
Seq. ID
                   BLASTN
Method
                   g625147
NCBI GI
                   81
BLAST score
                   1.0e-37
E value
Match length
                   211
                   90
% identity
                   Zea mays protein disulfide isomerase (pdi) mRNA, complete
NCBI Description
                   291913
Seq. No.
                   LIB3059-047-Q1-K1-F2
Seq. ID
                   BLASTN
Method
NCBI GI
                   q168685
BLAST score
                   235
E value
                   1.0e-129
                   331
Match length
 % identity
                   93
NCBI Description Maize 22 kd (Mw=26.99 kd) zein protein 3, mRNA
 Seq. No.
                    291914
                   LIB3059-047-Q1-K1-G2
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                    g16073
 BLAST score
                    202
 E value
                    2.0e-17
                    90
 Match length
                    61
 % identity
                   (X59526) zein protein [Acetabularia mediterranea]
 NCBI Description
```

Seq. ID

Method



```
291915
Seq. No.
                  LIB3059-047-Q1-K1-G3
Seq. ID
                  BLASTX
Method
                  g3885884
NCBI GI
                  233
BLAST score
                  1.0e-19
E value
Match length
                  53
% identity
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]
                  291916
Seq. No.
                  LIB3059-047-Q1-K1-H1
Seq. ID
                  BLASTX
Method
                  g399854
NCBI GI
                  289
BLAST score
                  6.0e-26
E value
                  64
Match length
                  92
% identity
                  HISTONE H2B.2 >gi 283042 pir S28049 histone H2B - maize
NCBI Description
                  >gi_22325_emb_CAA40565_ (X57313) H2B histone [Zea mays]
                  291917
Seq. No.
                  LIB3059-047-Q1-K1-H3
Seq. ID
                  BLASTN
Method
                   g2811133
NCBI GI
                   315
BLAST score
                   1.0e-177
E value
                   335
Match length
                   99
% identity
                   Zea mays starch synthase isoform zSTSII-1 (zSSIIa) mRNA,
NCBI Description
                   partial cds
                   291918
Seq. No.
                   LIB3059-047-Q1-K1-H5
Seq. ID
                   BLASTN
Method
                   g22528
NCBI GI
                   79
BLAST score
                   1.0e-36
E value
                   183
Match length
                   86
 % identity
NCBI Description Zea mays mRNA encoding a zein (clone A20)
                   291919
 Seq. No.
                   LIB3059-048-Q1-K1-A2
 Seq. ID
                   BLASTN
Method
                   g2331130
 NCBI GI
                   43
 BLAST score
                   4.0e-15
 E value
                   55
 Match length
                   95
 % identity
                   Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
 NCBI Description
                   291920
 Seq. No.
```

40645

LIB3059-048-Q1-K1-B5

BLASTX



```
q4006872
NCBI GI
                  261
BLAST score
                  1.0e-22
E value
                  104
Match length
% identity
                 (Z99707) methionyl aminopeptidase-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  291921
Seq. No.
                  LIB3059-048-Q1-K1-B8
Seq. ID
                  BLASTX
Method
                  g141603
NCBI GI
                  446
BLAST score
                  2.0e-44
E value
                  121
Match length
                  78
% identity
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
                  >gi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
                  >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
                  291922
Seq. No.
                  LIB3059-048-Q1-K1-C7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q82696
                  168
BLAST score
                   5.0e-12
E value
                   66
Match length
                   62
% identity
NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_
                   (X61121) glycine-rich protein [Zea mays]
                   291923
Seq. No.
Seq. ID
                   LIB3059-048-Q1-K1-F8
                   BLASTX
Method
                   q3763918
NCBI GI
                   191
BLAST score
                   2.0e-14
E value
                   44
Match length
% identity
                   (AC004450) putative isopropylmalate dehydratase
NCBI Description
                   [Arabidopsis thaliana]
                   291924
Seq. No.
Seq. ID
                   LIB3059-048-Q1-K1-G4
                   BLASTX
Method
                   q468516
NCBI GI
                   416
BLAST score
                   7.0e-41
E value
Match length
                   118
% identity
                   75
                  (X55724) zein [Zea mays]
NCBI Description
                   291925
 Seq. No.
                   LIB3059-048-Q1-K1-G5
 Seq. ID
 Method
                   BLASTX
                   g629861
 NCBI GI
```

453

BLAST score



```
E value
                  4.0e-45
Match length
                  114
                  82
% identity
                  zein Zd1, 19K - maize >gi 535020 emb CAA47639 (X67203)
NCBI Description
                  zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                  291926
Seq. ID
                  LIB3059-048-Q1-K1-G6
Method
                  BLASTN
NCBI GI
                  g22516
BLAST score
                  137
E value
                  3.0e-71
Match length
                  145
                  99
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.
                  291927
Seq. ID
                  LIB3059-048-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  g1176584
BLAST score
                  146
E value
                  3.0e-09
                  71
Match length
% identity
                  46
                  HYPOTHETICAL 32.3 KD PROTEIN IN KRE1-HXT14 INTERGENIC
NCBI Description
                  REGION >gi_1077427_pir__S51294 probable membrane protein
                  YNL320w - yeast (Saccharomyces cerevisiae)
                  >gi_633665_emb_CAA86377_ (Z46259) NO342 [Saccharomyces
                  cerevisiae] >gi 1302432_emb_CAA96251_ (Z71596) ORF YNL320w
                  [Saccharomyces cerevisiae]
Seq. No.
                  291928
Seq. ID
                  LIB3059-048-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  g141597
BLAST score
                  323
E value
                  6.0e-30
Match length
                  135
% identity
                  55
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
                  >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                  >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                  [Zea mays]
Seq. No.
                  291929
Seq. ID
                  LIB3059-049-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  q121472
BLAST score
                  262
E value
                  7.0e-23
Match length
                  66
% identity
                  80
```

NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)

>gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea

Seq. ID Method



mays] >gi 168485 (M16066) glutelin-2 [Zea mays]

```
291930
Seq. No.
Seq. ID
                  LIB3059-049-Q1-K1-A5
Method
                  BLASTN
NCBI GI
                  g168484
BLAST score
                  96
E value
                  1.0e-46
Match length
                  284
% identity
                  84
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                  291931
Seq. No.
Seq. ID
                  LIB3059-049-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  g141616
BLAST score
                  179
                  3.0e-13
E value
Match length
                  35
% identity
                  91
                  ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
NCBI Description
                  >gi 168662 (M12147) 15 kDa zein protein [Zea mays]
                  291932
Seq. No.
Seq. ID
                  LIB3059-049-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  g419803
BLAST score
                  234
E value
                  2.0e-26
Match length
                  134
% identity
                  54
                  zein protein - maize >gi 168705 (M72708) zein protein [Zea
NCBI Description
                  mays]
Seq. No.
                  291933
                  LIB3059-049-Q1-K1-C9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168661
BLAST score
                  38
E value
                  2.0e-12
Match length
                  70
% identity
                  89
NCBI Description Maize 15 kDa zein mRNA, clone cZ15A3, complete cds
Seq. No.
                  291934
Seq. ID
                  LIB3059-049-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  g121974
BLAST score
                  321
                  9.0e-30
E value
Match length
                  98
% identity
                   68
NCBI Description
                 HISTONE H2A.2.1 >gi 70710 pir HSWT2A histone H2A.2 - wheat
Seq. No.
                  291935
```

40648

LIB3059-049-Q1-K1-F1

BLASTX



```
g3914423
NCBI GI
                  264
BLAST score
                  4.0e-23
E value
                  94
Match length
                  60
% identity
NCBI Description PROFILIN 4 >gi_2642324 (AF032370) profilin [Zea mays]
                  291936
Seq. No.
                  LIB3059-049-Q1-K1-F11
Seq. ID
                  BLASTX
Method
                  g1923256
NCBI GI
                  346
BLAST score
                  1.0e-32
E value
Match length
                  120
                   58
% identity
                   (U86782) 26S proteasome-associated pad1 homolog [Homo
NCBI Description
                   sapiens]
                   291937
Seq. No.
                  LIB3059-049-Q1-K1-F8
Seq. ID
                  BLASTN
Method
NCBI GI
                   g168484
                   105
BLAST score
                   2.0e-52
E value
Match length
                   105
                   100
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                   291938
Seq. No.
                   LIB3059-049-Q1-K1-G10
Seq. ID
                   BLASTN
Method
                   g632737
NCBI GI
                   43
BLAST score
                   5.0e-15
E value
                   103
Match length
                   86
% identity
NCBI Description ADP-glucose pyrophosphorylase=grain Bt2 subunit homolog
                   [Zea mays=corn, leaves, mRNA Partial, 615 nt]
                   291939
 Seq. No.
                   LIB3059-049-Q1-K1-G4
Seq. ID
                   BLASTN
Method
                   g1037129
NCBI GI
BLAST score
                   199
                   1.0e-108
E value
                   295
Match length
                   92
 % identity
                   (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
 NCBI Description
                   Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                   291940
 Seq. No.
                   LIB3059-049-Q1-K1-G7
 Seq. ID
                   BLASTN
 Method
 NCBI GI
                   g2062705
 BLAST score
                    36
                    1.0e-10
 E value
```

36

Match length

BLAST score

E value Match length 87 2.0e-41

170



```
100
 % identity
 NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                     291941
 Seq. No.
                     LIB3059-049-Q1-K1-H1
 Seq. ID
 Method
                     BLASTX
 NCBI GI
                     q141617
 BLAST score
                     329
 E value
                     1.0e-30
                     103
 Match length
 % identity
                     65
                     ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
 NCBI Description
                     >gi_100941_pir__S12140_zein_Zc1 - maize
>gi_100945_pir__B29017_zein_2 - maize
>gi_22515_emb_CAA37595_(X53515)_zein_Zc1_[Zea_mays]
                     >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
 Seq. No.
                     291942
 Seq. ID
                     LIB3059-052-Q1-K1-A2
 Method
                     BLASTX
· NCBI GI
                     g3811009
 BLAST score
                     158
 E value
                     6.0e-11
 Match length
                     84
 % identity
                     44
                     (AB019328) NADP specific isocitrate dehydrogenase [Daucus
 NCBI Description
                     carota]
                     291943
 Seq. No.
 Seq. ID
                     LIB3059-052-Q1-K1-C4
 Method
                     BLASTN
 NCBI GI
                     q22524
 BLAST score
                     84
 E value
                     2.0e-39
 Match length
                     144
 % identity
                     90
 NCBI Description
                     Zea mays mRNA encoding a zein (clone ZG31A)
 Seq. No.
                     291944
                     LIB3059-052-Q1-K1-D4
 Seq. ID
 Method
                     BLASTX
 NCBI GI
                     g2117937
 BLAST score
                     265
                     2.0e-23
 E value
 Match length
                     91
  % identity
                     63
                     UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
 NCBI Description
                     barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose
                     pyrophosphorylase [Hordeum vulgare]
                     291945
  Seq. No.
 Seq. ID
                     LIB3059-052-Q1-K1-E1
 Method
                     BLASTN
 NCBI GI
                     g596079
```

BLAST score

% identity

E value Match length 440 9.0e-44

121

77



```
% identity
                  Zea mays thiamine biosynthetic enzyme (thi1-2) mRNA,
NCBI Description
                  complete cds
                  291946
Seq. No.
                  LIB3059-052-Q1-K1-H12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168681
BLAST score
                  62
                  1.0e-26
E value
Match length
                  195
                  89
% identity
NCBI Description
                  Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
                  >gi 270686 gb I03333 Sequence 8 from Patent US
Seq. No.
                  291947
Seq. ID
                  LIB3059-053-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  g82696
BLAST score
                  202
E value
                  1.0e-25
Match length
                  66
                  94
% identity
NCBI Description
                  glycine-rich protein - maize >gi 22293 emb CAA43431
                  (X61121) glycine-rich protein [Zea mays]
Seq. No.
                  291948
Seq. ID
                  LIB3059-053-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g168664
BLAST score
                  386
E value
                  2.0e-37
Match length
                  126
                  65
% identity
NCBI Description
                  (M13507) zein protein precursor [Zea mays]
                  291949
Seq. No.
                  LIB3059-053-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q266398
BLAST score
                  250
E value
                  1.0e-21
Match length
                  51
% identity
                  82
                  TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR
NCBI Description
                  INHIBITOR) (CHFI) >gi 68849 pir TIZM1 trypsin/factor XIIa
                  inhibitor precursor - maize >gi 22327 emb CAA37998
                  (X54064) corn Hageman factor inhibitor [Zea mays]
Seq. No.
                  291950
Seq. ID
                  LIB3059-053-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  g4185308
```

```
Mary Mary No.
```

```
NCBI Description (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
                   291951
Seq. No.
                   LIB3059-053-Q1-K1-D9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g16073
                   359
BLAST score
                   3.0e-34
E value
Match length
                   117
% identity
                   68
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
                   291952
Seq. No.
                   LIB3059-053-Q1-K1-H11
Seq. ID
Method
                   BLASTN
                   g22288
NCBI GI
                   120
BLAST score
                   4.0e-61
E value
Match length
                   188
                   92
% identity
NCBI Description Maize mRNA fragment for endosperm glutelin-2
Seq. No.
                   291953
                   LIB3059-054-Q1-K1-A6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g141605
                   221
BLAST score
                   2.0e-38
E value
                   123
Match length
% identity
                   73
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                   >gi 72312_pir _ZIZM92 19K zein precursor (clone cZ19C2) -
                   maize > gi_168\overline{68}0 (M12145) 19 kDa zein protein [Zea mays]
                   291954
 Seq. No.
                   LIB3059-054-Q1-K1-B5
 Seq. ID
                   BLASTX
 Method
                   q488571
 NCBI GI
                   279
 BLAST score
                   7.0e-25
 E value
                   59
 Match length
                    97
 % identity
                   (U09462) histone H3.2 [Medicago sativa]
 NCBI Description
                    291955
 Seq. No.
                    LIB3059-054-Q1-K1-E4
 Seq. ID
                    BLASTX
 Method
                    g3367596
 NCBI GI
                    169
 BLAST score
                    4.0e-12
 E value
                    80
 Match length
 % identity
 NCBI Description (AL031135) putative protein [Arabidopsis thaliana]
                    291956
 Seq. No.
                    LIB3059-054-Q1-K1-F10
 Seq. ID
```

40652

BLASTX

Method



```
NCBI GI
                  q141597
BLAST score
                  275
                  1.0e-25
E value
Match length
                  99
                  57
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
                  >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                  >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                  [Zea mays]
Seq. No.
                  291957
                  LIB3059-054-Q1-K1-G4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g168679
BLAST score
                  71
                  7.0e-32
E value
Match length
                  91
                  95
% identity
                  Maize 19 kDa zein mRNA, clone cZ19C2, complete cds.
NCBI Description
                  >gi_270687_gb_I03334_ Sequence 9 from Patent US
                  291958
Seq. No.
                  LIB3059-054-Q1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q629862
BLAST score
                  206
E value
                  1.0e-16
Match length
                  57
                  70
% identity
NCBI Description
                  zein Zd1, 19K - maize >gi 535021 emb CAA47640 (X67203)
                  zein Zd1 (19 kDa zein) [Zea mays]
                  291959
Seq. No.
                  LIB3059-054-Q1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1709619
BLAST score
                  347
E value
                  5.0e - 33
Match length
                  76
% identity
                  84
NCBI Description
                  PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) /
                  DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE
                  (GLYCOSYLATION SITE-BINDING CHAIN) (GSBP)
                  >gi_2146814_pir__S69181 protein disulfide isomerase (EC
                  5.3.4.1) precursor - maize >gi_625148 (L39014) protein
                  disulfide isomerase [Zea mays]
Seq. No.
                  291960
Seq. ID
                  LIB3059-054-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  q100940
BLAST score
                  336
E value
                  1.0e-31
Match length
                  85
```

zein zA1 - maize

% identity

NCBI Description

NCBI Description

291966

Seq. No.



```
291961
Seq. No.
                  LIB3059-055-Q1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1709619
BLAST score
                  359
                   3.0e-34
E value
Match length
                  78
                  90
% identity
NCBI Description
                  PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) /
                  DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE
                   (GLYCOSYLATION SITE-BINDING CHAIN) (GSBP)
                  >gi_2146814_pir__S69181 protein disulfide isomerase (EC
                  5.3.4.1) precursor - maize >gi_625148 (L39014) protein
                  disulfide isomerase [Zea mays]
Seq. No.
                  291962
Seq. ID
                  LIB3059-055-Q1-K1-B4
Method
                  BLASTX
                                          *
NCBI GI
                  g168695
BLAST score
                  179
E value
                   5.0e-13
Match length
                  56
                   66
% identity
                   (M16218) gamma zein [Zea mays] >gi 225315 prf 1211356A
NCBI Description
                  zein gamma [Zea mays]
                   291963
Seq. No.
Seq. ID
                  LIB3059-055-Q1-K1-B7
                  BLASTN
Method
NCBI GI
                  q16072
BLAST score
                   103
E value
                   8.0e-51
Match length
                  235
% identity
                  86
                  Acetabularia mediterranea zein gene
NCBI Description
Seq. No.
                  291964
                  LIB3059-055-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4185308
BLAST score
                   304
                   8.0e-28
E value
Match length
                  107
% identity
                   61
NCBI Description
                  (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
                   291965
Seq. No.
                   LIB3059-055-Q1-K1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3328221
BLAST score
                   365
                   7.0e-35
E value
                   80
Match length
                   85
% identity
```

40654

(AF076920) thioredoxin peroxidase [Secale cereale]



```
LIB3059-055-Q1-K1-D7
Seq. ID
                   BLASTX
Method
                   q1346109
NCBI GI
                   203
BLAST score
                   6.0e-16
E value
                   45
Match length
% identity
                   GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                   PROTEIN (GPB-LR) (RWD) >gi_540535_dbj_BAA07404_ (D38231)
                   RWD [Oryza sativa]
                   291967
Seq. No.
                   LIB3059-055-Q1-K1-D8
Seq. ID
                   BLASTX
Method
                   g2982297
NCBI GI
                   299
BLAST score
                   9.0e-28
E value
                   72
Match length
% identity
NCBI Description (AF051233) KIAA0107-like protein [Picea mariana]
                   291968
Seq. No.
                   LIB3059-055-Q1-K1-D9
Seq. ID
                   BLASTN
Method
                   q1244652
NCBI GI
                   35
BLAST score
                    4.0e-10
E value
                   99
Match length
                    84
% identity
                   Zea mays copia-type retroelement PREM-2 gag gene, complete
NCBI Description
                    291969
Seq. No.
                    LIB3059-055-Q1-K1-E12
Seq. ID
Method
                    BLASTX
NCBI GI
                    g16073
                    444
BLAST score
                    3.0e-44
E value
                    121
Match length
 % identity
                   (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
                    291970
 Seq. No.
                    LIB3059-055-Q1-K1-E2
 Seq. ID
                    BLASTX
 Method
                    q115484
 NCBI GI
                    189
 BLAST score
                    3.0e-14
 E value
                    45
 Match length
 % identity
                    CALMODULIN 1 >gi 71684_pir MCPZDC calmodulin - carrot
 NCBI Description
                    >gi_478632_pir__S22971 calmodulin - trumpet lily
                    >gi_541839_pir__S40301 calmodulin - Red bryony
                    >gi 2129970 pir S70768 calmodulin CAM81 - garden petunia
                    >gi_18326_emb_CAA42423_ (X59751) calmodulin [Daucus carota]
>gi_19447_emb_CAA78301_ (Z12839) calmodulin [Lilium
                    longiflorum] >gi_169207 (M80836) calmodulin [Petunia
```



hybrida] >gi_308900 (L18912) calmodulin [Lilium longiflorum] >gi_505154_emb_CAA43143_ (X60738) Calmodulin [Malus domestica] >gi_535444 (U13882) calmodulin [Pisum sativum] >gi_445602_prf__1909349A calmodulin [Daucus carota]

 Seq. No.
 291971

 Seq. ID
 LIB3059-055-Q1-K1-E5

 Method
 BLASTX

 NCBI GI
 g2696238

 BLAST score
 262

BLAST score 262 E value 4.0e-23 Match length 72 % identity 76

NCBI Description (D67042) aspartate aminotransferase [Oryza sativa]

 Seq. No.
 291972

 Seq. ID
 LIB3059-055-Q1-K1-E8

 Mathod
 BLASTY

Method BLASTX
NCBI GI g4185308
BLAST score 245
E value 7.0e-21
Match length 98
% identity 55

NCBI Description (AF090446) 22-kDa alpha zein protein 21 [Zea mays]

Seq. No. 291973

Seq. ID LIB3059-055-Q1-K1-F12

Method BLASTX
NCBI GI g463152
BLAST score 218
E value 6.0e-18
Match length 73
% identity 62

NCBI Description (L29505) zein [Zea mays] >gi_1094858_prf__2106415A Met-rich

seed storage protein [Zea mays]

Seq. No. 291974

Seq. ID LIB3059-055-Q1-K1-H10

Method BLASTX
NCBI GI g141603
BLAST score 439
E value 1.0e-43
Match length 112
% identity 81

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)

>gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize

>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 291975

Seq. ID LIB3059-055-Q1-K1-H12

Method BLASTN
NCBI GI g22222
BLAST score 202
E value 1.0e-110
Match length 218
% identity 98



```
NCBI Description Z.mays ZSF4C4 gene for zein
                        291976
      Seq. No.
                        LIB3059-056-Q1-K1-A2
     Seq. ID -
                        BLASTN
     Method
     NCBI GI
                        g2345153
                        54
     BLAST score
      E value
                        8.0e-22
     Match length
                        94
                        89
      % identity
     NCBI Description Zea mays ribsomal protein S4 (rps4) mRNA, complete cds
                        291977
      Seq. No.
                        LIB3059-056-Q1-K1-A9
      Seq. ID
                        BLASTX
      Method
                        g419803
      NCBI GI
                        274
      BLAST score
                        3.0e-24
      E value
                        111
      Match length
                        51
      % identity
      NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea
mays]
                        291978
      Seq. No.
                        LIB3059-056-Q1-K1-B11
      Seq. ID
                        BLASTX
      Method
                        q2832246
      NCBI GI
                        218
      BLAST score
                         1.0e-17
      E value
                         99
      Match length
                         51
      % identity
      NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]
                         291979
      Seq. No.
                         LIB3059-056-Q1-K1-B8
      Seq. ID
      Method
                         BLASTX
      NCBI GI
                         g1709129
                         528
      BLAST score
                         5.0e-54
      E value
      Match length
                         121
                         81
      % identity
                         GLYCOGEN SYNTHASE KINASE-3 HOMOLOG MSK-3
      NCBI Description
                         >gi_481018_pir__S37642 protein kinase MSK-3 (EC 2.7.1.-) -
                         alfalfa >gi 313148_emb_CAA48472_ (X68409) protein kinase
                         [Medicago sativa]
      Seq. No.
                         291980
                         LIB3059-056-Q1-K1-D10
      Seq. ID
      Method
                         BLASTX
      NCBI GI
                         g82065
                         213
      BLAST score
      E value
                         3.0e-17
                         88
      Match length
                         52
       % identity
                         ribosomal protein S3a - Madagascar periwinkle
       NCBI Description
```

>gi_217903_dbj_BAA00860_ (D01058) ORF [Catharanthus roseus]

Seq. ID

```
Seq. No.
                  LIB3059-056-Q1-K1-D5
Seq. ID
                  BLASTX
Method
                  g3281867
NCBI GI
                  452
BLAST score
                  4.0e-45
E value
                  113
Match length
                  78
% identity
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]
                  291982
Seq. No.
                  LIB3059-056-Q1-K1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4263711
                   162
BLAST score
                   1.0e-14
E value
                   135
Match length
                   39
% identity
                   (AC006223) putative CCR4-associated transcription factor
NCBI Description
                   [Arabidopsis thaliana]
                   291983
Seq. No.
                   LIB3059-056-Q1-K1-E3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g141598
                   248
BLAST score
                   3.0e-21
E value
                   76
Match length
                   68
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE ZG99)
NCBI Description
                   >gi 72313_pir__ZIZM99 19K zein precursor (clone ZG99) -
                   maize > gi 225\overline{19} emb CAA24717 (V01470) zein [Zea mays]
                   >qi 22534 emb CAA24726 (V01479) zein [Zea mays]
                   291984
Seq. No.
Seq. ID
                   LIB3059-056-Q1-K1-E9
                   BLASTX
Method
NCBI GI
                   g960289
                   494
BLAST score
                   6.0e-50
E value
                   130
Match length
% identity
                   (L34343) anthranilate synthase alpha subunit [Ruta
NCBI Description
                   graveolens]
                   291985
Seq. No.
                   LIB3059-056-Q1-K1-F11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2655029
BLAST score
                   224
                   8.0e-36
E value
                   127
Match length
% identity
                   (AF019296) starch synthase isoform zSTSII-1 [Zea mays]
NCBI Description
                   291986
 Seq. No.
```

40658

LIB3059-056-Q1-K1-G11

Seq. ID



```
BLASTX
Method
                  g168586
NCBI GI
BLAST score
                  169
                  1.0e-20
E value
                  83
Match length
% identity
                  73
NCBI Description (M58656) pyruvate, orthophosphate dikinase [Zea mays]
Seq. No.
                  291987
                  LIB3059-056-Q1-K1-G2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q141602
                  327
BLAST score
E value
                  2.0e-30
                  87
Match length
                   77
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6)
NCBI Description
                   >gi 82658 pir A22831 19K zein precursor (clone M6) - maize
                   >gi 22538 emb CAA26294 (X02450) zein precursor [Zea mays]
                   291988
Seq. No.
                  LIB3059-056-Q1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g141599
BLAST score
                   309
E value
                   3.0e-28
Match length
                   126
                   53
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19A2)
NCBI Description
                   >gi 72316 pir ZIZMA2 19K zein precursor (clone cZ19A2) -
                   maize (fragment) >gi_168670 (M12142) 19 kDa zein protein
                   [Zea mays]
                   291989
Seq. No.
                   LIB3059-057-Q1-K1-A5
Seq. ID
                   BLASTX
Method
                   g141603
NCBI GI
                   270
BLAST score
                   7.0e-24
E value
                   75
Match length
                   76
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                   >gi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
                   >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
                   291990
Seq. No.
                   LIB3059-057-Q1-K1-A7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g224513
                   161
BLAST score
                   4.0e-11
E value
                   91
Match length
 % identity
                   47
NCBI Description
                   zein M6 [Zea mays]
                   291991
 Seq. No.
```

40659

LIB3059-057-Q1-K1-B10



```
Method
                  BLASTX
NCBI GI
                  g100675
BLAST score
                  235
E value
                  2.0e-24
Match length
                  102
                  66
% identity
                  glucose-1-phosphate adenylyltransferase (EC 2.7.7.27)
NCBI Description
                  precursor - rice >gi_169759 (J04960) ADP-glucose
                  pyrophosphorylase 51kD subunit (EC 2.7.7.27) [Oryza sativa]
                  291992
Seq. No.
Seq. ID
                  LIB3059-057-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  g141617
BLAST score
                  313
E value
                  5.0e-29
Match length
                  105
% identity
                  60
                  ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                  >gi 100941 pir S12140 zein Zc1 - maize
                  >gi 100945 pir B29017 zein 2 - maize
                  >gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                  >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
                  291993
Seq. No.
                  LIB3059-057-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141603
BLAST score
                  240
E value
                  5.0e-28
Match length
                  118
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >gi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
                  >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
                  291994
Seq. No.
Seq. ID
                  LIB3059-057-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g3641838
BLAST score
                  220
E value
                  6.0e-18
Match length
                  70
% identity
                  57
                  (AL023094) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                  291995
Seq. No.
                  LIB3059-057-Q1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g629862
BLAST score
                  294
```

E value 9.0e-27 Match length 94 % identity 64

NCBI Description zein Zd1, 19K - maize >gi 535021 emb CAA47640 (X67203)

zein Zd1 (19 kDa zein) [Zea mays]

Method

NCBI GI BLAST score BLASTN g22524

108



```
291996
Seq. No.
                  LIB3059-057-Q1-K1-D12
Seq. ID
Method
                  BLASTX
                  q3687251
NCBI GI
BLAST score
                  227
                  6.0e-19
E value
                  86
Match length
                  53
% identity
NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]
                  291997
Seq. No.
                  LIB3059-057-Q1-K1-F10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q22544
BLAST score
                  36
                  7.0e-11
E value
Match length
                  68
% identity
                  88
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
                  291998
Seq. No.
Seq. ID
                  LIB3059-057-Q1-K1-F11
Method
                  BLASTX
                  q2668742
NCBI GI
BLAST score
                  332
E value
                  4.0e-31
Match length
                  90
% identity
                  76
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]
                  291999
Seq. No.
                  LIB3059-057-Q1-K1-F4
Seq. ID
Method
                  BLASTX
                  g4371290
NCBI GI
BLAST score
                  196
E value
                  3.0e-15
Match length
                  49
% identity
                  73
NCBI Description (AC006260) unknown protein [Arabidopsis thaliana]
                  292000
Seq. No.
                  LIB3059-057-Q1-K1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1184776
BLAST score
                  166
E value
                  1.0e-15
                  70
Match length
% identity
                  (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC4 [Zea mays]
Seq. No.
                  292001
                  LIB3059-057-Q1-K1-G6
Seq. ID
```

Match length

% identity

87

61



```
4.0e-54
E value
Match length
                   163
                   92
% identity
NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)
                   292002
Seq. No.
                   LIB3059-057-Q1-K1-G8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3236242
                   242
BLAST score
E value
                   9.0e-21
                   73
Match length
                   67
% identity
                   (AC004684) putative ribosomal protein L36 [Arabidopsis
NCBI Description
                   thaliana]
                   292003
Seq. No.
                   LIB3059-057-Q1-K1-H6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3935184
                  \frac{1}{2} 207
BLAST score
                   2.0e-16
E value
Match length
                   124
% identity
                   44
                   (AC004557) F17L21.27 [Arabidopsis thaliana]
NCBI Description
                   292004
Seq. No.
                   LIB3059-058-Q1-K1-A10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g567893
BLAST score
                   161
                   6.0e-11
E value
Match length
                   105
% identity
                   25
                   (L37382) beta-galactosidase-complementation protein
NCBI Description
                    [Cloning vector]
                   292005
Seq. No.
                   LIB3059-058-Q1-K1-A6
 Seq. ID
                   BLASTX
Method
NCBI GI
                   g72307
                   242
 BLAST score
                    4.0e-30
 E value
                   116
 Match length
                    65
 % identity
                   22K zein precursor (clone pZ22.3) - maize >gi_168686
 NCBI Description
                    (J01246) 26.99 kd zein protein [Zea mays]
                    292006
 Seq. No.
                   LIB3059-058-Q1-K1-A8
 Seq. ID
                    BLASTX
 Method
                    g3023356
 NCBI GI
                    159
 BLAST score
                    2.0e-16
 E value
```

NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR



musculus]

```
292007
Seq. No.
                  LIB3059-058-Q1-K1-C5
Seq. ID
                  BLASTX
Method
                  q3548818
NCBI GI
                  422
BLAST score
                  1.0e-41
E value
                  141
Match length
                  62
% identity
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]
                  292008
Seq. No.
                  LIB3059-058-Q1-K1-D9
Seq. ID
                  BLASTX
Method
                  g4220517
NCBI GI
                  251
BLAST score
                   2.0e-21
E value
                  91
Match length
                   49
% identity
NCBI Description (AL035356) hypothetical protein [Arabidopsis thaliana]
                   292009
Seq. No.
                  LIB3059-058-Q1-K1-E12
Seq. ID
                   BLASTX
Method
                   g224508
NCBI GI
                   177
BLAST score
                   1.0e-17
E value
                   118
Match length
                   59
% identity
NCBI Description zein A20 [Zea mays]
                   292010
Seq. No.
                   LIB3059-058-Q1-K1-E8
Seq. ID
                   BLASTX
Method
                   g451193
NCBI GI
                   210
BLAST score
                   2.0e-25
E value
                   109
Match length
                   63
 % identity
                   (L28008) wali7 [Triticum aestivum]
 NCBI Description
                   >gi 1090845_prf__2019486B wali7 gene [Triticum aestivum]
                   292011
 Seq. No.
                   LIB3059-058-Q1-K1-G4
 Seq. ID
                   BLASTX
 Method
                   q549638
 NCBI GI
 BLAST score
                   163
                   4.0e-11
 E value
                   131
 Match length,
 % identity
                   HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC
 NCBI Description
                   REGION >gi_539279_pir__S38159 hypothetical protein YKR081c
                    - yeast (Saccharomyces cerevisiae) >gi_415901_emb_CAA81632_
```

>gi 2623222 (AF030559) ATP synthase beta-subunit [Mus

40663

(Z27116) ORF YKR401 [Saccharomyces cerevisiae] >gi 486561_emb_CAA82160_ (Z28306) ORF YKR081c



NCBI Description zein E19 [Zea mays]

[Saccharomyces cerevisiae]

```
292012
Seq. No.
                   LIB3059-058-Q1-K1-H2
Seq. ID
                   BLASTX
Method
                   g121472
NCBI GI
                   156
BLAST score
E value
                   2.0e-10
Match length
                   88
                   41
% identity
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
                   [Zea mays] >gi 22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
                   mays] >gi 1684\overline{8}5 (M1\overline{6}066) gluteli\overline{n}-2 [Zea mays]
                   292013
Seq. No.
                   LIB3059-058-Q1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3915826
BLAST score
                   442
E value
                   5.0e-44
Match length
                   110
                   75
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L5
                   292014
Seq. No.
                   LIB3059-059-Q1-K1-A11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g141610
BLAST score
                   159
E value
                   1.0e-10
Match length
                   113
% identity
                   40
NCBI Description ZEIN-ALPHA PRECURSOR (CLONE Z4)
                   292015
Seq. No.
                   LIB3059-059-Q1-K1-E4
Seq. ID
                   BLASTN
Method
                    g168704
NCBI GI
                    38
BLAST score
                    5.0e-12
E value
                    52
Match length
                    94
 % identity
NCBI Description Zea mays zein protein gene, complete cds
                    292016
 Seq. No.
                    LIB3059-059-Q1-K1-H12
 Seq. ID
                    BLASTX
 Method
                    g224509
 NCBI GI
                    229
 BLAST score
                    6.0e-19
 E value
                    98
 Match length
                    54
 % identity
```



```
292017
Seq. No.
                  LIB3059-060-Q1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4519539
                  332
BLAST score
                  3.0e - 31
E value
                  85
Match length
                  71
% identity
                   (AB016256) NAD-dependent sorbitol dehydrogenase [Malus
NCBI Description
                  domestica]
                   292018
Seq. No.
                   LIB3059-060-Q1-K1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2668742
BLAST score
                   391
                   5.0e-38
E value
Match length
                   82
% identity
                   (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                   292019
Seq. No.
                   LIB3059-060-Q1-K1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2832243
BLAST score
                   291
                   3.0e-26
E value
Match length
                   102
                   62
% identity
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
                   292020
Seq. No.
                   LIB3060-001-Q1-K1-D11
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4519187
BLAST score
                   35
                   4.0e-10
E value
                   79
Match length
                   86
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
NCBI Description
                   K1G2, complete sequence
                   292021
Seq. No.
                   LIB3060-001-Q1-K2-B7
Seq. ID
                   BLASTX
Method
                   g2921304
NCBI GI
                   164
BLAST score
                   3.0e-11
E value
                   81
Match length
% identity
                   (AF033496) herbicide safener binding protein [Zea mays]
NCBI Description
                   292022
Seq. No.
Seq. ID
                   LIB3060-001-Q1-K2-C12
```

BLASTX

573

q312179

Method

NCBI GI

BLAST score



3.0e-59 E value Match length 123 92 % identity

NCBI Description (X73151) glyceraldehyde 3-phosphate dehydrogenase

(phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]

>gi 1185554 (U45858) glyceraldehyde-3-phosphate

dehydrogenase [Zea mays]

Seq. No.

Seq. ID

LIB3060-001-Q1-K2-C2

Method BLASTX g1743354 NCBI GI BLAST score 255 E value 4.0e-22 Match length 114 48 % identity

(Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum] NCBI Description

Seq. No.

292024 Seq. ID

LIB3060-002-Q1-K2-A12

Method BLASTX NCBI GI q2632254 BLAST score 407 7.0e-40 E value Match length 110 % identity 68

NCBI Description (Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.

Seq. ID

LIB3060-002-Q1-K2-A2

Method BLASTX q1778149 NCBI GI BLAST score 171 3.0e-12E value Match length 61 64 % identity

NCBI Description (U66404) phosphate/phosphoenolpyruvate translocator

precursor [Zea mays]

Seq. No.

292026

292025

Seq. ID

LIB3060-002-Q1-K2-D12

Method BLASTX NCBI GI g2911073 BLAST score 262 E value 8.0e-23 Match length 120 % identity 50

(AL021960) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

292027

Seq. ID

LIB3060-002-Q1-K2-F12

Method BLASTX NCBI GI g283038 BLAST score 206 2.0e-16 E value 107 Match length



```
% identity
                  chlorophyll a/b-binding protein (cab-m7) precursor - maize
NCBI Description
                  >gi 22230_emb_CAA37474_ (X53398) light harvesting
                  chlorophyll a /b binding protein [Zea mays]
Seq. No.
                  292028
                  LIB3060-002-Q1-K2-F5
Seq. ID
Method
                  BLASTX
                  g2326947
NCBI GI
BLAST score
                  285
                  2.0e-28
E value
                  107
Match length
% identity
                  63
                  (Z50801) Chlorophyll a/b-binding protein CP29 precursor
NCBI Description
                   [Zea mays]
Seq. No.
                  292029
                  LIB3060-002-Q1-K2-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1935021
                  356
BLAST score
E value
                  8.0e - 34
                  142
Match length
% identity
                   49
NCBI Description (Z93775) monosaccharid transport protein [Vicia faba]
                   292030
Seq. No.
                   LIB3060-002-Q1-K2-H3
Sea. ID
Method
                   BLASTX
NCBI GI
                   g3914005
                   228
BLAST score
                   3.0e-19
E value
                   79
Match length
                   67
% identity
NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 1816586
                   (U85494) LON1 protease [Zea mays]
                   292031
Seq. No.
                   LIB3060-003-Q1-K1-B6
Seq. ID
                   BLASTX
Method
                   g2407790
NCBI GI
                   163
BLAST score
                   1.0e-19
E value
                   119
Match length
                   42
% identity
NCBI Description (AF019910) grr1 [Glycine max]
                   292032
Seq. No.
                   LIB3060-003-Q1-K1-C10
Seq. ID
                   BLASTX
Method
                   g3024018
NCBI GI
                   457
BLAST score
                   1.0e-45
E value
Match length
                   113
% identity
                   82
                   INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
NCBI Description
                   >gi_1546919_emb_CAA69225_ (Y07920) translation initiation
```



factor 5A [Zea mays] >gi_2668738 (AF034943) translation initiation factor 5A [Zea mays]

292033 Seq. No.

LIB3060-003-Q1-K1-C12 Seq. ID

Method BLASTN NCBI GI g4502326 BLAST score 123 E value 9.0e-63 Match length 211 90 % identity

Homo sapiens AU RNA-binding protein/enoyl-Coenzyme A NCBI Description

hydratase (AUH) mRNA >gi 780240_emb_X79888_HSAUHMR

H.sapiens AUH mRNA >gi_1912084_gb_G31445_G31445 human STS

SHGC-31547

Seq. No. Seq. ID

292034 LIB3060-003-Q1-K1-C5

Method BLASTX NCBI GI g2766596 230 BLAST score 5.0e-19 E value Match length 81 % identity

(AF002857) homologue of Bacillus subtilis ribG [Shigella NCBI Description

flexneri]

Seq. No. 292035

LIB3060-003-Q1-K1-E11 Seq. ID

Method BLASTX g4127346 NCBI GI BLAST score 268 2.0e-23 E value 102 Match length % identity 53

NCBI Description (AJ010448) glutathione transferase [Alopecurus myosuroides]

292036 Seq. No.

LIB3060-003-Q1-K1-E2 Seq. ID

BLASTX Method g3885896 NCBI GI BLAST score 169 3.0e-12 E value 89 Match length % identity

NCBI Description (AF093636) plastocyanin precursor [Oryza sativa]

292037 Seq. No.

Seq. ID LIB3060-003-Q1-K1-E6

BLASTN Method NCBI GI g1658314 BLAST score 54 2.0e-21 E value 58 Match length % identity 98

NCBI Description O.sativa osr40g3 gene

Seq. No.

Seq. ID

292043

LIB3060-004-Q1-K1-G4



```
292038
Seq. No.
                   LIB3060-003-Q1-K1-F12
Seq. ID
Method
                   BLASTX
                   g4154281
NCBI GI
                   239
BLAST score
                   2.0e-20
E value
                   76
Match length
% identity
                   71
NCBI Description (AF082347) C13 endopeptidase NP1 precursor [Zea mays]
                   292039
Seq. No.
                   LIB3060-003-Q1-K1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4512654
BLAST score
                   162
E value
                   3.0e-11
Match length
                   105
                   40
% identity
NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]
Seq. No.
                   292040
                   LIB3060-004-Q1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g128688
                   379
BLAST score
E value
                   1.0e-36
Match length
                   73
                   100
% identity
                   NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST
NCBI Description
                   >gi_1363566_pir__S58557 NADH dehydrogenase (ubiquinone) (EC
1.6.5.3) chain 3 - maize chloroplast
                   >gi_902227_emb_CAA60291_ (X86563) NADH dehydrogenase D3
                   [Zea mays]
Seq. No.
                   292041
                   LIB3060-004-Q1-K1-E12
Seq. ID
                   BLASTX
Method
                   q100880
NCBI GI
BLAST score
                   148
                   6.0e-10
E value
                   29
Match length
                   93
% identity
                   glyceraldehyde-3-phosphate dehydrogenase (NADP+)
NCBI Description
                    (phosphorylating) (EC 1.2.1.13) A, chloroplast - maize
Seq. No.
                   292042
                   LIB3060-004-Q1-K1-G12
Seq. ID
                   BLASTN
Method
                   g3970828
NCBI GI
BLAST score
                   48
                   4.0e-18
E value
                   89
Match length
                   89
% identity
                   Homo sapiens HSP105 beta mRNA, complete cds
NCBI Description
```

Seq. ID Method

NCBI GI



```
Method
                  BLASTX
NCBI GI
                  g283038
                  377
BLAST score
                  2.0e-36
E value
                                 ÷,
                  96
Match length
                  79
% identity
                  chlorophyll a/b-binding protein (cab-m7) precursor - maize
NCBI Description
                  >gi 22230 emb_CAA37474 (X53398) light harvesting
                  chlorophyll a /b binding protein [Zea mays]
                  292044
Seq. No.
Seq. ID
                  LIB3060-004-Q1-K1-H2
                  BLASTX
Method
                  g2654870
NCBI GI
                  374
BLAST score
                  5.0e-36
E value
                  118
Match length
                  79
% identity
NCBI Description (AF015302) RbohAOsp [Oryza sativa]
Seq. No.
                  292045
                  LIB3060-005-Q1-K1-A4
Seq. ID
                  BLASTX
Method
                  g3080392
NCBI GI
                  153
BLAST score
                  1.0e-10
E value
                   49
Match length
% identity
                   63
NCBI Description (AL022603) glucose transporter [Arabidopsis thaliana]
                   292046
Seq. No.
                   LIB3060-005-Q1-K1-B5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1946371
                   529
BLAST score
E value
                   3.0e-54
Match length
                   121
                   82
% identity
                   (U93215) regulatory protein Viviparous-1 isolog
NCBI Description
                   [Arabidopsis thaliana]
                   292047
Seq. No.
Seq. ID
                   LIB3060-005-Q1-K1-B8
Method
                   BLASTX
                   q4185513
NCBI GI
BLAST score
                   223
                   2.0e-18
E value
                   88
Match length
% identity
                   (AF102823) actin depolymerizing factor 5 [Arabidopsis
NCBI Description
                   thaliana] >gi 4185517 (AF102825) actin depolymerizing
                   factor 5 [Arabidopsis thaliana]
Seq. No.
                   292048
```

40670

LIB3060-005-Q1-K1-F2

BLASTX g1853970

% identity

NCBI Description



```
BLAST score
                  2.0e-10
E value
                  99
Match length
% identity
                  36
NCBI Description (D88122) CPRD46 protein [Vigna unguiculata]
                  292049
Seq. No.
Seq. ID
                  LIB3060-005-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  q3402684
BLAST score
                  390
                   7.0e-38
E value
Match length
                   100
                   76
% identity
                   (AC004697) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   292050
                   LIB3060-005-Q1-K1-G3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2624416
BLAST score
                   87
                   2.0e-41
E value
Match length
                   207
% identity
                   86
                   Zea mays mRNA for ubiquitin carrier protein UBC7
NCBI Description
                   292051
Seq. No.
                   LIB3060-005-Q1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3021270
                   159
BLAST score
E value
                   1.0e-10
                   115
Match length
% identity
                   30
                   (AL022347) serine/threonine kinase -like protein
NCBI Description
                   [Arabidopsis thaliana]
                   292052
Seq. No.
Seq. ID
                   LIB3060-006-Q1-K1-B2
                   BLASTN
Method
                   g3342027
NCBI GI
                   40
BLAST score
                   3.0e-13
E value
                   120
Match length
                   83
% identity
                   Anigozanthos flavidus 18S small subunit ribosomal RNA gene,
NCBI Description
                   complete sequence
                   292053
Seq. No.
                   LIB3060-006-Q1-K1-B7
Seq. ID
                   BLASTX
Method
                   q3236253
NCBI GI
                   206
BLAST score
E value
                   3.0e-16
Match length
                   116
```

(AC004684) receptor-like protein kinase [Arabidopsis



thaliana]

```
292054
Seq. No.
                  LIB3060-006-Q1-K1-E2
Seq. ID
                  BLASTX
Method
                  g3287951
NCBI GI
                  221
BLAST score
E value
                  5.0e-18
                  118
Match length
% identity
                  44
                  HYPOTHETICAL 41.6 KD PROTEIN IN FMT-SPOVM INTERGENIC REGION
NCBI Description
                  >gi 2337804_emb CAA74265_ (Y13937) YloN protein [Bacillus
                  subtilis] >gi_2633947_emb_CAB13448_ (Z99112) similar to
                  hypothetical proteins [Bacillus subtilis]
                  292055
Seq. No.
                  LIB3060-006-Q1-K1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3341978
                   198
BLAST score
                   2.0e-15
E value
Match length
                   88
                   50
% identity
NCBI Description (AF044603) cytokinin oxidase [Zea mays]
                   292056
Seq. No.
                   LIB3060-006-Q1-K1-H4
Seq. ID
                   BLASTX
Method
                   g3292814
NCBI GI
BLAST score
                   160
                   2.0e-11
E value
                   49
Match length
% identity
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
                   292057
Seq. No.
                   LIB3060-007-Q1-K1-C10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2435522
                   298
BLAST score
                   5.0e-27
E value
                   145
Match length
                   46
% identity
                   (AF024504) contains similarity to other AMP-binding enzymes
NCBI Description
                   [Arabidopsis thaliana]
                   292058
Seq. No.
Seq. ID
                   LIB3060-007-Q1-K1-D6
                   BLASTX
Method
                   q112994
NCBI GI
                   358
BLAST score
E value
                   4.0e-34
                   85
Match length
 % identity
                   GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                   >gi 82685_pir S04536 embryonic abundant protein,
```

40672

glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)



ABA-inducible gene protein [Zea mays] >gi_226091_prf__1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 292059 Seq. ID LIB3060-008-Q1-K1-A4

Method BLASTN
NCBI GI g22378
BLAST score 50
E value 4.0e-19
Match length 130
% identity 85

NCBI Description Z.mays gene for nucleic acid binding protein

Seq. No. 292060

Seq. ID LIB3060-008-Q1-K1-D3

Method BLASTX
NCBI GI g3335347
BLAST score 284
E value 1.0e-25
Match length 96
% identity 57

NCBI Description (AC004512) Contains similarity to ARI, RING finger protein

gb_X98309 from Drosophila melanogaster. ESTs gb_T44383, gb_W43120, gb_N65868, gb_H36013, gb_AA042241, gb_T76869 and gb_AA042359 come from this gene. [Arabidopsis thaliana]

Seq. No. 292061

Seq. ID LIB3060-008-Q1-K1-D6

Method BLASTN
NCBI GI g22229
BLAST score 44
E value 7.0e-16
Match length 115

% identity 85

NCBI Description Z.mays cab-m7 gene for light harvesting chlorophyll a/b binding protein

Seq. No. 292062

Seq. ID LIB3060-008-Q1-K1-D9

Method BLASTX
NCBI GI g118104
BLAST score 536
E value 6.0e-55
Match length 120
% identity 86

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)

>gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -

maize >gi 168461 (M55021) cyclophilin [Zea mays]

>gi 829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 292063

Seq. ID LIB3060-008-Q1-K1-E11

Method BLASTX NCBI GI g3319342 BLAST score 237

Match length



```
6.0e-20
E value
                   90
Match length
% identity
                   (AF077407) similar to mitochondrial carrier proteins (Pfam:
NCBI Description
                  mit carr.hmm, score: 79.74 and 42.50) [Arabidopsis
                  thaliana]
Seq. No.
                   292064
                  LIB3060-008-Q1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g100880
BLAST score
                   163
E value
                   9.0e-12
Match length
                   47
                   77
% identity
                   glyceraldehyde-3-phosphate dehydrogenase (NADP+)
NCBI Description
                   (phosphorylating) (EC 1.2.1.13) A, chloroplast - maize
Seq. No.
                   292065
                   LIB3060-008-Q1-K1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3450842
BLAST score
                   454
E value
                   2.0e-45
Match length
                   130
% identity
                   (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                   sativa]
Seq. No.
                   292066
                   LIB3060-009-Q1-K1-A6
Seq. ID
Method
                   BLASTN
                   g643596
NCBI GI
BLAST score
                   101
                   9.0e-50
E value
                   188
Match length
                   89
% identity
NCBI Description Corn mRNA for cysteine proteinase, clone CCP, complete cds
                   292067
Seq. No.
                   LIB3060-009-Q1-K1-B3
Seq. ID
                   BLASTX
Method
                   g730536
NCBI GI
BLAST score
                   239
E value
                   1.0e-20
                   67
Match length
                   75
% identity
                   60S RIBOSOMAL PROTEIN L23 >gi 310933 (L18915) 60S ribosomal
NCBI Description
                   protein subunit L17 [Nicotiana tabacum]
                   292068
Seq. No.
                   LIB3060-009-Q1-K1-C2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2262107
BLAST score
                   278
                   4.0e-25
E value
```

BLAST score

E value

611 1.0e-63



```
% identity
                   (ACO02343) Ser/Thr protein kinase isolog [Arabidopsis
NCBI Description
                  thaliana]
                   292069
Seq. No.
                  LIB3060-009-Q1-K1-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                   g266578
BLAST score
                   268
E value
                   1.0e-23
                   56
Match length
                   89
% identity
                  METALLOTHIONEIN-LIKE PROTEIN 1 >gi_100898_pir__S17560
NCBI Description
                   metallothionein-like protein - mai\overline{z}e >gi \overline{2}367\overline{30} bbs 57629
                   (S57628) metallothionein homologue [Zea mays, Peptide, 76
                   aa] [Zea mays] >gi_559536_emb_CAA57676_ (X82186)
                   metallothionein- like protein [Zea mays]
                   >gi 228095_prf__1717215A metallothionein-like protein [Zea
                   mays]
                   292070
Seq. No.
                   LIB3060-009-Q1-K1-G4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g643596
BLAST score
                   104
                   1.0e-51
E value
                   156
Match length
                   92
% identity
NCBI Description Corn mRNA for cysteine proteinase, clone CCP, complete cds
                   292071
Seq. No.
                   LIB3060-010-Q1-K1-A7
Seq. ID
                   BLASTX
Method
                   g21697
NCBI GI
BLAST score
                   168
                   8.0e-12
E value
                   73
Match length
                   51
% identity
NCBI Description (X66015) cathepsin B [Triticum aestivum]
                   292072
Seq. No.
Seq. ID
                   LIB3060-010-Q1-K1-B8
                   BLASTX
Method
NCBI GI
                   g4558556
BLAST score
                   156
                   2.0e-10
E value
                   71
Match length
                   49
% identity
                   (AC007138) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                   292073
Seq. No.
                   LIB3060-010-Q1-K1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115771
```



Match length 128 % identity 89

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll

a/b-binding protein precursor - maize

>gi 22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No. 292074

Seq. ID LIB3060-010-Q1-K1-E3

Method BLASTX
NCBI GI g3023693
BLAST score 248
E value 4.0e-21
Match length 50
% identity 98

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_1364060_pir__JC4253 translation elongation factor 1alpha - Aureobasidium pullulans >gi_643455 (U19723) translation elongation factor 1-alpha [Aureobasidium

pullulans]

Seq. No. 292075

Seq. ID LIB3060-010-Q1-K1-G5

Method BLASTX
NCBI GI g3395443
BLAST score 307
E value 4.0e-28
Match length 85
% identity 67

NCBI Description (AC004683) putative ammonium transporter, 3' partial

[Arabidopsis thaliana]

Seq. No. 292076

Seq. ID LIB3060-010-Q1-K1-H11

Method BLASTX
NCBI GI g2827141
BLAST score 307
E value 5.0e-28
Match length 142
% identity 45

NCBI Description (AF027173) cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Seq. No. 292077

Seq. ID LIB3060-010-Q1-K1-H12

Method BLASTX
NCBI GI 94006872
BLAST score 265
E value 4.0e-23
Match length 97
% identity 51

NCBI Description (Z99707) methionyl aminopeptidase-like protein [Arabidopsis

thaliana]

Seq. No. 292078

Seq. ID LIB3060-011-Q1-K1-A12



Method BLASTX
NCBI GI g2492519
BLAST score 540
E value 2.0e-55
Match length 141
% identity 73

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi 1395191 dbj_BAA13021_ (D86121) 26S proteasome ATPase

subunit [Spinacia oleracea]

Seq. No. 292079

Seq. ID LIB3060-011-Q1-K1-A7

Method BLASTX
NCBI GI g1491774
BLAST score 253
E value 5.0e-22
Match length 77
% identity 70

NCBI Description (X99936) cysteine protease [Zea mays]

Seq. No. 292080

Seq. ID LIB3060-011-Q1-K1-B12

Method BLASTX
NCBI GI g115771
BLAST score 604
E value 7.0e-63
Match length 114
% identity 97

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll

a/b-binding protein precursor - maize

>gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No. 292081

Seq. ID LIB3060-011-Q1-K1-B4

Method BLASTX
NCBI GI g1346883
BLAST score 645
E value 1.0e-67
Match length 126
% identity 99

NCBI Description PHYTOENE SYNTHASE PRECURSOR >gi_2130144_pir__568307

phytoene synthase - maize >gi 1098665 (U32636) phytoene

synthase [Zea mays]

Seq. No. 292082

Seq. ID LIB3060-011-Q1-K1-C9

Method BLASTX
NCBI GI g2425066
BLAST score 148
E value 2.0e-09
Match length 62
% identity 48

NCBI Description (AF019147) cysteine proteinase Mir3 [Zea mays]

Seq. No. 292083



```
LIB3060-011-Q1-K1-D6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4091117
                   357
BLAST score
                   2.0e-34
E value
Match length
                   108
                   72
% identity
NCBI Description (AF047428) nucleic acid binding protein [Oryza sativa]
                   292084
Seq. No.
                   LIB3060-011-Q1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g295855
BLAST score
                   246
E value
                   4.0e-21
Match length
                   114
                   47
% identity
                  (X15642) P-pyruvate carboxylase [Zea mays]
NCBI Description
Seq. No.
                   292085
                   LIB3060-011-Q1-K1-G9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g556685
                   97
BLAST score
E value
                   3.0e-47
Match length
                   185
                   89
% identity
NCBI Description Z.mays mRNA for ADP-ribosylation factor
                   292086
Seq. No.
                   LIB3060-011-Q1-K1-H11
Seq. ID
                   BLASTX
Method
                   g3176874
NCBI GI
BLAST score
                   221
                   2.0e-18
E value
                   74
Match length
                   57
% identity
                   (AF065639) cucumisin-like serine protease [Arabidopsis
NCBI Description
                   thaliana]
                   292087
Seq. No.
                   LIB3060-012-Q1-K1-A9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2408068
BLAST score
                   211
                   8.0e-17
E value
                   102
Match length
                   39
 % identity
NCBI Description (Z99165) hypothetical protein [Schizosaccharomyces pombe]
                   292088
Seq. No.
                   LIB3060-012-Q1-K1-D11
Seq. ID
                   BLASTN
Method
NCBI GI
                   g22223
BLAST score
                   84
```

1.0e-39

157

E value

Match length



```
% identity
NCBI Description Maize cab-1 gene for chlorophyll a/b-binding protein
                  292089
Seq. No.
                  LIB3060-012-Q1-K1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2687357
BLAST score
                  89
E value
                  2.0e-42
Match length
                  173
% identity
                   90
                  Zea mays nonphototropic hypocotyl 1 (nph1) mRNA, complete
NCBI Description
Seq. No.
                   292090
                  LIB3060-012-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4585873
BLAST score
                   165
E value
                   2.0e-11
Match length
                   73
                   48
% identity
NCBI Description (AC005850) Putative protein kinase [Arabidopsis thaliana]
                   292091
Seq. No.
                   LIB3060-012-Q1-K1-H9
Seq. ID
                   BLASTX
Method
                   q3176874
NCBI GI
                   344
BLAST score
                   9.0e-40
E value
Match length
                   116
                   72
% identity
                   (AF065639) cucumisin-like serine protease [Arabidopsis
NCBI Description
                   thaliana]
                   292092
Seq. No.
                   LIB3060-013-Q1-K1-A1
Seq. ID
                   BLASTX
Method
                   q3047111
NCBI GI
                   524
BLAST score
E value
                   2.0e-53
                   139
Match length
                   71
% identity
                  (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   292093
                   LIB3060-013-Q1-K1-D1
Seq. ID
                   BLASTN
Method
                   g1698669
NCBI GI
BLAST score
                   46
                   9.0e-17
E value
                   133
Match length
                   85
% identity
                  Zea mays S-like RNase (kin1) mRNA, complete cds
NCBI Description
```

292094

LIB3060-013-Q1-K1-D2

Seq. No.

Seq. ID



```
Method
                  BLASTX
NCBI GI
                  g112994
                  374
BLAST score
                  4.0e-36
E value
                  79
Match length
% identity
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi 226091 prf 1410284A abscisic acid inducible gene [Zea
                  mays]
                  292095
Seq. No.
Seq. ID
                  LIB3060-013-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  g3024122
BLAST score
                  578
                  7.0e-60
E value
                  132
Match length
% identity
                  85
                  S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821
                   (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]
                  292096
Seq. No.
Seq. ID
                  LIB3060-014-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  g4587556
BLAST score
                  214
E value
                   4.0e-17
Match length
                  72
% identity
                   (AC006577) Similar to gi 1653162 (p)ppGpp
NCBI Description
                   3-pyrophosphohydrolase from Synechocystis sp genome
                   gb D90911. EST gb W43807 comes from this gene.
                   [Arabidopsis thaliana]
                  292097
Seq. No.
Seq. ID
                  LIB3060-014-Q1-K1-C10
Method
                  BLASTN
NCBI GI
                   q169818
BLAST score
                   131
E value
                   2.0e-67
Match length
                   326
% identity
                   88
NCBI Description Rice 25S ribosomal RNA gene
Seq. No.
                   292098
                   LIB3060-014-Q1-K1-C2
Seq. ID
Method
                  BLASTX
                   q115791
NCBI GI
BLAST score
                   148
```

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

2.0e-09

57 54

E value Match length

% identity



(CAB-2) (LHCP) >gi_81770_pir__S01961 chlorophyll a/b-binding protein 2 precursor - soybean >gi_18548_emb_CAA31418_ (X12980) chlorophyll a/b binding preprotein (AA -33 to 223) [Glycine max]

Seq. No. 292099

Seq. ID LIB3060-014-Q1-K1-C6

Method BLASTX
NCBI GI g168586
BLAST score 149
E value 1.0e-09
Match length 40
% identity 75

NCBI Description (M58656) pyruvate, orthophosphate dikinase [Zea mays]

Seq. No. 292100

Seq. ID LIB3060-014-Q1-K1-D1

Method BLASTX
NCBI GI g4191796
BLAST score 161
E value 5.0e-11
Match length 83
% identity 42

NCBI Description (AC005917) putative senescence-associated protein 5

[Arabidopsis thaliana]

Seq. No. 292101

Seq. ID LIB3060-014-Q1-K1-D2

Method BLASTX
NCBI GI g4589961
BLAST score 200
E value 2.0e-15
Match length 135
% identity 5

NCBI Description (AC007169) unknown protein [Arabidopsis thaliana]

Seq. No. 292102

Seq. ID LIB3060-014-Q1-K1-D8

Method BLASTX
NCBI GI g4589981
BLAST score 184
E value 1.0e-13
Match length 50
% identity 70

NCBI Description (AC007195) amidophosphoribosyltransferase [Arabidopsis

thaliana]

Seq. No. 292103

Seq. ID LIB3060-014-Q1-K1-G6

Method BLASTX
NCBI GI g2842484
BLAST score 472
E value 2.0e-47
Match length 137
% identity 63

NCBI Description (AL021749) tyrosine transaminase-like protein [Arabidopsis

thaliana]



```
Seq. No.
                  292104
                  LIB3060-014-Q1-K1-G9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g548605
BLAST score
                  249
E value
                  2.0e-21
Match length
                  98
% identity
                  61
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
                  - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
                  292105
Seq. No.
Seq. ID
                  LIB3060-015-Q1-K1-B3
                  BLASTX
Method
NCBI GI
                  g1353352
BLAST score
                  407
                  9.0e-40
E value
Match length
                  126
% identity
                  63
                  (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                  reinhardtii]
                  292106
Seq. No.
                  LIB3060-015-Q1-K1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3335374
BLAST score
                  196
                  4.0e-15
E value
                  101
Match length
% identity
                   43
NCBI Description (AC003028) glutaredoxin-like protein [Arabidopsis thaliana]
                  292107
Seq. No.
Seq. ID
                  LIB3060-015-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g3805845
BLAST score
                  274
                  3.0e-24
E value
                  114
Match length
                   54
% identity
NCBI Description (AL031986) putative protein [Arabidopsis thaliana]
                   292108
Seq. No.
Seq. ID
                  LIB3060-015-Q1-K1-F3
Method
                  BLASTX
```

Method BLASTX
NCBI GI g4581156
BLAST score 148
E value 1.0e-09
Match length 43
% identity 63

NCBI Description (AC006919) putative pyruvate kinase [Arabidopsis thaliana]

Seq. No. 292109

BLAST score

E value

269 1.0e-23



```
LIB3060-015-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1890152
BLAST score
                  184
                  1.0e-13
E value
                  57
Match length
                  56
% identity
                  (X92510) allene oxide synthase [Arabidopsis thaliana]
NCBI Description
                  292110
Seq. No.
                  LIB3060-015-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4006850
BLAST score
                  403
E value
                  2.0e-39
Match length
                  133
% identity
                  56
NCBI Description (Z99707) cytochrome like protein [Arabidopsis thaliana]
Seq. No.
                  292111
                  LIB3060-015-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q733458
BLAST score
                  373
E value
                   7.0e-36
                  79
Match length
% identity
                   90
                   (U23190) chlorophyll a/b-binding apoprotein CP24 precursor
NCBI Description
                   [Zea mays]
                   292112
Seq. No.
                  LIB3060-016-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3292814
BLAST score
                   200
E value
                   4.0e-26
                   107
Match length
                   58
% identity
                  (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
                   292113
Seq. No.
Seq. ID
                   LIB3060-016-Q1-K1-A3
                   BLASTX
Method
NCBI GI
                   g3860263
BLAST score
                   269
E value
                   1.0e-23
                   106
Match length
                   52
% identity
                   (AC005824) putative cytochrome p450 protein [Arabidopsis
NCBI Description
                   thaliana]
                   292114
Seq. No.
                   LIB3060-016-Q1-K1-B2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4262232
```



```
Match length
                  111
                  52
% identity
                  (AC006200) putative ribosomal protein L7 [Arabidopsis
NCBI Description
                  thaliana]
                  292115
Seq. No.
                  LIB3060-016-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3894172
BLAST score
                  251
                  2.0e-21
E value
                  127
Match length
% identity
                  45
                  (ACO05312) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                  thaliana]
                  292116
Seq. No.
Seq. ID
                  LIB3060-016-Q1-K1-G6
Method
                  BLASTN
NCBI GI
                  g2981206
BLAST score
                  45
E value
                  3.0e-16
                  77
Match length
                  90
% identity
                  Zea mays photosystem I complex PsaH subunit precursor
NCBI Description
                   (psaH) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
                  292117
Seq. No.
                  LIB3060-016-Q1-K1-G7
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3080389
BLAST score
                  147
                   3.0e-09
E value
Match length
                   91
                   43
% identity
                   (AL022603) putative membrane associated protein
NCBI Description
                   [Arabidopsis thaliana]
                   292118
Seq. No.
Seq. ID
                  LIB3060-016-Q1-K1-H4
                   BLASTN
Method
                   g342579
NCBI GI
BLAST score
                   35
                   3.0e-10
E value
Match length
                   51
                   92
% identity
                  Maize chloroplast phosphorylation coupling factor alpha
NCBI Description
                   subunit (atpA) and proteolipid subunit (atpH) genes,
                   complete cds
                   292119
Seq. No.
                   LIB3060-016-Q1-K1-H8
```

Seq. ID

Method BLASTX NCBI GI g114649 BLAST score 192 1.0e-14 E value



Match length 80 % identity 55

NCBI Description ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III)

>gi_67899_pir__LWLVA H+-transporting ATP synthase (EC
3.6.1.34) lipid-binding protein - liverwort (Marchantia
polymorpha) chloroplast >gi_11653_emb_CAA28066_ (X04465)

atpH [Marchantia polymorpha]

Seq. No. 292120

Seq. ID LIB3060-017-Q1-K1-A1

Method BLASTX
NCBI GI g115786
BLAST score 504
E value 3.0e-51
Match length 114
% identity 84

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB) (LHCP) >gi_82680_pir__A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea

mays]

Seq. No. 292121

Seq. ID LIB3060-017-Q1-K1-A10

Method BLASTX
NCBI GI g1172977
BLAST score 275
E value 1.0e-24
Match length 93
% identity 57

NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic

ribosomal protein L18 [Arabidopsis thaliana]

Seq. No. 292122

Seq. ID LIB3060-017-Q1-K1-B11

Method BLASTX
NCBI GI g4154281
BLAST score 353
E value 2.0e-33
Match length 73
% identity 90

NCBI Description (AF082347) C13 endopeptidase NP1 precursor [Zea mays]

Seq. No. 292123

Seq. ID LIB3060-017-Q1-K1-D10

Method BLASTX
NCBI GI g131388
BLAST score 280
E value 5.0e-25
Match length 93
% identity 73

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir__S16260

photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum

aestivum]



```
292124
Seq. No.
                  LIB3060-017-Q1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3219781
                  151
BLAST score
E value
                  9.0e-10
Match length
                  60
% identity
                  53
                  CCR4-ASSOCIATED FACTOR 1 (CAF1) >gi_726134 (U21854) cCAF1
NCBI Description
                  protein [Caenorhabditis elegans]
                  292125
Seq. No.
                  LIB3060-018-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q295825
BLAST score
                  331
E value
                  7.0e-31
Match length
                  108
% identity
                   66
NCBI Description (X15819) nitrate reductase apoenzyme [Oryza sativa]
Seq. No.
                   292126
                  LIB3060-018-Q1-K1-C8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q607751
BLAST score
                  58
                   8.0e-24
E value
Match length
                  94
% identity
                   90
                  Urochloa panicoides phosphoenolpyruvate carboxykinase
NCBI Description
                   (PCK1) mRNA, complete cds
Seq. No.
                   292127
                  LIB3060-018-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2623310
BLAST score
                   214
                   4.0e-17
E value
Match length
                   55
                   73
% identity
                   (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3402721 (AC004261) unknown protein [Arabidopsis
                   thaliana]
Seq. No.
                   292128
Seq. ID
                  LIB3060-018-Q1-K1-G10
                  BLASTX
Method
                   g2854153
NCBI GI
BLAST score
                   234
                   2.0e-19
E value
Match length
                   128
                   45
% identity
                  (AF045640) No definition line found [Caenorhabditis
NCBI Description
```

elegans]

292129

Seq. No.

E value



```
LIB3060-018-Q1-K1-H12
Seq. ID
                  BLASTX
Method
                  g2984709 .*
NCBI GI
                  272
BLAST score
                   6.0e-24
E value
                  75
Match length
                   72
% identity
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
NCBI Description
Seq. No.
                   292130
                  LIB3060-018-Q1-K1-H5
Seq. ID
                  BLASTX
Method
                   q4490702
NCBI GI
BLAST score
                   372
                   1.0e-35
E value
                   124
Match length
% identity
                   56
                  (AL035680) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   292131
                   LIB3060-019-Q1-K1-A11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g168608
BLAST score
                   206
E value
                   1.0e-112
Match length
                   354
                   90
% identity
                  Maize 17S ribosomal RNA gene and flanks
NCBI Description
Seq. No.
                   292132
                   LIB3060-019-Q1-K1-B11
Seq. ID
Method
                   BLASTX
                   g3695005
NCBI GI
BLAST score
                   290
E value
                   5.0e-43
Match length
                   120
                   74
% identity
                   (AF038586) pyruvate dehydrogenase kinase isoform 2; PDK2
NCBI Description
                   [Zea mays]
                   292133
Seq. No.
                   LIB3060-019-Q1-K1-B5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g629727
BLAST score
                   180
E value
                   8.0e-14
Match length
                   51
                   67
% identity
                   phosphoenolpyruvate carboxylase (EC 4.1.1.31) - potato
NCBI Description
                   (fragment)
                   292134
Seq. No.
                   LIB3060-019-Q1-K1-C5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1076724
                   219
BLAST score
                   8.0e-18
```



```
Match length
                  60
                  70
% identity
                  LHCI-680, photosystem I antenna protein - barley
NCBI Description
                  >gi 666054 emb CAA59049 (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
                  292135
Seq. No.
                  LIB3060-019-Q1-K1-D1
Seq. ID
Method
                  BLASTX
                  g3176689
NCBI GI
                  226
BLAST score
                  2.0e-18
E value
                  57
Match length
                  72
% identity
                   (AC003671) Contains similarity to ubiquitin
NCBI Description
                  carboxyl-terminal hydrolase 14 gb_Z35927 from S.
                  cerevisiae. [Arabidopsis thaliana]
Seq. No.
                  292136
                  LIB3060-019-Q1-K1-D2
Seq. ID
Method
                  BLASTX -
NCBI GI
                   q2130042
BLAST score
                  148
                   5.0e-10
E value
                   36
Match length
                   78
% identity
                  Mg-chelatase chain Xantha-f - barley >gi 861199 (U26916)
NCBI Description
                   protoporphyrin IX Mg-chelatase subunit precursor [Hordeum
                   vulgare]
                   292137
Seq. No.
                   LIB3060-019-Q1-K1-H2
Seq. ID
                  BLASTX
Method
                   g4558665
NCBI GI
                   173
BLAST score
                   2.0e-12
E value
Match length
                   86
                   45
% identity
                  (AC007063) putative white protein [Arabidopsis thaliana]
NCBI Description
                   292138
Seq. No.
                   LIB3060-020-Q1-K1-B1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g120670
BLAST score
                   293
                   3.0e-36
E value
Match length
                   111
                   77
% identity
```

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi_100879_pir__S06879_glyceraldehyde-3-phosphate

dehydrogenase (EC 1.2.1.12) C - maize

>gi 295853 emb_CAA33620_ (X15596) GAPDH [Zea mays]

Seq. No. 292139

Seq. ID LIB3060-020-Q1-K1-D6

Method BLASTN NCBI GI g4240040

Match length

% identity

97

29



```
BLAST score
                  7.0e-37
E value
                  127
Match length
                  91
% identity
NCBI Description Zea mays ZmGR2c mRNA, complete cds
Seq. No.
                  292140
Seq. ID
                  LIB3060-020-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g1076678
BLAST score
                  266
E value
                  1.0e-23
Match length
                  65
% identity
                  83
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)
                  292141
Seq. No.
                  LIB3060-020-Q1-K1-F3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g313759
BLAST score
                  40
E value
                  1.0e-13
                  75
Match length
                  87
% identity
                  Z.mays hsp 70-1 gene for heat shock protein
NCBI Description
                  292142
Seq. No.
Seq. ID
                  LIB3060-020-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g68029
BLAST score
                  165
                   5.0e-12
E value
                   53
Match length
                   68
% identity
                  phosphoenolpyruvate carboxylase (EC 4.1.1.31) - maize
NCBI Description
                   >qi 22408 emb CAA33317 (X15239) PEP carboxylase [Zea mays]
                   >gi 228619 prf 1807332A phosphoenolpyruvate carboxylase
                   [Zea mays]
                   292143
Seq. No.
                  LIB3060-021-Q1-K1-A6
Seq. ID
Method
                  BLASTN
NCBI GI
                   g169818
BLAST score
                   112
                   3.0e-56
E value
Match length
                  171
% identity
                   92
NCBI Description Rice 25S ribosomal RNA gene
                  292144
Seq. No.
                   LIB3060-021-Q1-K1-A8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3603456
BLAST score
                   466
E value
                   7.0e-47
```



NCBI Description (AF088848) polyubiquitin [Capsicum chinense]

Seq. No. 292145

Seq. ID LIB3060-021-Q1-K1-B8

Method BLASTX
NCBI GI g4314363
BLAST score 182
E value 1.0e-13
Match length 95
% identity 38

NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No.

292146

Seq. ID LIB3060-021-Q1-K1-C1

Method BLASTX
NCBI GI g548605
BLAST score 226
E value 1.0e-18
Match length 73
% identity 71

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR

(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

Seq. No. 292147

Seq. ID LIB3060-021-Q1-K1-D8

Method BLASTX
NCBI GI g2668742
BLAST score 305
E value 5.0e-28
Match length 86
% identity 73

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No.

292148

Seq. ID LIB3060-021-Q1-K1-E6

Method BLASTX
NCBI GI g3789954
BLAST score 324
E value 3.0e-30
Match length 111
% identity 58

NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza

sativa]

Seq. No.

292149

Seq. ID LIB3060-021-Q1-K1-G2

Method BLASTN
NCBI GI g4105122
BLAST score 69
E value 1.0e-30
Match length 121
% identity 89

NCBI Description Zea mays cell wall invertase (incw3) gene, complete cds



```
Seq. No.
Seq. ID
                  LIB3060-021-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  g116526
BLAST score
                  523
                  2.0e-53
E value
Match length
                  108
% identity
                  92
                  PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) (ORF 216)
NCBI Description
                  >gi 82522 pir JQ0251 hypothetical 24.7K protein
                  (rps12-psbN intergenic region) - rice chloroplast
                  >gi_12012_emb_CAA33972_ (X15901) ORF216 [Oryza sativa]
                  >gi 226633 prf 1603356BG ORF 216 [Oryza sativa]
                  292151
Seq. No.
Seq. ID
                  LIB3060-022-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  g2407279
BLAST score
                  240
                  2.0e-20
E value
Match length
                  57
                  88
% identity
NCBI Description (AF017362) aldolase [Oryza sativa]
                  292152
Seq. No.
Seq. ID
                  LIB3060-022-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  g1777312
BLAST score
                  188
E value
                  2.0e-14
Match length
                  95
% identity
                  45
NCBI Description
                  (D30622) novel serine/threonine protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  292153
Seq. ID
                  LIB3060-022-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g3790102
BLAST score
                  269
E value
                  8.0e-24
Match length
                  106
% identity
                  54
NCBI Description
                  (AF095521) pyrophosphate-dependent phosphofructokinase
                  alpha subunit [Citrus X paradisi]
Seq. No.
                  292154
Seq. ID
                  LIB3060-022-Q1-K1-E5
Method
                  BLASTX
                  g3228517
NCBI GI
BLAST score
                  242
```

E value 2.0e-20 Match length 82 % identity 55

(AF007788) ETTIN [Arabidopsis thaliana] NCBI Description

292155 Seq. No.

Method

NCBI GI

BLASTX

g3450842



```
LIB3060-022-Q1-K1-F2
Seq. ID
                  BLASTX
Method
                  g1255199
NCBI GI
BLAST score
                  150
E value
                  1.0e-09
Match length
                  118
% identity
                  30
NCBI Description (U50828) sel-1 gene product [Caenorhabditis elegans]
                  292156
Seq. No.
Seq. ID
                  LIB3060-022-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  g3080396
BLAST score
                  153
E value
                  4.0e-10
Match length
                  66
% identity
                  47
NCBI Description (AL022603) putative protein [Arabidopsis thaliana]
                  292157
Seq. No.
Seq. ID
                  LIB3060-023-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  q1041815
BLAST score
                  160
E value
                  8.0e-11
Match length
                  55
                  51
% identity
NCBI Description (U16721) lipid transfer protein [Oryza sativa]
                  292158
Seq. No.
Seq. ID
                  LIB3060-023-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g115771
BLAST score
                  500
E value
                  8.0e-51
Match length
                  106
% identity
                  88
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-1) (LHCP) >gi 82682 pir S04453 chlorophyll
                  a/b-binding protein precursor - maize
                  >gi_22224_emb_CAA32900 (X14794) chlorophyll a/b-binding
                  preprotein (AA 1 - 262) [Zea mays]
Seq. No.
                  292159
Seq. ID
                  LIB3060-024-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  q168643
BLAST score
                  309
E value
                  2.0e-28
Match length
                  101
% identity
NCBI Description (L02540) NADPH HC-toxin reductase [Zea mays]
Seq. No.
                  292160
                  LIB3060-024-Q1-K1-B3
Seq. ID
```



```
BLAST score
                  1.0e-15
E value
                  138
Match length
                  44
% identity
                  (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                  sativa]
                  292161
Seq. No.
                  LIB3060-024-Q1-K1-C10
Seq. ID
                  BLASTX
Method
                  g120657
NCBI GI
BLAST score
                  220
                  4.0e-18
E value
                  95
Match length
                  55
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
NCBI Description
                  CHLOROPLAST >gi 66024 pir DEZMG3
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                   (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                  maize >gi_168479 (M18976) glyceraldehyde-3-phosphate
                  dehydrogenase [Zea mays] >gi 763035 emb CAA33455 (X15408)
                  glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
                  292162
Seq. No.
                  LIB3060-024-Q1-K1-F12
Seq. ID
                  BLASTX
Method
                  g2651310
NCBI GI
BLAST score
                  166
                  1.0e-11
E value
                  63
Match length
                   52
% identity
                  (AC002336) putative PTR2-B peptide transporter [Arabidopsis
NCBI Description
                  thaliana]
                   292163
Seq. No.
Seq. ID
                  LIB3060-024-Q1-K1-H1
                   BLASTX
Method
NCBI GI
                   g2511541
BLAST score
                   440
                   1.0e-43
E value
                   100
Match length
                   84
% identity
NCBI Description (AF020787) DNA-binding protein GBP16 [Oryza sativa]
Seq. No.
                   292164
                   LIB3060-025-Q1-K1-C8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2326947
BLAST score
                   198
E value
                   8.0e-20
                   121
Match length
                   47
% identity
                  (Z50801) Chlorophyll a/b-binding protein CP29 precursor
NCBI Description
                   [Zea mays]
```

40693

292165

LIB3060-025-Q1-K1-D1

Seq. No.

Seq. ID

NCBI GI

BLAST score

q3355308

302



```
Method
                  BLASTX
NCBI GI
                  g3169179
BLAST score
                  151
                  6.0e-10
E value
Match length
                  38
% identity
                  68
                  (AC004401) putative N-acetyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                  292166
Seq. No.
Seq. ID
                  LIB3060-025-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g2586083
BLAST score
                  264
                  4.0e-23
E value
Match length
                  132
% identity
                  (U72725) receptor kinase-like protein [Oryza
NCBI Description
                  longistaminata]
                  292167
Seq. No.
Seq. ID
                  LIB3060-025-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  q2262107
BLAST score
                  167
                  1.0e-11
E value
Match length
                  41
% identity
                  (AC002343) Ser/Thr protein kinase isolog [Arabidopsis
NCBI Description
                  thaliana]
                  292168
Seq. No.
Seq. ID
                  LIB3060-025-Q1-K1-F2
Method
                  BLASTX
                  g2129627
NCBI GI
BLAST score
                  484
E value
                  8.0e-49
Match length
                  143
                  60
% identity
NCBI Description K+-channel - Arabidopsis thaliana >gi 1165000 emb CAA63601_
                  (X93022) K+ channel [Arabidopsis thaliana]
Seq. No.
                  292169
Seq. ID
                  LIB3060-025-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  g2980804
BLAST score
                  148
E value
                  2.0e-09
Match length
                  44
                  75
% identity
NCBI Description (AL022197) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  292170
                  LIB3060-025-Q1-K1-H5
Seq. ID
Method
                  BLASTX
```

Match length

41



```
E value
                  1.0e-27
                  98
Match length
% identity
                  60
                  (AJ009695) wall-associated kinase 4 [Arabidopsis thaliana]
NCBI Description
                  292171
Seq. No.
Seq. ID
                  LIB3060-025-Q1-K1-H8
Method
                  BLÄSTX
NCBI GI
                  g4336436
BLAST score
                  355
E value
                  1.0e-33
Match length
                  110
                   65
% identity
                  (AF092432) protein phosphatase type 2C [Lotus japonicus]
NCBI Description
                  292172
Seq. No.
Seq. ID
                  LIB3060-026-Q1-K1-A1
                  BLASTX
Method
NCBI GI
                  g479256
BLAST score
                  205
E value
                   4.0e-16
                   99
Match length
                   49
% identity
                  ribosomal protein L12.1, chloroplast - rye
NCBI Description
                  >qi 1345575 emb CAA48400 (X68325) ribosomal protein L12
                   [Secale cereale]
                   292173
Seq. No.
Seq. ID
                  LIB3060-026-Q1-K1-B11
                  {\tt BLASTX}
Method
NCBI GI
                   g631955
BLAST score
                   276
                   2.0e-24
E value
Match length
                   47
                   98
% identity
                  chlorophyll a/b binding protein type II (LHCI) - Lolium
NCBI Description
                   temulentum L
                   292174
Seq. No.
Seq. ID
                   LIB3060-026-Q1-K1-B6
Method
                   BLASTX
NCBI GI
                   q82080
BLAST score
                   307
E value
                   3.0e-28
                   80
Match length
% identity
                   chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                   >gi 226872 prf 1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
Seq. No.
                   292175
                   LIB3060-026-Q1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g401114
                   193
BLAST score
                   9.0e-15
E value
```



% identity SUCROSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE NCBI Description GLUCOSYLTRANSFERASE) >gi 82726 pir JQ1329 sucrose-phosphate synthase (EC 2.4.1.14) - maize >gi 168626 (M97550) sucrose phosphate synthase [Zea mays] Seq. No. 292176 Seq. ID LIB3060-026-Q1-K1-F3 Method BLASTX NCBI GI q3641837 BLAST score 290 E value 4.0e-26 Match length 67 84 % identity NCBI Description (AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana] 292177 Seq. No. LIB3060-026-Q1-K1-F5 Seq. ID Method BLASTX NCBI GI g3641837 BLAST score 283 E value 2.0e-25 77 Match length 75 % identity NCBI Description (AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana] 292178 Seq. No. Seq. ID LIB3060-026-Q1-K1-H6 Method BLASTX NCBI GI g115815 BLAST score 454 2.0e-45 E value Match length 105 83 % identity NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-M9) (LHCP) >gi 100866 pir S13098 chlorophyll a/b-binding protein precursor - maize >qi 22355 emb CAA39376 (X55892) light-harvesting chlorophyll a/b binding protein [Zea mays] Seq. No. 292179 Seq. ID LIB3060-027-Q1-K1-A10 Method BLASTX

NCBI GI q4539677 BLAST score 255 E value 5.0e-22 Match length 95 % identity 54

NCBI Description (AF061282) patatin-like protein [Sorghum bicolor]

Seq. No. Seq. ID

LIB3060-027-Q1-K1-G3

292180

BLASTX Method g1237250 NCBI GI BLAST score 271

```
E value
                   7.0e-24
Match length
                   135
                   39
% identity
NCBI Description (X96784) cytochrome P450 [Nicotiana tabacum]
                   292181
Seq. No.
Seq. ID
                   LIB3060-027-Q1-K1-G8
                   BLASTX
Method
NCBI GI
                   g121446
BLAST score
                   233
E value
                   1.0e-19
                   114
Match length
% identity
                   48
                   FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE PRECURSOR
NCBI Description
                   (FD-GOGAT) >gi_100877_pir__A38596 glutamate synthase (ferredoxin) (EC 1.4.7.1) - maize >gi_168477 (M59190)
                   ferredoxin-dependent glutamate synthase [Zea mays]
                   292182
Seq. No.
Seq. ID
                   LIB3060-028-Q1-K1-B3
Method
                   BLASTX
NCBI GI
                   g1352830
BLAST score
                   182
E value
                   1.0e-17
                   81
Match length
                   60
% identity
                   VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
NCBI Description
                   SUBUNIT) >gi 1049253 (U36436) vacuolar ATPase 69 kDa
                   subunit [Zea mays]
Seq. No.
                   292183
                   LIB3060-028-Q1-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g21693
BLAST score
                   184
E value
                   9.0e-14
Match length
                   66
% identity
                   48
NCBI Description (X66012) cathepsin B [Triticum aestivum]
                   292184
Seq. No.
                   LIB3060-028-Q1-K1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4468807
BLAST score
                   214
E value
                   3.0e-17
Match length
                   89
```

43 % identity

NCBI Description (AL035601) cytochrome P450 monooxygenase-like protein

[Arabidopsis thaliana]

Seq. No. 292185

Seq. ID LIB3060-028-Q1-K1-H4

Method BLASTN NCBI GI g175854 BLAST score 41 8.0e-14 E value



Match length 49 % identity 96

NCBI Description O.sativa 28S large subunit rRNA, 5' end

Seq. No.

292186

Seq. ID LIB3060-029-Q1-K1-A6

Method BLASTX
NCBI GI g3080389
BLAST score 177
E value 8.0e-13
Match length 36
% identity 92

NCBI Description (AL022603) putative membrane associated protein

[Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3060-029-Q1-K1-B4

292187

Method BLASTX
NCBI GI g115815
BLAST score 518
E value 6.0e-53
Match length 122
% identity 84

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-M9) (LHCP) >gi_100866_pir__S13098 chlorophyll

a/b-binding protein precursor - maize

>gi_22355_emb_CAA39376_ (X55892) light-harvesting

chlorophyll a/b binding protein [Zea mays]

Seq. No. 292188

Seq. ID LIB3060-029-Q1-K1-C8

Method BLASTX
NCBI GI g4325282
BLAST score 208
E value 2.0e-16
Match length 62
% identity 60

NCBI Description (AF123310) NAC domain protein NAM [Arabidopsis thaliana]

>gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM

[Arabidopsis thaliana]

Seq. No. 292189

Seq. ID LIB3060-029-Q1-K1-G12

Method BLASTX
NCBI GI g3080738
BLAST score 258
E value 2.0e-22
Match length 85
% identity 61

NCBI Description (U77365) pasticcino 1-A [Arabidopsis thaliana]

Seq. No. 292190

Seq. ID LIB3060-029-Q1-K1-G9

Method BLASTX
NCBI GI g115771
BLAST score 686
E value 1.0e-72



Match length % identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll

a/b-binding protein precursor - maize

>gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

292191 Seq. No.

Seq. ID LIB3060-029-Q1-K1-H9

Method BLASTX NCBI GI q479406 BLAST score 543 8.0e-56 E value 114 Match length 86 % identity

chlorophyll a/b-binding protein - garden pea NCBI Description

>gi 20671 emb CAA49149 (X69215) chlorophyll a/b-binding

protein [Pisum sativum]

Seq. No. 292192

Seq. ID LIB3060-030-Q1-K1-A10

Method BLASTX g2570517 NCBI GI BLAST score 196 4.0e-15 E value 79 Match length % identity 63

NCBI Description (AF022741) thioredoxin F isoform [Oryza sativa]

Seq. No. 292193

Seq. ID LIB3060-030-Q1-K1-B2

Method BLASTX NCBI GI q3881978 158 BLAST score E value 1.0e-10 Match length 52 % identity

(Y11348) annexin-like protein [Medicago sativa] NCBI Description

Seq. No.

292194

Seq. ID LIB3060-030-Q1-K1-B9

Method BLASTX NCBI GI q131388 BLAST score 189 E value 1.0e-14 Match length 75

% identity

OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD NCBI Description

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi 100831_pir__S16260

photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi 21844 emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum

aestivum]

Seq. No. 292195



```
LIB3060-030-Q1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115771
BLAST score
                  457
                  7.0e-46
E value
Match length
                  92
% identity
                  92
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-1) (LHCP) >gi 82682_pir__S04453 chlorophyll
                  a/b-binding protein precursor - maize
                  >gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding
                  preprotein (A\overline{A} 1 - 262) [Zea mays]
                  292196
Seq. No.
Seq. ID
                  LIB3060-030-Q1-K1-D12
                  BLASTN
Method
NCBI GI
                  g4321761
BLAST score
                  114
E value
                  2.0e-57
Match length
                  126
                  98
% identity
NCBI Description Zea mays transcription factor MYC7E mRNA, partial cds
                  292197
Seq. No.
Seq. ID
                  LIB3060-030-Q1-K1-D6
                  BLASTX
Method
                  g4154281
NCBI GI
BLAST score
                  289
                  3.0e-26
E value
Match length
                  95
% identity
NCBI Description (AF082347) C13 endopeptidase NP1 precursor [Zea mays]
Seq. No.
                  292198
                  LIB3060-030-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115815
BLAST score
                  421
                  1.0e-41
E value
Match length
                  96
                  84
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-M9) (LHCP) >gi 100866 pir S13098 chlorophyll
                  a/b-binding protein precursor - maize
                  >gi 22355 emb CAA39376 (X55892) light-harvesting
                   chlorophyll a/b binding protein [Zea mays]
Seq. No.
                  292199
Seq. ID
                  LIB3060-030-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g3258575
```

Method BLASTX
NCBI GI g3258575
BLAST score 480
E value 2.0e-48
Match length 131
% identity 72

NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]

```
Seq. No.
Seq. ID
                  LIB3060-032-Q1-K1-B8
Method
                  BLASTN
NCBI GI
                  g643596
BLAST score
                  58
                  6.0e-24
E value
Match length
                  58
                  100
% identity
NCBI Description Corn mRNA for cysteine proteinase, clone CCP, complete cds
                  292201
Seq. No.
Seq. ID
                  LIB3060-032-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  q115771
BLAST score
                  179
E value
                  3.0e-13
                  77
Match length
                  52
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-1) (LHCP) >gi 82682 pir S04453 chlorophyll
                  a/b-binding protein precursor - maize
Seq. No.
                  292202
Seq. ID
                  LIB3060-032-Q1-K1-E5
```

```
BLASTX
Method
NCBI GI
                   g3122914
BLAST score
                   394
                   4.0e-50
E value
Match length
                   122
                   80
% identity
```

VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS) NCBI Description >qi 1890130 (U89986) valyl tRNA synthetase [Arabidopsis

thaliana]

292203

```
Seq. ID
                   LIB3060-032-Q1-K1-G6
Method
                   BLASTX
NCBI GI
                   g266578
BLAST score
                   187
                   3.0e-14
E value
Match length
                   56
% identity
                   57
```

Seq. No.

BLAST score

METALLOTHIONEIN-LIKE PROTEIN 1 >qi 100898 pir S17560 NCBI Description metallothionein-like protein - maize >gi 236730 bbs 57629 (S57628) metallothionein homologue [Zea mays, Peptide, 76

aa] [Zea mays] >gi 559536 emb CAA57676_ (X82186)

metallothionein- like protein [Zea mays]

>gi 228095 prf 1717215A metallothionein-like protein [Zea

mays]

Seq. No. 292204 Seq. ID LIB3060-034-Q1-K1-F2 Method BLASTN NCBI GI g22263

76



```
E value
                  7.0e-35
Match length
                  80
                  99
% identity
NCBI Description Z.mays Ds insertion element
Seq. No.
                  292205
                  LIB3060-034-Q1-K1-F7
Seq. ID
Method
                  BLASTX
                  q1086586
NCBI GI
BLAST score
                  146
E value
                  8.0e-10
Match length
                  122
                  34
% identity
NCBI Description (U41007) similar to G beta repeats (PROSITE:PS00670)
                  [Caenorhabditis elegans]
Seq. No.
                  292206
                  LIB3060-034-Q1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1680686
BLAST score
                  321
E value
                  1.0e-29
Match length
                  70
                  87
% identity
NCBI Description (U51330) rust resistance kinase Lr10 [Triticum aestivum]
                  292207
Seq. No.
Seq. ID
                  LIB3060-035-Q1-K1-A4
                  BLASTX
Method
NCBI GI
                  g115771
BLAST score
                  349
E value
                  3.0e-42
Match length
                  90
% identity
                  91
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-1) (LHCP) >gi 82682 pir S04453 chlorophyll
                  a/b-binding protein precursor - maize
                  >gi 22224 emb CAA32900 (X14794) chlorophyll a/b-binding
                  preprotein (AA 1 - 262) [Zea mays]
Seq. No.
                  292208
Seq. ID
                  LIB3060-035-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  q451193
BLAST score
                  175
E value
                  1.0e-12
Match length
                  70
% identity
                  50
NCBI Description (L28008) wali7 [Triticum aestivum]
                  >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]
                  292209
Seq. No.
Seq. ID
                  LIB3060-035-Q1-K1-C8
```

Method BLASTX
NCBI GI g2129677
BLAST score 180
E value 3.0e-13



```
59
Match length
% identity
                  probablel N-acetyltransferase hookless 1 - Arabidopsis
NCBI Description
                  thaliana >gi_1277090 (U50399) putative N-acetyltransferase
                  hookless1 [Arabidopsis thaliana] >gi_1277092 (U50400)
                  putative N-acetyltransferase hookless1 [Arabidopsis
                  thaliana] >gi_4468983_emb_CAB38297 (AL035605) probable
                  N-acetyltransferase hookless 1 [Arabidopsis thaliana]
                  292210
Seq. No.
Seq. ID
                  LIB3060-035-Q1-K1-C9
                  \mathtt{BLASTX}
Method
NCBI GI
                  g4097549
                  153
BLAST score
                  5.0e-10
E value
                  62
Match length
                  48
% identity
NCBI Description (U64907) ATFP4 [Arabidopsis thaliana]
                  292211
Seq. No.
Seq. ID
                  LIB3060-035-Q1-K1-D9
                  BLASTN
Method
NCBI GI
                  g998429
BLAST score
                  34
                  2.0e-09
E value
Match length
                  38
% identity
                  97
                  GRF1=general regulatory factor [Zea mays, XL80, Genomic,
NCBI Description
                  5348 nt]
Seq. No.
                  292212
                  LIB3060-035-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115815
BLAST score
                  473
E value
                  1.0e-47
                  102
Match length
% identity
                  86
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-M9) (LHCP) >gi 100866 pir S13098 chlorophyll
                  a/b-binding protein precursor - maize
                  >gi 22355 emb CAA39376 (X55892) light-harvesting
                  chlorophyll a/b binding protein [Zea mays]
```

Seq. No. 292213

Seq. ID LIB3060-035-Q1-K1-F11

Method BLASTX q2306981 NCBI GI BLAST score 159 3.0e-17 E value Match length 109 % identity

NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]

Seq. No. 292214

LIB3060-035-Q1-K1-F7 Seq. ID

Method BLASTX



```
NCBI GI
                  g3913427
BLAST score
                  330
                  7.0e-31
E value
Match length
                  126
                  58
% identity
NCBI Description
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                  (SAMDC) >gi 1532073 emb CAA69075 (Y07767)
                  S-adenosylmethionine decarboxylase [Zea mays]
Seq. No.
                  292215
Seq. ID
                  LIB3060-035-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g141608
BLAST score
                  330
E value
                  9.0e-31
Match length
                  124
% identity
                  57
                  ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943 pir S15655
NCBI Description
                  zein, 19K - maize >gi 22446 emb CAA37651 (X53582) 19 kDa
                  zein [Zea mays]
Seq. No.
                  292216
Seq. ID
                  LIB3060-036-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  q4586378
BLAST score
                  370
E value
                  2.0e-35
Match length
                  98
% identity
NCBI Description (AB021746) nicotianamine synthase 1 [Oryza sativa]
Seq. No.
                  292217
Seq. ID
                  LIB3060-036-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  q4115938
BLAST score
                  343
E value
                  2.0e-32
Match length
                  110
% identity
                  69
                  (AF118223) contains similarity several bacterial
NCBI Description
                  glutathione-regulated potassium efflux system proteins
                  [Arabidopsis thaliana]
Seq. No.
                  292218
                  LIB3060-036-Q1-K1-D1
Seq. ID
Method
                  BLASTX
                  g3341747
                  311
                  1.0e-28
```

NCBI GI BLAST score E value Match length 117 % identity

NCBI Description (AF077130) receptor-like protein kinase [Oryza sativa]

Seq. No. 292219

LIB3060-036-Q1-K1-G10 Seq. ID

Method BLASTX NCBI GI g283038



BLAST score 461 E value 3.0e-46 Match length 106 % identity 84

NCBI Description chlorophyll a/b-binding protein (cab-m7) precursor - maize

>gi 22230 emb CAA37474_ (X53398) light harvesting

chlorophyll a /b binding protein [Zea mays]

Seq. No. 292220

Seq. ID LIB3060-036-Q1-K1-G11

Method BLASTX
NCBI GI g2627181
BLAST score 495
E value 4.0e-50
Match length 119
% identity 76

NCBI Description (D89619) cycloartenol synthase [Pisum sativum]

Seq. No. 292221

Seq. ID LIB3060-036-Q1-K1-H1

Method BLASTX
NCBI GI g2668742
BLAST score 208
E value 2.0e-24
Match length 81
% identity 81

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 292222

Seq. ID LIB3060-036-Q1-K1-H7

Method BLASTX
NCBI GI g4262224
BLAST score 271
E value 6.0e-24
Match length 84
% identity 64

NCBI Description (AC006200) putative amino acid or GABA permease

[Arabidopsis thaliana]

Seq. No. 292223

Seq. ID LIB3060-037-Q1-K1-A11

Method BLASTX
NCBI GI g120663
BLAST score 361
E value 2.0e-34
Match length 113
% identity 61

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR,

CHLOROPLAST >gi 66027 pir DEPMNB

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - garden pea >gi_309671 (M55147) glyceraldehyde-3-phosphate

dehydrogenase B subunit [Pisum sativum]

Seq. No. 292224

Seq. ID LIB3060-037-Q1-K1-C6

Method BLASTN



NCBI GI g342582 BLAST score 179 E value 4.0e-96 Match length 295 % identity 94

NCBI Description Maize chloroplast cytochrome b559 alpha- and beta-subunit

(psbE and F), cytochrome b6-f complex (petE), and

photosystem II polypeptide, complete cds, Pro-tRNA and

Trp-tRNA

Seq. No. 292225

Seq. ID LIB3060-037-Q1-K1-D2

Method BLASTX
NCBI GI g116527
BLAST score 164
E value 3.0e-11
Match length 48
% identity 52

NCBI Description PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) (ORF 196)

>gi_1143166 (U32397) ClpP protease [Nicotiana tabacum]
>gi_2924270 emb_CAA77422 (Z00044) ATP-dependent protease

proteolytic subuni [Nicotiana tabacum]

Seq. No. 292226

Seq. ID LIB3060-037-Q1-K1-F12

Method BLASTX
NCBI GI g4262240
BLAST score 325
E value 3.0e-30
Match length 102
% identity 61

NCBI Description (AC006200) putative stress protein [Arabidopsis thaliana]

Seq. No. 292227

Seq. ID LIB3060-038-Q1-K1-D1

Method BLASTX
NCBI GI g2501189
BLAST score 281
E value 1.0e-25
Match length 67
% identity 87

NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR

>gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
- maize >gi_596078 (U17350) thiamine biosynthetic enzyme

[Zea mays]

Seq. No. 292228

Seq. ID LIB3060-038-Q1-K1-D12

Method BLASTX
NCBI GI g2244786
BLAST score 188
E value 3.0e-14
Match length 55
% identity 67

NCBI Description (Z97335) ribonucleoprotein homolog [Arabidopsis thaliana]

Seq. No. 292229

Match length

% identity

79 48



```
LIB3060-038-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4416302
BLAST score
                  407
E value
                  8.0e-40
Match length
                  79
                  97
% identity
                  (AF105716) copia-type pol polyprotein [Zea mays]
NCBI Description
                  292230
Seq. No.
Seq. ID
                  LIB3060-038-Q1-K1-G6
Method
                  BLASTN
NCBI GI
                  g451192
BLAST score
                  45
                  3.0e-16
E value
Match length
                  109
% identity
                  85
NCBI Description Triticum aestivum (wali7) mRNA, 3' end, partial cds
                  292231
Seq. No.
                  LIB3060-039-Q1-K1-C4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g236729
BLAST score
                  40
E value
                  4.0e-13
Match length
                  174
                  86
% identity
NCBI Description metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]
                  292232
Seq. No.
Seq. ID
                  LIB3060-039-Q1-K1-D11
                  BLASTN
Method
NCBI GI
                  g2463566
BLAST score
                  67
E value
                  3.0e-29
Match length
                  103
% identity
                  91
NCBI Description Zea mays mRNA for squalene synthase, complete cds
Seq. No.
                  292233 -
Seq. ID
                  LIB3060-039-Q1-K1-E4
Method
                  BLASTN
NCBI GI
                  q168520
BLAST score
                  48
                  2.0e-18
E value
Match length
                  124
% identity
                  85
NCBI Description Maize glyceraldehyde-3-phosphate dehydrogenase mRNA, 5' end
                  292234
Seq. No.
                  LIB3060-039-Q1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g129231
BLAST score
                  187
                  4.0e-14
E value
```



NCBI Description ORYZAIN ALPHA CHAIN PRECURSOR >gi_67644_pir_KHRZOA oryzain

(EC 3.4.22.-) alpha precursor - rice

>gi_218181_dbj_BAA14402_ (D90406) oryzain alpha precursor

[Oryza sativa]

Seq. No. 292235

Seq. ID LIB3060-039-Q1-K1-G1

Method BLASTX
NCBI GI g115772
BLAST score 167
E value 1.0e-11
Match length 48
% identity 75

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll

a/b-binding protein 1R precursor - rice

>gi_20178_emb_CAA32108_ (X13908) chlorophyll a/b-binding

preprotein (AA -31 to 235) [Oryza sativa]

Seq. No. 292236

Seq. ID LIB3060-039-Q1-K1-H1

Method BLASTX
NCBI GI g116526
BLAST score 172
E value 6.0e-16
Match length 72
% identity 65

NCBI Description PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) (ORF 216)

>gi_82522_pir__JQ0251 hypothetical 24.7K protein
(rps12-psbN intergenic region) - rice chloroplast
>gi_12012_emb_CAA33972_ (X15901) ORF216 [Oryza sativa]

>gi_226633_prf__1603356BG ORF 216 [Oryza sativa]

Seq. No. 292237

Seq. ID LIB3060-039-Q1-K1-H8

Method BLASTX
NCBI GI g1345683
BLAST score 314
E value 4.0e-29
Match length 80
% identity 76

NCBI Description CATALASE ISOZYME 3 >gi_487045_pir__S37379 catalase (EC

1.11.1.6) 3 - maize $>g\bar{i}$ 16843 $\bar{7}$ (L $\bar{05}$ 934) catalase [Zea mays]

Seq. No. 292238

Seq. ID LIB3060-040-Q1-K1-B11

Method BLASTX
NCBI GI g1076809
BLAST score 212
E value 1.0e-17
Match length 43
% identity 95

NCBI Description H+-transporting ATPase (EC 3.6.1.35) - maize

>gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase

[Zea mays]

Seq. No. 292239

Seq. ID

```
LIB3060-040-Q1-K1-B9
Seq.
                  BLASTN
Meth
                  g1181672
NCB1
                  52
BLAS
       core
                  2.0e-20
E va
                  116
       ength
Matc
% ia__ity
NCBI Description
                  87
                  Sorghum bicolor heat shock protein 70 cognate (hsc70) mRNA,
                  partial cds
                  292240
Seq. No.
Seq. ID
                  LIB3060-040-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g168435
                  196
BLAST score
                   4.0e-15
E value
                   43
Match length
                   88
% identity
NCBI Description (M33103) catalase isozyme 3 (EC 1.11.1.6) [Zea mays]
                   292241
Seq. No.
                  LIB3060-040-Q1-K1-D11
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4249402
BLAST score
                   217
                   1.0e-17
E value
Match length
                   128
                   42
% identity
                  (AC006072) unknown protein [Arabidopsis thaliana]
NCBI Description
                   292242
Seq. No.
                   LIB3060-040-Q1-K1-E8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g113621
BLAST score
                   287
                   2.0e-26
E value
Match length
                   61
% identity
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
NCBI Description
                   >gi 68196 pir ADZM fructose-bisphosphate aldolase (EC
                   4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
                   [Zea mays] >gi 295850_emb_CAA31366_ (X12872) fructose
                   bisphosphate aldolase [Zea mays] >gi 225624 prf 1307278A
                   cytoplasmic aldolase [Zea mays]
                   292243
Seq. No.
                   LIB3060-040-Q1-K1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4249402
BLAST score
                   197
                   1.0e-15
E value
Match length
                   58
% identity
                  (AC006072) unknown protein [Arabidopsis thaliana]
NCBI Description
                   292244
Seq. No.
```

40709

LIB3060-040-Q1-K1-G6



```
Method
                  BLASTN
NCBI GI
                  g22464
BLAST score
                  87
                   4.0e-41
E value
                  151
Match length
                  89
% identity
                  Maize rbcS gene for ribulose-1,5-bisphosphate
NCBI Description
                  carboxylase/oxygenase small subunit (EC 4.1.1.39)
                  292245
Seq. No.
Seq. ID
                  LIB3060-041-Q1-K1-B12
                  {\tt BLASTX}
Method
NCBI GI
                  g131388
                  158
BLAST score
                   6.0e-11
E value
Match length
                   64
                   56
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                   SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                   THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir__S16260
                  photosystem II oxygen-evolving complex protein 1 - common
                  wheat x Sanduri wheat >gi_21844 emb_CAA40670 (X57408)
                   33kDa oxygen evolving protein of photosystem II [Triticum
                   aestivum]
                   292246
Seq. No.
Seq. ID
                  LIB3060-041-Q1-K1-F7
                   BLASTX
Method
                   g3914465
NCBI GI
                   266
BLAST score
E value
                   2.0e-23
Match length
                   85
                   67
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                   >qi 2981207 (AF052076) photosystem I complex PsaH subunit
                   precursor [Zea mays]
                   292247
Seq. No.
                   LIB3060-041-Q1-K1-F8
Seq. ID
                   {\tt BLASTX}
Method
                   q3785994
NCBI GI
BLAST score
                   209
E value
                   1.0e-16
                   104
Match length
                   44
% identity
NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   292248
                   LIB3060-041-Q1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q168523
```

Method BLASTX
NCBI GI g168523
BLAST score 420
E value 2.0e-41
Match length 122
% identity 71

NCBI Description

(M31483) glyceraldehyde-3-phosphate dehydrogenase precursor



[Zea mays]

```
292249
Seq. No.
                  LIB3060-041-Q1-K1-H5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q902200
                  55
BLAST score
                  2.0e-22
E value
                  187
Match length
                  83
% identity
NCBI Description Z.mays complete chloroplast genome
                  292250
Seq. No.
                  LIB3060-042-Q1-K1-A2
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4490325
BLAST score
                   146
                   1.0e-09
E value
Match length
                   38
                   68
% identity
NCBI Description (AL035656) hypothetical protein [Arabidopsis thaliana]
                   292251
Seq. No.
Seq. ID
                   LIB3060-042-Q1-K1-B10
                   BLASTX
Method
                   g3688186
NCBI GI
                   232
BLAST score
                   2.0e-19
E value
                   102
Match length
                   44
% identity
NCBI Description (AL031804) putative protein [Arabidopsis thaliana]
                   292252
Seq. No.
                   LIB3060-042-Q1-K1-C11
Seq. ID
                   BLASTX
Method
                   q2791834
NCBI GI
                   181
BLAST score
E value
                   8.0e-15
                   77
Match length
                   62
% identity
                  (AF041463) elongation factor 1-alpha [Manihot esculenta]
NCBI Description
                   292253
Seq. No.
                   LIB3060-042-Q1-K1-C4
Seq. ID
                   BLASTN
Method
                   q4105562
NCBI GI
BLAST score
                   190
                   1.0e-103
E value
Match length
                   256
                   94
 % identity
                   Zea mays zeta-carotene desaturase precursor, mRNA, complete
NCBI Description
 Seq. No.
                   292254
                   LIB3060-042-Q1-K1-D9
 Seq. ID
 Method
                   BLASTX
```

40711

g120657

NCBI GI



BLAST score 182 E value 1.0e-13 Match length 95 % identity 45

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,

CHLOROPLAST >gi 66024 pir DEZMG3

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) A precursor, chloroplast maize >gi_168479 (M18976) glyceraldehyde-3-phosphate
dehydrogenase [Zea mays] >gi_763035_emb_CAA33455_ (X15408)

glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No. 292255

Seq. ID LIB3060-042-Q1-K1-E12

Method BLASTX
NCBI GI g3687235
BLAST score 254
E value 7.0e-22
Match length 77
% identity 66

NCBI Description (AC005169) putative copia-like transposable element

[Arabidopsis thaliana]

Seq. No. 292256

Seq. ID LIB3060-042-Q1-K1-E6

Method BLASTX
NCBI GI g3694807
BLAST score 302
E value 7.0e-28
Match length 85
% identity 72

NCBI Description (AF055898) alanine aminotransferase [Zea mays]

Seq. No. 292257

Seq. ID LIB3060-042-Q1-K1-E7

Method BLASTX
NCBI GI g730510
BLAST score 234
E value 7.0e-20
Match length 87
% identity 55

NCBI Description RAS-RELATED PROTEIN RIC1 > gi 542150 pir S38740 GTP-binding

protein - rice >gi_432607_gb_AAB28535_ (S66160) ras-related GTP binding protein possessing GTPase activity=ric1 [Oryza sativa=rice, var. Yamahoushi, callus, Peptide, 202 aa]

[Oryza sativa]

Seq. No. 292258

Seq. ID LIB3060-042-Q1-K1-F11

Method BLASTN
NCBI GI g5579440
BLAST score 56
E value 7.0e-23
Match length 132
% identity 86

NCBI Description Zea mays histone acetyltransferase HAT B mRNA, complete cds



```
Seq. No.
                  LIB3060-042-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131388
BLAST score
                  168
E value
                  5.0e-12
Match length
                  66
                  71
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260
                  photosystem II oxygen-evolving complex protein 1 - common
                  wheat x Sanduri wheat >gi 21844 emb CAA40670 (X57408)
                  33kDa oxygen evolving protein of photosystem II [Triticum
                  aestivum]
Seq. No.
                  292260
Seq. ID
                  LIB3060-042-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  g4049399
BLAST score
                  215
E value
                  3.0e-17
Match length
                  118
% identity
                  38
NCBI Description (Y09581) FRO2 [Arabidopsis thaliana]
                  292261
Seq. No.
                  LIB3060-042-Q1-K1-H7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g11957
BLAST score
                  163
E value
                  1.0e-86
Match length
                  195
% identity
                  48
NCBI Description Rice complete chloroplast genome
Seq. No.
                  292262
Seq. ID
                  LIB3060-043-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  q131388
BLAST score
                  214
E value
                  2.0e-17
Match length
                  110
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
```

THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260

photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi 21844 emb CAA40670 (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum

aestivum]

Seq. No.

292263

LIB3060-043-Q1-K1-B3 Seq. ID

Method BLASTX NCBI GI g731426 BLAST score 321



E value 1.0e-29 Match length 109 % identity 51

NCBI Description HYPOTHETICAL 56.5 KD PROTEIN IN HXT8 5'REGION AND IN PAU6

5'REGION >gi_1077619_pir__S50519 hypothetical protein YEL070w - yeast (Saccharomyces cerevisiae) >gi_603248

(U18795) Yel070wp [Saccharomyces cerevisiae] >gi_1302610_emb_CAA96356_ (Z71688) ORF YNR073c

[Saccharomyces cerevisiae]

Seq. No. 292264

Seq. ID LIB3060-043-Q1-K1-B5

Method BLASTX
NCBI GI g112994
BLAST score 403
E value 2.0e-39
Match length 86
% identity 94

NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN

>gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)

ABA-inducible gene protein [Zea mays]

>gi 226091 prf 1410284A abscisic acid inducible gene [Zea

mays]

Seq. No. 292265

Seq. ID LIB3060-043-Q1-K1-B9

Method BLASTX
NCBI GI g3885896
BLAST score 496
E value 3.0e-50
Match length 115
% identity 83

NCBI Description (AF093636) plastocyanin precursor [Oryza sativa]

Seq. No. 292266

Seq. ID LIB3060-043-Q1-K1-C7

Method BLASTN
NCBI GI g607751
BLAST score 43
E value 5.0e-15
Match length 59
% identity 93

NCBI Description Urochloa panicoides phosphoenolpyruvate carboxykinase

(PCK1) mRNA, complete cds

Seq. No. 292267

Seq. ID LIB3060-043-Q1-K1-H6

Method BLASTX
NCBI GI g3747111
BLAST score 148
E value 2.0e-09
Match length 52
% identity 50

NCBI Description (AF095641) MTN3 homolog [Arabidopsis thaliana]

Seq. No. 292268



```
LIB3060-044-Q1-K1-B6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2443886
                  254
BLAST score
                  8.0e-22
E value
                  70
Match length
% identity
NCBI Description (AC002294) Unknown protein [Arabidopsis thaliana]
                  292269
Seq. No.
                  LIB3060-044-Q1-K1-C3
Seq. ID
Method
                  BLASTN
                  g3819221
NCBI GI
                  71
BLAST score
                  1.0e-31
E value
                  239
Match length
                  82
% identity
NCBI Description Hordeum vulgare partial mRNA; clone cMWG0721
                  292270
Seq. No.
                  LIB3060-044-Q1-K1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3928543
BLAST score
                  143
                  5.0e-09
E value
                  44
Match length
                  52
% identity
                  (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                  292271
Seq. No.
Seq. ID
                  LIB3060-044-Q1-K1-D12
Method
                  BLASTX
                  g401114
NCBI GI
BLAST score
                  547
                  2.0e-56
E value
                  114
Match length
% identity
                   96
                  SUCROSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE
NCBI Description
                  GLUCOSYLTRANSFERASE) >gi 82726 pir JQ1329
                   sucrose-phosphate synthase (EC 2.4.1.14) - maize >gi_168626
                   (M97550) sucrose phosphate synthase [Zea mays]
Seq. No.
                   292272
                  LIB3060-044-Q1-K1-F3
Seq. ID
                  BLASTN
Method
NCBI GI
                   q902200
BLAST score
                  165
E value
                   1.0e-87
Match length
                   336
% identity
                   44
NCBI Description Z.mays complete chloroplast genome
```

Seq. No. 292273

Seq. ID LIB3060-045-Q1-K1-B3

Method BLASTX NCBI GI g2632254



```
BLAST score
E value
                  6.0e-31
Match length
                  77
                  84
% identity
NCBI Description (Y12465) serine/threonine kinase [Sorghum bicolor]
Seq. No.
                  292274
Seq. ID
                  LIB3060-045-Q1-K1-C5
Method
                  BLASTN
NCBI GI
                  g22356
BLAST score
                  111
E value
                  1.0e-55
Match length
                  166
                  91
% identity
                  Maize mRNA for light-harvesting chlorophyll a/b binding
NCBI Description
                  protein LHCP
                  292275
Seq. No.
Seq. ID
                  LIB3060-045-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  251
E value
                  1.0e-21
                  74
Match length
                  69
% identity
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                  292276
Seq. No.
Seq. ID
                  LIB3060-045-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g2828012
BLAST score
                  382
E value
                  7.0e-37
                  87
Match length
% identity
                  89
                  (AF036891) starch synthase I precursor [Zea mays]
NCBI Description
                  292277
Seq. No.
Seq. ID
                  LIB3060-045-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g82040
BLAST score
                  437
E value
                  2.0e-43
Match length
                  118
                  22
% identity
NCBI Description
                  ubiquitin precursor - flax (fragment) >qi 168304 (M57895)
                  ubiquitin [Linum usitatissimum]
Seq. No.
                  292278
Seq. ID
                  LIB3060-045-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g1332579
```

Method BLASTX
NCBI GI g1332579
BLAST score 188
E value 1.0e-14
Match length 78
% identity 7

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]



```
292279
Seq. No.
                  LIB3060-045-Q1-K1-G6
Seq. ID
Method
                  BLASTX
                  g1418990
NCBI GI
BLAST score
                  186
E value
                  5.0e-14
                  67
Match length
                  55
% identity
                  (Z75524) unknown [Lycopersicon esculentum]
NCBI Description
                  292280
Seq. No.
Seq. ID
                  LIB3060-045-Q1-K1-H10
                  BLASTX
Method
NCBI GI
                  g67155
BLAST score
                  282
                   3.0e-25
E value
                  126
Match length
                   80
% identity
                  pyruvate, orthophosphate dikinase (EC 2.7.9.1) precursor -
NCBI Description
                  maize
                  292281
Seq. No.
Seq. ID
                  LIB3060-045-Q1-K1-H12
                  BLASTX
Method
                   g1778095
NCBI GI
                   239
BLAST score
                   3.0e-20
E value
                   120
Match length
                   42
% identity
                   (U64903) putative sugar transporter; member of major
NCBI Description
                   facilitative superfamily; integral membrane protein [Beta
                   vulgaris]
                   292282
Seq. No.
Seq. ID
                   LIB3060-045-Q1-K1-H2
Method
                   BLASTX
NCBI GI
                   g3738329
BLAST score
                   141
                   2.0e-14
E value
                   73
Match length
% identity
                   63
NCBI Description
                  (AC005170) unknown protein [Arabidopsis thaliana]
                   292283
Seq. No.
Seq. ID
                   LIB3060-046-Q1-K1-A2
Method
                   BLASTX
NCBI GI
                   g2586083
BLAST score
                   247
E value
                   5.0e-21
Match length
                   127
% identity
NCBI Description
                   (U72725) receptor kinase-like protein [Oryza
                   longistaminata]
```

40717

292284

LIB3060-046-Q1-K1-B12

Seq. No.

Seq. ID



Method BLASTX
NCBI GI g113626
BLAST score 288
E value 4.0e-26
Match length 79
% identity 75

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE >gi_68202_pir__ADBY2 fructose-bisphosphate aldolase (EC 4.1.2.13) II - yeast (Saccharomyces cerevisiae) >gi_3696_emb_CAA33111_ (X15003) fructose-bisphosphate aldolase [Saccharomyces cerevisiae]

>gi 433637 emb CAA53412 (X75781) yeast

fructose-bisphate-aldolase [Saccharomyces cerevisiae]

>gi 486081 emb CAA81897_ (Z28060) ORF YKL060c

[Saccharomyces cerevisiae] >gi_1587557_prf_2206495F fructosebisphosphate aldolase [Saccharomyces cerevisiae]

Seq. No. 292285

Seq. ID LIB3060-046-Q1-K1-F3

Method BLASTN
NCBI GI g902200
BLAST score 83
E value 7.0e-39
Match length 298
% identity 90

NCBI Description Z.mays complete chloroplast genome

Seq. No. 292286

Seq. ID LIB3060-046-Q1-K1-F7

Method BLASTX
NCBI GI g1361979
BLAST score 180
E value 3.0e-13
Match length 61
% identity 57

NCBI Description serine O-acetyltransferase (EC 2.3.1.30) - watermelon

>gi_1350550_dbj_BAA12843_ (D85624) serine acetyltransferase

[Citrullus lanatus] >gi_1841312_dbj_BAA08479_ (D49535)

serine acetyltransferase. [Citrullus lanatus] >gi 2337772 dbj BAA21827 (AB006530) serine

acetyltransferase [Citrullus lanatus]

Seq. No. 292287

Seq. ID LIB3060-046-Q1-K1-H11

Method BLASTX
NCBI GI g2347195
BLAST score 174
E value 7.0e-13
Match length 75
% identity 47

NCBI Description (AC002338) hypothetical protein [Arabidopsis thaliana]

Seq. No. 292288

Seq. ID LIB3060-047-Q1-K1-A1

Method BLASTN
NCBI GI g3309177
BLAST score 376
E value 0.0e+00



Match length 391 % identity 99

NCBI Description Zea mays starch branching enzyme I (sbe1) gene, complete

cds

Seq. No. 292289

Seq. ID LIB3060-047-Q1-K1-A12

Method BLASTX
NCBI GI g2190540
BLAST score 209
E value 1.0e-16
Match length 82
% identity 51

NCBI Description (AC001229) Similar to Arabidopsis TFL1 (gb_U77674).

[Arabidopsis thaliana]

Seq. No. 292290

Seq. ID LIB3060-047-Q1-K1-A2

Method BLASTX
NCBI GI g82080
BLAST score 303
E value 1.0e-28
Match length 97
% identity 75

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

>gi_226872_prf__1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

Seq. No. 292291

Seq. ID LIB3060-047-Q1-K1-B2

Method BLASTX
NCBI GI g1491774
BLAST score 337
E value 1.0e-48
Match length 106
% identity 92

NCBI Description (X99936) cysteine protease [Zea mays]

Seq. No. 292292

Seq. ID LIB3060-047-Q1-K1-C1

Method BLASTX
NCBI GI g115771
BLAST score 617
E value 2.0e-64
Match length 137
% identity 86

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >gi 82682 pir S04453 chlorophyll

a/b-binding protein precursor - maize

>gi 22224 emb CAA32900 (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No. 292293

Seq. ID LIB3060-047-Q1-K1-C4

Method BLASTX NCBI GI g1658315 BLAST score 199



```
E value
                  1.0e-15
Match length
                  93
% identity
                  43
                  (Y08988) osr40g3 [Oryza sativa]
NCBI Description
                  292294
Seq. No.
                  LIB3060-047-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g230348
BLAST score
                  177
E value
                 8.0e-13
Match length
                  104
% identity
                  42
NCBI Description Triacylglycerol Acylhydrolase (E.C.3.1.1.3)
                  292295
Seq. No.
                  LIB3060-047-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82696
BLAST score
                  214
                  4.0e-17
E value
Match length
                  78
% identity
                  63
                  glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
                  292296
Seq. No.
                  LIB3060-047-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462749
                  533
BLAST score
                  1.0e-54
E value
Match length
                  134
                  78
% identity
                   (AC002292) Putative Serine/Threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                  292297
Seq. No.
Seq. ID
                  LIB3060-048-Q1-K1-D7
                  BLASTX
Method
                  g4220594
NCBI GI
BLAST score
                  172
                   2.0e-12
E value
Match length
                  59
% identity
                  (AB011264) nicochianamine synthase 3 [Hordeum vulgare]
NCBI Description
                   292298
Seq. No.
Seq. ID
                  LIB3060-048-Q1-K1-E7
                  BLASTN
Method
                   g596077
NCBI GI
                   63
BLAST score
                   2.0e-27
E value
Match length
                   83
% identity
                  Zea mays thiamine biosynthetic enzyme (thi1-1) mRNA,
NCBI Description
```

40720

complete cds

NCBI Description



```
292299
Seq. No.
                   LIB3060-048-Q1-K1-E9
Seq. ID
                   BLASTX
Method
                   g141605
NCBI GI
                   414
BLAST score
                   7.0e-46
E value
Match length
                   107
                   96
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                   >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                   maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
                   292300
Seq. No.
                   LIB3060-048-Q1-K1-F12
Seq. ID
                   BLASTX
Method
                    g141601
NCBI GI
                    171
BLAST score
                    3.0e-12
E value
                    83
Match length
                    47
% identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
NCBI Description
                    >gi_82657_pir__S03417 19K zein precursor (clone gZ19AB11) -
maize >gi_22543_emb_CAA29340_ (X05911) 19 kd alpha zein (AA
                    1 - 234) [Zea mays]
Seq. No.
                    292301
                    LIB3060-048-Q1-K1-G1
Seq. ID
                    BLASTN
Method
                    g169818
NCBI GI
                    40
BLAST score
                    1.0e-13
E value
                    52
Match length
                    94
% identity
NCBI Description Rice 25S ribosomal RNA gene
                    292302
Seq. No.
Seq. ID
                    LIB3060-048-Q1-K1-G10
                    BLASTX
Method
                    q168699
NCBI GI
                    204
BLAST score
                    8.0e-22
E value
                    100
Match length
                    65
% identity
                    (M60836) zein [Zea mays]
NCBI Description
                    292303
Seq. No.
                    LIB3060-048-Q1-K1-G12
Seq. ID
                    BLASTN
Method
                    g2828011
NCBI GI
                    35
BLAST score
                    1.0e-10
E value
                    95
Match length
 % identity
                     84
```

gene encoding plastid protein, complete cds

Zea mays starch synthase I precursor (Ss1) mRNA, nuclear



```
Seq. No.
                  292304
                  LIB3060-048-Q1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4038030
BLAST score
                  249
                   3.0e-21
E value
Match length
                  138
                   40
% identity
                   (AC005936) putative protein kinase, 5' partial [Arabidopsis
NCBI Description
                   thaliana]
                   292305
Seq. No.
                   LIB3060-048-Q1-K1-G9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2832246
BLAST score
                   201
                   1.0e-19
E value
Match length
                   89
                   61
% identity
                   (AF031569) 22-kDa alpha zein 8 [Zea mays]
NCBI Description
                   292306
Seq. No.
                   LIB3060-049-Q1-K1-B2
Seq. ID
Method
                   BLASTN
                   g3256034
NCBI GI
BLAST score
                   71
                   1.0e-31
E value
                   272
Match length
% identity
                   90
                   Sorghum bicolor mRNA for SNFL3, putative serine/threonine
NCBI Description
                   protein kinase
                   292307
Seq. No.
                   LIB3060-049-Q1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g534982
                   150
BLAST score
                   1.0e-09
E value
                   39
Match length
                   82
% identity
                   (X75898) phosphoglucomutase [Spinacia oleracea]
NCBI Description
                   292308
Seq. No.
Seq. ID
                   LIB3060-049-Q1-K1-D3
Method
                   BLASTX
NCBI GI
                   q118104
BLAST score
                   296
                   1.0e-47
E value
                   132
Match length
                   83
% identity
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                   >gi 68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                   maize >gi 168461 (M55021) cyclophilin [Zea mays]
```

Seq. No. 292309

>qi 829148 emb CAA48638 (X68678) cyclophilin [Zea mays]

E value

Match length

1.0e-18 57



```
LIB3060-049-Q1-K1-H4
Seq. ID
                   BLASTX
Method
                   q3559816
NCBI GI
BLAST score
                   402
E value
                   3.0e-39
                   144
Match length
                   53
% identity
                   (Y15782) transketolase 2 [Capsicum annuum]
NCBI Description
                   292310
Seq. No.
                   LIB3060-050-Q1-K1-A4
Seq. ID
                   BLASTX
Method
                   q1076678
NCBI GI
                   239
BLAST score
E value
                   3.0e-20
                   66
Match length
                   77
% identity
                  ubiquitin / ribosomal protein S27a - potato (fragment)
NCBI Description
                   292311
Seq. No.
                   LIB3060-050-Q1-K1-B2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1772985
BLAST score
                   302
E value
                   9.0e-28
Match length
                   80
                   79
% identity
                   (Z83835) zeaxanthin epoxidase [Lycopersicon esculentum]
NCBI Description
                   292312
Seq. No.
                   LIB3060-050-Q1-K1-B6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4539315
BLAST score
                   169
E value
                   7.0e-12
Match length
                   66
% identity
                   50
                   (AL035679) putative zinc finger protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   292313
                   LIB3060-050-Q1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2911072
                   209
BLAST score
E value
                   1.0e-16
Match length
                   69
                   62
% identity
                   (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                   292314
Seq. No.
                   LIB3060-050-Q1-K1-C4
Seq. ID
                   BLASTX
Method
                   g2708741
NCBI GI
BLAST score
                   226
```

Match length

% identity

71

15



```
% identity
NCBI Description (AC003952) hypothetical protein [Arabidopsis thaliana]
                  292315
Seq. No.
Seq. ID
                  LIB3060-050-Q1-K1-D4
                  BLASTX
Method
NCBI GI
                  g4204265
                  307
BLAST score
                  5.0e-28
E value
                  103
Match length
                  61
% identity
                 (AC005223) 45643 [Arabidopsis thaliana]
NCBI Description
                  292316
Seq. No.
                  LIB3060-050-Q1-K1-D9
Seq. ID
                  BLASTX
Method
                  g82696
NCBI GI
BLAST score
                  185
                  2.0e-14
E value
                  37
Match length
                  92
% identity
                  glycine-rich protein - maize >gi_22293_emb_CAA43431
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
                  292317
Seq. No.
                  LIB3060-050-Q1-K1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1173218
BLAST score
                  226
                  1.0e-18
E value
                  59
Match length
                   81
% identity
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                   292318
Seq. No.
Seq. ID
                  LIB3060-051-Q1-K1-A2
                   BLASTX
Method
                   g3024018
NCBI GI
                   395
BLAST score
                   2.0e-38
E value
Match length
                   115
% identity
                   69
                   INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
NCBI Description
                   >qi 1546919 emb CAA69225 (Y07920) translation initiation
                   factor 5A [Zea mays] >gi 2668738 (AF034943) translation
                   initiation factor 5A [Zea mays]
                   292319
Seq. No.
                   LIB3060-051-Q1-K1-B10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3789942
BLAST score
                   244
E value
                   7.0e-21
```

سرتين



NCBI Description (AF093505) polyubiquitin [Saccharum hybrid cultivar H32-8560]

Seq. No. 292320

Seq. ID LIB3060-051-Q1-K1-B2

Method BLASTN
NCBI GI g22312
BLAST score 168
E value 1.0e-89
Match length 200
% identity 96

NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA =

abscisic acid)

Seq. No. 292321

Seq. ID LIB3060-051-Q1-K1-D6

Method BLASTX
NCBI GI g4559358
BLAST score 237
E value 5.0e-20
Match length 86
% identity 53

NCBI Description (AC006585) putative steroid binding protein [Arabidopsis

thaliana]

Seq. No. 292322

Seq. ID LIB3060-051-Q1-K1-D8

Method BLASTX
NCBI GI g2194132
BLAST score 294
E value 1.0e-26
Match length 138
% identity 47

NCBI Description (AC002062) No definition line found [Arabidopsis thaliana]

Seq. No. 292323

Seq. ID LIB3060-051-Q1-K1-E12

Method BLASTN
NCBI GI g3360288
BLAST score 61
E value 1.0e-25
Match length 100
% identity 91

NCBI Description Zea mays leucine-rich repeat transmembrane protein kinase 1

(ltk1) mRNA, partial cds

Seq. No. 292324

Seq. ID LIB3060-051-Q1-K1-E3

Method BLASTX
NCBI GI g136125
BLAST score 278
E value 4.0e-30
Match length 129
% identity 60

NCBI Description PUTATIVE AC TRANSPOSASE (ORFA) >gi_22113_emb_CAA29005_

(X05424) ORFa [Zea mays]



```
292325
 Seq. No.
                    LIB3060-051-Q1-K1-H2
 Seq. ID
Method
                    BLASTX
                    g3928543
 NCBI GI
                    304
 BLAST score
                    9.0e-28
 E value
                    101
 Match length
                    53
 % identity
                    (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
 NCBI Description
                    thaliana]
                    292326
 Seq. No.
                    LIB3060-052-Q1-K1-C9
 Seq. ID
                    BLASTN
 Method
 NCBI GI
                    g2894376
 BLAST score
                    45
                    4.0e-16
 E value
                    156
 Match length
 % identity
                    88
 NCBI Description Hordeum vulgare DNA for chromosome 4H
                    292327
 Seq. No.
                    LIB3060-052-Q1-K1-E10
 Seq. ID
                    BLASTN
 Method
                    g564023
 NCBI GI
 BLAST score
                    87
                    4.0e-41
 E value
 Match length
                    119
 % identity
                    94
                    Zea mays dihydrolipoamide acetyl transferase (ZM/DHLAAT)
 NCBI Description
                    mRNA, complete cds
                    292328
 Seq. No.
                    LIB3060-052-Q1-K1-E3
 Seq. ID
 Method
                    BLASTX
                    g3334115
 NCBI GI
                    291
 BLAST score
 E value
                    3.0e-26
                    118
 Match length
                    58
 % identity
                    ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
 NCBI Description
                    (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 2463664
                    (AF006489) adenine nucleotide translocator 1 [Gossypium
                    hirsutum]
                    292329
 Seq. No.
                    LIB3060-052-Q1-K1-E4
 Seq. ID
                    BLASTN
 Method
 NCBI GI
                    g452340
                    86
 BLAST score
 E value
                    7.0e-41
                    110
 Match length
  % identity
                    Z.mays mRNA for type II light-harvesting chlorophyll
 NCBI Description
```

Seq. No. 292330

40726

a/b-binding protein

Method

NCBI GI BLAST score BLASTX g3822223

243



```
LIB3060-052-Q1-K1-F1
Seq. ID
Method
                  BLASTN
                  g22165
NCBI GI
BLAST score
                  48
                  6.0e-18
E value
Match length
                  115
                  87
% identity
                  Maize gene for mitochondrial adenine nucleotide
NCBI Description
                  translocator (ANT-G1)
                  292331
Seq. No.
                  LIB3060-053-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3786009
BLAST score
                  224
E value
                  2.0e-18
Match length
                  112
% identity
                  48
                  (AC005499) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  292332
                  LIB3060-053-Q1-K1-C4
Seq. ID
Method
                  BLASTX
                   g4154281
NCBI GI
BLAST score
                   300
E value
                  2.0e-27
Match length
                  66
% identity
                  85
                  (AF082347) C13 endopeptidase NP1 precursor [Zea mays]
NCBI Description
Seq. No.
                  292333
                  LIB3060-053-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4337195
BLAST score
                   530
                   3.0e-54
E value
Match length
                   111
% identity
                   89
                  (AC006403) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   292334
Seq. No.
                  LIB3060-053-Q1-K1-H10
Seq. ID
Method
                  BLASTX
                   g1076809
NCBI GI
BLAST score
                   280
E value
                   2.0e-25
Match length
                   79
                   67
% identity
                  H+-transporting ATPase (EC 3.6.1.35) - maize
NCBI Description
                   >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase
                   [Zea mays]
                   292335
Seq. No.
                  LIB3060-054-Q1-K1-B3
Seq. ID
```

Seq. ID Method

NCBI GI



```
E value
                  2.0e-26
Match length
                  99
% identity
                   (AF077955) branched-chain alpha keto-acid dehydrogenase E1
NCBI Description
                  alpha subunit [Arabidopsis thaliana]
Seq. No.
                  292336
                  LIB3060-054-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115771
BLAST score
                  393
E value
                  3.0e-38
                  101
Match length
                  77
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll
                  a/b-binding protein precursor - maize
                  >gi 22224 emb CAA32900 (X14794) chlorophyll a/b-binding
                  preprotein (AA 1 - 262) [Zea mays]
Seq. No.
                  292337
Seq. ID
                  LIB3060-054-Q1-K1-D2
Method
                  BLASTN
NCBI GI
                  q3789951
BLAST score
                  46
E value
                  1.0e-16
Match length
                  82
% identity
                  89
                  Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
Seq. No.
                  292338
Sea. ID
                  LIB3060-054-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  q4154281
BLAST score
                  251
E value
                   1.0e-27
Match length
                  90
                   77
% identity
NCBI Description
                  (AF082347) C13 endopeptidase NP1 precursor [Zea mays]
Seq. No.
                   292339
                  LIB3061-001-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q168695
BLAST score
                  147
                   6.0e-10
E value
Match length
                  36
% identity
                   81
                  (M16218) gamma zein [Zea mays] >gi 225315 prf 1211356A
NCBI Description
                   zein gamma [Zea mays]
Seq. No.
                   292340
```

40728

LIB3061-001-Q1-K1-C12

BLASTX

g224509

```
149
```

BLAST score

```
E value
                  4.0e-10
Match length
                  51
% identity
                  61
NCBI Description
                  zein E19 [Zea mays]
Seq. No.
                  292341
                  LIB3061-001-Q1-K1-D10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22526
BLAST score
                  73
E value
                  4.0e-33
Match length
                  152
% identity
                  88
                  Zea mays mRNA encoding a zein (clone zA1)
NCBI Description
Seq. No.
                  292342
Seq. ID
                  LIB3061-001-Q1-K1-F11
Method
                  BLASTN
NCBI GI
                  g168704
BLAST score
                  74
                  7.0e-34
E value
Match length
                  158
                  86
% identity
NCBI Description
                  Zea mays zein protein gene, complete cds
Seq. No.
                  292343
Seq. ID
                  LIB3061-001-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  q629861
BLAST score
                  215
E value
                  6.0e-18
Match length
                  59
                  75
% identity
                  zein Zd1, 19K - maize >gi 535020 emb CAA47639 (X67203)
NCBI Description
                  zein Zd1 (19 kDa zein) [Zea mays]
                  292344
Seq. No.
                  LIB3061-001-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g224514
BLAST score
                  243
E value
                  5.0e-21
Match length
                  67
% identity
                  78
NCBI Description
                  zein M8 [Zea mays]
Seq. No.
                  292345
Seq. ID
                  LIB3061-001-Q1-K2-C5
Method
                  BLASTX
NCBI GI
                  g141601
BLAST score
                  219
E value
                  6.0e-18
Match length
                  103
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
                  >gi 82657 pir S03417 19K zein precursor (clone gZ19AB11) -
```

maize >gi_22543_emb_CAA29340_ (X05911) 19 kd alpha zein (AA 1 - 234) [Zea mays]

292346 Seq. No. LIB3061-001-Q1-K2-D2 Seq. ID BLASTX Method NCBI GI q168691 BLAST score 162 2.0e-11 E value 80 Match length 50 % identity NCBI Description (M29628) zein [Zea mays] 292347 Seq. No. LIB3061-001-Q1-K2-D6 Seq. ID BLASTX Method g4558664 NCBI GI 199 BLAST score 2.0e-15 E value 128 Match length % identity 13 NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana] 292348 Seq. No. LIB3061-001-Q1-K2-E2 Seq. ID BLASTX Method NCBI GI g121472 144 BLAST score 5.0e-09 E value Match length 54 61 % identity GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) NCBI Description (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)

>gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) maize >gi_22289 emb CAA26149 (X02230) glutelin-2 precursor

[Zea mays] >gi 22517_emb_CAA37594_ (X53514) zein Zc2 [Zea

mays] >gi $1684\overline{8}5$ (M $\overline{16066}$) glutelin-2 [Zea mays]

292349 Seq. No.

LIB3061-001-Q1-K2-F11 Seq. ID

BLASTX Method g419803 NCBI GI 253 BLAST score 5.0e-22 E value Match length 87 56 % identity

zein protein - maize >gi_168705 (M72708) zein protein [Zea NCBI Description

mays]

292350 Seq. No.

LIB3061-001-Q1-K2-F12 Seq. ID

BLASTX Method q419803 NCBI GI BLAST score 351 E value 2.0e-33 80 Match length 88 % identity



NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 292351

Seq. ID LIB3061-001-Q1-K2-G4

Method BLASTN
NCBI GI g22542
BLAST score 45
E value 2.0e-16
Match length 125
% identity 85

NCBI Description Maize gene for Mr 19000 alpha zein and 5'-flanking region

Seq. No. 292352

Seq. ID LIB3061-001-Q1-K2-G5

Method BLASTX
NCBI GI g224507
BLAST score 161
E value 3.0e-11
Match length 40
% identity 80

NCBI Description zein Al [Zea mays]

Seq. No. 292353

Seq. ID LIB3061-001-Q1-K2-H1

Method BLASTX
NCBI GI g312179
BLAST score 272
E value 2.0e-38
Match length 103
% identity 84

NCBI Description (X73151) glyceraldehyde 3-phosphate dehydrogenase

(phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]

>gi 1185554 (U45858) glyceraldehyde-3-phosphate

dehydrogenase [Zea mays]

Seq. No. 292354

Seq. ID LIB3061-001-Q1-K2-H2

Method BLASTX
NCBI GI g2832246
BLAST score 266
E value 2.0e-23
Match length 102
% identity 61

NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]

Seq. No. 292355

Seq. ID LIB3061-001-Q1-K2-H9

Method BLASTN
NCBI GI g168681
BLAST score 44
E value 7.0e-16
Match length 76
% identity 89

NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.

>gi 270686 gb I03333 Sequence 8 from Patent US

% identity

NCBI Description



```
292356
Seq. No.
Seq. ID
                  LIB3061-002-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g141599
BLAST score
                  233
E value
                  1.0e-19
                  53
Match length
                  89
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19A2)
NCBI Description
                  >qi 72316 pir ZIZMA2 19K zein precursor (clone cZ19A2) -
                  maize (fragment) >gi 168670 (M12142) 19 kDa zein protein
                  [Zea mays]
Seq. No.
                  292357
Seq. ID
                  LIB3061-002-Q1-K1-C11
Method
                  BLASTN
NCBI GI
                  g459169
BLAST score
                  41
E value
                  3.0e-14
Match length
                  53
                   94
% identity
                  Zea mays B73 antifungal zeamatin-like protein mRNA,
NCBI Description
                  complete cds
Seq. No.
                  292358
Seq. ID
                  LIB3061-002-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g141608
BLAST score
                  257
E value
                   8.0e-24
Match length
                  76
% identity
                   75
                  ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943 pir S15655
NCBI Description
                   zein, 19K - maize >gi 22446 emb CAA37651 (X53582) 19 kDa
                   zein [Zea mays]
Seq. No.
                   292359
Seq. ID
                  LIB3061-002-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g508545
BLAST score
                   186
E value
                   2.0e-14
Match length
                   50
% identity
NCBI Description
                  (L34340) zein [Zea mays]
Seq. No.
                   292360
Seq. ID
                   LIB3061-002-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                   g16073
BLAST score
                   227
E value
                   5.0e-19
Match length
                   52
```

(X59526) zein protein [Acetabularia mediterranea]

Seq. ID Method



```
Seq. No.
                  292361
                  LIB3061-002-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141602
BLAST score
                  217
                  5.0e-18
E value
Match length
                  55
                  82
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6)
NCBI Description
                  >gi_82658_pir__A22831 19K zein precursor (clone M6) - maize
                  >gi 22538 emb CAA26294 (X02450) zein precursor [Zea mays]
                  292362
Seq. No.
                  LIB3061-002-Q1-K2-A3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q168701
BLAST score
                   316
E value
                   3.0e-29
                   92
Match length
                   75
% identity
NCBI Description (M60837) zein [Zea mays]
                   292363
Seq. No.
                   LIB3061-002-Q1-K2-A5
Seq. ID
                   BLASTN
Method
                   g168669
NCBI GI
BLAST score
                   45
                   2.0e-16
E value
                   129
Match length
% identity
                   84
NCBI Description Maize 19 kDa zein mRNA, clone cZ19A2, partial cds
Seq. No.
                   292364
                   LIB3061-002-Q1-K2-B12
Seq. ID
Method
                   BLASTX
                   g629862
NCBI GI
BLAST score
                   170
                   3.0e-12
E value
Match length
                   86
% identity
                   50
                   zein Zd1, 19K - maize >gi 535021_emb_CAA47640_ (X67203)
NCBI Description
                   zein Zd1 (19 kDa zein) [Zea mays]
                   292365
Seq. No.
                   LIB3061-002-Q1-K2-D3
Seq. ID
                   BLASTX
Method
                   g82696
NCBI GI
BLAST score
                   329
                   6.0e-31
E value
                   76
Match length
                   84
% identity
                   glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
                   292366
Seq. No.
```

40733

LIB3061-002-Q1-K2-D4

BLASTN



```
g16072
NCBI GI
BLAST score
                  45
                  1.0e-16
E value
                  57
Match length
                  95
% identity
NCBI Description Acetabularia mediterranea zein gene
Seq. No.
                  292367
Seq. ID
                  LIB3061-002-Q1-K2-E3
                  BLASTN
Method
NCBI GI
                  g2832242
BLAST score
                  42
E value
                  1.0e-14
                  58
Match length
                  16
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.
                  292368
Seq. ID
                  LIB3061-002-Q1-K2-F10
Method
                  BLASTX
NCBI GI
                  g2668742
                  371
BLAST score
                  1.0e-35
E value
Match length
                  94
% identity
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                  292369
Seq. No.
Seq. ID
                  LIB3061-002-Q1-K2-H2
                  BLASTN
Method
NCBI GI
                   g22447
BLAST score
                  131
                   2.0e-67
E value
Match length
                  147
% identity
                   97
NCBI Description Zea mays ZMPMS2 gene for 19 kDa zein protein
Seq. No.
                   292370
                  LIB3061-003-Q1-K1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g141605
BLAST score
                   478
E value
                   4.0e-48
Match length
                   112
                   89
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                   >qi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >qi 168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                   292371
Seq. ID
                   LIB3061-003-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   g100938
BLAST score
                   227
                   4.0e-19
E value
Match length
                   65
```

75

% identity

% identity

89



```
zein precursor - maize >gi_22442_emb_CAA32513 (X14335)
NCBI Description
                  zein precursor (AA -21 to 90) [Zea mays]
Seq. No.
                  292372
Seq. ID
                  LIB3061-003-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  q322870
BLAST score
                  158
                  5.0e-13
E value
                  54
Match length
% identity
                  glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) -
NCBI Description
                  maize (fragment)
                  292373
Seq. No.
Seq. ID
                  LIB3061-003-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g141603
                  245
BLAST score
                  4.0e-21
E value
Match length
                  78
                  69
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >gi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
                  >gi_22529_emb_CAA24723 (V01476) zein [Zea mays]
                  292374
Seq. No.
                  LIB3061-003-Q1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141597
BLAST score
                  280
                  7.0e-33
E value
Match length
                  105
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                  >gi 72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
                   [Zea mays]
                  292375
Seq. No.
Seq. ID
                  LIB3061-003-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  g16073
BLAST score
                  318
E value
                   2.0e-29
Match length
                   96
% identity
                   72
NCBI Description
                  (X59526) zein protein [Acetabularia mediterranea]
Seq. No.
                   292376
                  LIB3061-003-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g141605
BLAST score
                   424
                   6.0e-42
E value
Match length
                   97
```



```
ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                  292377
Seq. ID
                  LIB3061-003-Q1-K1-F3
                  BLASTN
Method
                  q168675
NCBI GI
                  42
BLAST score
                  1.0e-14
E value
Match length
                  80
                  90
% identity
NCBI Description Maize mutant zein (zE19) gene, complete cds
                  292378
Seq. No.
Seq. ID
                  LIB3061-003-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  q3169174
                  183
BLAST score
                  1.0e-13
E value
Match length
                  65
                  48
% identity
NCBI Description (AC004401) putative serine carboxypeptidase I [Arabidopsis
                  thaliana]
                  292379
Seq. No.
Seq. ID
                  LIB3061-003-Q1-K1-G1
Method
                  BLASTX
                  g168701
NCBI GI
BLAST score
                  160
                  6.0e-14
E value
                  74
Match length
% identity
NCBI Description (M60837) zein [Zea mays]
                  292380
Seq. No.
Seq. ID
                  LIB3061-003-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  g16073
BLAST score
                  400
E value
                  5.0e-39
Match length
                  108
% identity
                  77
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
                  292381
Seq. No.
                  LIB3061-003-Q1-K1-H9
Seq. ID
Method
                  BLASTX
                  g542157
NCBI GI
```

247 BLAST score 2.0e-21 E value 74 Match length % identity 61

NCBI Description ribosomal 5S RNA-binding protein - Rice

292382 Seq. No.

LIB3061-004-Q1-K1-A12 Seq. ID



```
BLASTX
Method
                  g3426062
NCBI GI
                  153
BLAST score
                  3.0e-10
E value
Match length
                  71
% identity
                  45
NCBI Description (AJ007587) monooxygenase [Arabidopsis thaliana]
                  292383
Seq. No.
                  LIB3061-004-Q1-K1-C11
Seq. ID
Method
                  BLASTX
                  g419803
NCBI GI
                  370
BLAST score
                  2.0e-35
E value
Match length
                  126
                   61
% identity
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea
                  mays]
                   292384
Seq. No.
                  LIB3061-004-Q1-K1-E4
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2832243
BLAST score
                  312
                   1.0e-28
E value
Match length
                  116
                   59
% identity
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
                   292385
Seq. No.
                   LIB3061-004-Q1-K1-F4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g168697
BLAST score
                   286
                   1.0e-25
E value
                   106
Match length
% identity
                   60
NCBI Description (M60835) zein [Zea mays]
Seq. No.
                   292386
Seq. ID
                   LIB3061-005-Q1-K1-A9
Method
                   BLASTX
NCBI GI
                   g2665356
BLAST score
                   250
E value
                   1.0e-21
Match length
                   107
% identity
                   48
NCBI Description (Y15748) PkB kinase [Rattus norvegicus]
                   292387
Seq. No.
                   LIB3061-005-Q1-K1-B2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g224508
BLAST score
                   419
                   3.0e-41
E value
Match length
                   113
```

40737

78

% identity



NCBI Description zein A20 [Zea mays]

```
292388
Seq. No.
                  LIB3061-005-Q1-K1-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q121475
                  158
BLAST score
                  1.0e-10
E value
                  59
Match length
                  53
% identity
NCBI Description GLUTELIN TYPE II PRECURSOR >gi_100678_pir__A34332 glutelin
                  II precursor - rice >gi 20219 emb CAA29151 (X05663)
                  glutelin [Oryza sativa] >gi_20221_emb_CAA29152_ (X05664)
                  glutelin [Oryza sativa] >gi_20236_emb_CAA68683 (Y00687)
                  glutelin [Oryza sativa] >gi_556398 (M28158) glutelin [Oryza
                  sativa] >gi_556399 (M28156) glutelin [Oryza sativa]
                  292389
Seq. No.
                  LIB3061-005-Q1-K1-B9
Seq. ID
                  BLASTX
Method
                  q2832246
NCBI GI
                  206
BLAST score
E value
                  2.0e-16
                  104
Match length
                  45
% identity
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]
                  292390
Seq. No.
                  LIB3061-005-Q1-K1-D11
Seq. ID
Method
                  BLASTX
                  q2832247
NCBI GI
                  154
BLAST score
E value
                  3.0e-10
                  52
Match length
% identity
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]
Seq. No.
                  292391
                  LIB3061-005-Q1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g136140
BLAST score
                  155
E value
                   3.0e-10
Match length
                   65
                   45
% identity
NCBI Description PUTATIVE AC9 TRANSPOSASE >gi_72973_pir__TQZMCA probable
                  transposase - maize transposon Ac9
                   292392
Seq. No.
                   LIB3061-005-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   g141602
NCBI GI
BLAST score
                   147
                   2.0e-09
E value
                   106
Match length
                   38
% identity
```

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6)



>gi_82658_pir__A22831 19K zein precursor (clone M6) - maize
>gi_22538_emb_CAA26294_ (X02450) zein precursor [Zea mays]

Seq. No. 292393

Seq. ID LIB3061-005-Q1-K1-F8

Method BLASTX
NCBI GI g141603
BLAST score 206
E value 1.0e-29
Match length 96
% identity 81

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)

>gi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize

>gi 22529 emb CAA24723 (V01476) zein [Zea mays]

Seq. No. 292394

Seq. ID LIB3061-005-Q1-K1-G12

Method BLASTX
NCBI GI g629861
BLAST score 421
E value 2.0e-41
Match length 112
% identity 79

NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)

zein Zdl (19 kDa zein) [Zea mays]

Seq. No. 292395

Seq. ID LIB3061-005-Q1-K1-H3

Method BLASTX
NCBI GI g82660
BLAST score 330
E value 7.0e-31
Match length 106
% identity 65

NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)

>gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 292396

Seq. ID LIB3061-005-Q1-K1-H6

Method BLASTX
NCBI GI g3916255
BLAST score 147
E value 2.0e-09
Match length 116
% identity 26

NCBI Description (AF087669) ExbD [Bordetella bronchiseptica]

Seq. No. 292397

Seq. ID LIB3061-006-Q1-K1-A11

Method BLASTN
NCBI GI g168690
BLAST score 94
E value 2.0e-45
Match length 189
% identity 91

NCBI Description Maize zein mRNA, complete cds, clone ZG124



```
292398
Seq. No.
                  LIB3061-006-Q1-K1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22526
BLAST score
                  51
E value
                  6.0e-20
                  99
Match length
                  88
% identity
NCBI Description Zea mays mRNA encoding a zein (clone zA1)
                  292399
Seq. No.
                  LIB3061-006-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141613
BLAST score
                  146
E value
                  2.0e-09
Match length
                  85
% identity
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
NCBI Description
                  >gi 72305 pir ZIZM21 22K zein precursor (clone pZ22.1) -
                  maize >gi 22532 emb CAA24725 (V01478) zein [Zea mays]
Seq. No.
                  292400
                  LIB3061-006-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82660
BLAST score
                  236
E value
                  8.0e-20
Match length
                  80
% identity
                  19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                  >gi 809117 emb CAA24720 (V01473) zein [Zea mays]
Seq. No.
                  292401
                  LIB3061-006-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3395439
BLAST score
                  329
E value
                  1.0e-30
Match length
                  123
% identity
NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]
                  292402
Seq. No.
                  LIB3061-006-Q1-K1-E4
Seq. ID
Method
                  BLASTX
                  g224508
NCBI GI
BLAST score
                  285
                  4.0e-34
E value
Match length
                  111
% identity
                  70
NCBI Description zein A20 [Zea mays]
                  292403
Seq. No.
```

Seq. ID LIB3061-006-Q1-K1-E7

Method BLASTX NCBI GI g168691



```
BLAST score
E value
                  1.0e-25
                  129
Match length
% identity
                  56
NCBI Description (M29628) zein [Zea mays]
                  292404
Seq. No.
                  LIB3061-006-Q1-K1-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22292
BLAST score
                  146
                  1.0e-76
E value
Match length
                  182
% identity
                  95
NCBI Description Z.mays mRNA for glycine-rich protein
                  292405
Seq. No.
                  LIB3061-006-Q1-K1-G5
Seq. ID
                  BLASTN
Method
NCBI GI
                  q3128143
BLAST score
                  67
                  3.0e-29
E value
Match length
                  67
                  100
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MTI20, complete sequence [Arabidopsis thaliana]
                  292406
Seq. No.
                  LIB3061-006-Q1-K1-G8
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2832242
BLAST score
                  108
                  1.0e-53
E value
                  120
Match length
% identity
                   16
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                  292407
Seq. No.
                  LIB3061-007-Q1-K1-A11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22516
BLAST score
                   255
                   1.0e-141
E value
Match length
                   381
                   92
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                   292408
Seq. No.
                  LIB3061-007-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g82660
BLAST score
                   392
                   5.0e-38
E value
Match length
                   122
% identity
                   67
NCBI Description
                  19K zein precursor (clone ZG31A) - maize (fragment)
```

>gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. ID Method

BLASTN



```
292409
Seq. No.
                  LIB3061-007-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g629862
BLAST score
                  358
                  5.0e-34
E value
                  103
Match length
% identity
                  72
                  zein Zd1, 19K - maize >gi 535021 emb CAA47640 (X67203)
NCBI Description
                  zein Zd1 (19 kDa zein) [Zea mays]
                  292410
Seq. No.
Seq. ID
                  LIB3061-007-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  q4185308
BLAST score
                  455
E value
                  2.0e-45
Match length
                  116
                  86
% identity
NCBI Description (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
                  292411
Seq. No.
                  LIB3061-007-Q1-K1-E8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g16073
BLAST score
                  433
E value
                  8.0e-43
                  137
Match length
% identity
                   67
                  (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
Seq. No.
                  292412
Seq. ID
                  LIB3061-007-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  q141605
BLAST score
                  334
E value
                   2.0e-31
Match length
                  74
% identity
                   91
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
                   >gi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >qi 168680 (M12145) 19 kDa zein protein [Zea mays]
Seg. No.
                   292413
                  LIB3061-008-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g16073
BLAST score
                   440
                   3.0e-44
E value
                  117
Match length
                  85
% identity
                  (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
                  292414
Seq. No.
                  LIB3061-008-Q1-K1-B11
```



```
g433039
NCBI GI
BLAST score
                  73
                  8.0e-33
E value
                  101
Match length
% identity
                  Zea mays W-22 clone PREM-1 retroelement PREM-1, partial
NCBI Description
                  sequence
                  292415
Seq. No.
Seq. ID
                  LIB3061-008-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  q2660669
BLAST score
                  278
                  1.0e-24
E value
                  102
Match length
% identity
                  (AC002342) human Mi-2 autoantigen-like protein [Arabidopsis
NCBI Description
                  thaliana]
                   292416
Seq. No.
                  LIB3061-008-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2660669
BLAST score
                   488
                   5.0e-61
E value
                   138
Match length
% identity
NCBI Description
                  (AC002342) human Mi-2 autoantigen-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   292417
Seq. ID
                   LIB3061-008-Q1-K1-F1
Method
                   BLASTX
                   g468516
NCBI GI
BLAST score
                   226
                   1.0e-18
E value
Match length
                   132
% identity
                   42
NCBI Description
                  (X55724) zein [Zea mays]
                   292418
Seq. No.
                   LIB3061-008-Q1-K1-G12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g121472
BLAST score
                   361
E value
                   2.0e-34
                   115
Match length
                   59
% identity
                  GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
```

maize >gi_22289 emb_CAA26149 (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594 (X53514) zein Zc2 [Zea

mays] >gi 168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 292419

LIB3061-009-Q1-K1-A1 Seq. ID



```
Method
                  BLASTX
NCBI GI
                  g168699
                  254
BLAST score
                  6.0e-22
E value
                  76
Match length
                  70
% identity
NCBI Description (M60836) zein [Zea mays]
                  292420
Seq. No.
Seq. ID
                  LIB3061-009-Q1-K1-A6
                  BLASTN
Method
                  g168669
NCBI GI
                  120
BLAST score
                  3.0e-61
E value
                  140
Match length
                  96
% identity
NCBI Description Maize 19 kDa zein mRNA, clone cZ19A2, partial cds
                  292421
Seq. No.
Seq. ID
                  LIB3061-009-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  g168691
BLAST score
                  189
                  1.0e-14
E value
                  87
Match length
                  46
% identity
NCBI Description (M29628) zein [Zea mays]
                  292422
Seq. No.
Seq. ID
                  LIB3061-009-Q1-K1-D5
Method
                  BLASTX
                   q629861
NCBI GI
BLAST score
                   263
                   3.0e-23
E value
Match length
                   64
                   84
% identity
NCBI Description zein Zd1, 19K - maize >gi 535020 emb CAA47639 (X67203)
                   zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                   292423
Seq. ID
                   LIB3061-009-Q1-K1-E3
Method
                   BLASTX
NCBI GI
                   g4185308
BLAST score
                   149
                   1.0e-09
E value
Match length
                   87
% identity
                  (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
NCBI Description
                   292424
Seq. No.
                   LIB3061-009-Q1-K1-F5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g16073
                   190
BLAST score
                   1.0e-20
E value
```

50

Match length % identity

NCBI Description



```
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
                    292425
  Seq. No.
  Seq. ID
                    LIB3061-009-Q1-K1-F6
 Method
                    BLASTX
                    g168691
 NCBI GI
                    332
 BLAST score
                    4.0e-31
. E value
 Match length
                    95
  % identity
                    72
                    (M29628) zein [Zea mays]
 NCBI Description
  Seq. No.
                    292426
                    LIB3061-009-Q1-K1-F7
  Seq. ID
  Method
                    BLASTN
  NCBI GI
                    q22544
  BLAST score
                    104
  E value
                    2.0e-51
 Match length
                    402
  % identity
                    87
  NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
  Seq. No.
                    292427
                    LIB3061-010-Q1-K1-A6
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g82660
  BLAST score
                    286
  E value
                    8.0e-26
  Match length
                    63
                    90
  % identity
                    19K zein precursor (clone ZG31A) - maize (fragment)
  NCBI Description
                    >gi 809117_emb_CAA24720_ (V01473) zein [Zea mays]
                    292428
  Seq. No.
                    LIB3061-010-Q1-K1-B6
  Seq. ID
                    BLASTX
  Method
                    g141617
  NCBI GI
                    341
  BLAST score
                     4.0e-32
  E value
  Match length
                    117
  % identity
                    57
                    ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
  NCBI Description
                    >gi_100941_pir__S12140 zein Zc1 - maize
                    >gi_100945_pir__B29017 zein 2 - maize
                    >gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                    >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
                    292429
  Seq. No.
                    LIB3061-010-Q1-K1-B8
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g16073
  BLAST score
                     457
  E value
                    1.0e-45
  Match length
                    116
                     81
  % identity
```

(X59526) zein protein [Acetabularia mediterranea]



```
Seq. No.
Seq. ID
                  LIB3061-010-Q1-K1-C6
                  BLASTX
Method
                  q168695
NCBI GI
BLAST score
                  199
                  6.0e-16
E value
                  76
Match length
% identity
                  (M16218) gamma zein [Zea mays] >gi_225315 prf__1211356A
NCBI Description
                  zein gamma [Zea mays]
                  292431
Seq. No.
Seq. ID
                  LIB3061-010-Q1-K1-D4
Method
                  BLASTN
                  g4185305
NCBI GI
BLAST score
                  261
E value
                  1.0e-145
Match length
                  391
% identity
                  92
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                  (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes
Seq. No.
                  292432
                  LIB3061-010-Q1-K1-F1
Seq. ID
Method
                  BLASTX
                  q141617
NCBI GI
                  529
BLAST score
E value
                  3.0e-54
                  118
Match length
% identity
                  ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                  >gi 100941 pir S12140 zein Zc1 - maize
                  >gi 100945 pir B29017 zein 2 - maize
                  >gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                  >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
Seq. No.
                  292433
                  LIB3061-011-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g141597
BLAST score
                  289
E value
                   5.0e-26
                   110
Match length
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
                   [Zea mays]
                   292434
Seq. No.
```

Seq. ID LIB3061-011-Q1-K1-B7

Method BLASTX g72307 NCBI GI BLAST score 307 E value 4.0e-28

```
Match length
                  108
% identity
                  62
                  22K zein precursor (clone pZ22.3) - maize >gi 168686
NCBI Description
                   (J01246) 26.99 kd zein protein [Zea mays]
Seq. No.
                  292435
                  LIB3061-011-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g629861
BLAST score
                  206
E value
                  1.0e-16
                   67
Match length
                   63
% identity
                  zein Zd1, 19K - maize >gi 535020_emb_CAA47639_ (X67203)
NCBI Description
                   zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                  292436
Seq. ID
                  LIB3061-011-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  q2194093
BLAST score
                   218
E value
                   6.0e-18
                   76
Match length
% identity
                  Chain A, Stearoyl-Acyl Carrier Protein Desaturase From
NCBI Description
                   Castor Seeds >gi_2194094_pdb_1AFR_B Chain B, Stearoyl-Acyl
                   Carrier Protein Desaturase From Castor Seeds
                   >gi_2194095_pdb_1AFR_C Chain C, Stearoyl-Acyl Carrier
                   Protein Desaturase From Castor Seeds >gi_2194096_pdb_1AFR D
                   Chain D, Stearoyl-Acyl Carrier Protein Desaturase From
                   Castor Seeds >gi_2194097_pdb_1AFR_E Chain E, Stearoyl-Acyl
                   Carrier Protein Desaturase From Castor Seeds
                   >gi 2194098 pdb 1AFR F Chain F, Stearoyl-Acyl Carrier
                   Protein Desaturase From Castor Seeds
                   292437
Seq. No.
                   LIB3061-011-Q1-K1-D2
Seq. ID
                   BLASTN
Method
                   g1037129
NCBI GI
                   323
BLAST score
                   0.0e + 00
E value
                   414
```

Match length % identity 95

(gamma-zeinA) = opaque2 modifier {5' region} [Zea mays=maize, NCBI Description Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 292438

LIB3061-011-Q1-K1-E8 Seq. ID

BLASTX Method g141597 NCBI GI BLAST score 274 E value 3.0e-24 107 Match length 57 % identity

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30) NCBI Description

>gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize >gi 22545 emb CAA24728 (V01481) reading frame zein [2]

Seq. ID



[Zea mays]

```
Seq. No.
                  292439
Seq. ID
                  LIB3061-011-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g141610
BLAST score
                  257
E value
                  3.0e-22
Match length
                  134
% identity
                  50
NCBI Description ZEIN-ALPHA PRECURSOR (CLONE Z4)
Seq. No.
                  292440
Seq. ID
                  LIB3061-011-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  q4262232
BLAST score
                  161
                  6.0e-11
E value
Match length
                  81
% identity
                  48
NCBI Description (AC006200) putative ribosomal protein L7 [Arabidopsis
                  thaliana]
Seq. No.
                  292441
Seq. ID
                  LIB3061-011-Q1-K1-F8
                ~ BLASTX
Method
NCBI GI
                  g468516
BLAST score
                  426
E value
                  5.0e-42
Match length
                  102
% identity
                  86
NCBI Description (X55724) zein [Zea mays]
Seq. No.
                  292442
Seq. ID
                  LIB3061-011-Q1-K1-G4
Method
                  BLASTN
NCBI GI
                  g22531
BLAST score
                  66
E value
                  4.0e-29
Match length
                  98
% identity
                  92
NCBI Description
                  Zea mays mRNA encoding a zein (clone pZ22.1)
                  >gi_270688_gb_I03336_ Sequence 10 from Patent US 4885357
                  >gi_270741_gb_I03273 Sequence 2 from Patent US
Seq. No.
                  292443
Seq. ID
                  LIB3061-011-Q1-K1-H6
Method
                  BLASTN
NCBI GI
                  g22537
BLAST score
                  105
E value
                  3.0e-52
Match length
                  189
% identity
                  89
NCBI Description Maize mRNA for zein polypeptide (clone M6)
Seq. No.
                  292444
```

40748

LIB3061-011-Q1-K1-H7



```
BLASTN
Method
NCBI GI
                  g22516
BLAST score
                   362
E value
                  0.0e+00
Match length
                   434
% identity
                  96
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.
                  292445
                  LIB3061-012-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141601
BLAST score
                  149
E value
                   1.0e-09
Match length
                  103
% identity
                   41
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
NCBI Description
                  >gi 82657 pir S03417 19K zein precursor (clone gZ19AB11) -
                  maize >gi 225\overline{43} emb CAA29340 (X05911) 19 kd alpha zein (AA
                  1 - 234) [Zea mays]
Seq. No.
                  292446
                  LIB3061-012-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g508545
BLAST score
                   329
E value
                   1.0e-30
Match length
                   116
% identity
                   63
NCBI Description
                  (L34340) zein [Zea mays]
Seq. No.
                  292447
                  LIB3061-012-Q1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g141597
BLAST score
                   196
                   2.0e-31
E value
Match length
                   129
% identity
                   63
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
                   [Zea mays]
                   292448
Seq. No.
Seq. ID
                  LIB3061-012-Q1-K1-A5
Method
                   BLASTX
                   g141597
NCBI GI
BLAST score
                   236
E value
                   1.0e-23
Match length
                   86
                   77
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
```

[Zea mays]

>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]

Seq. No.

Seq. ID

292454

LIB3061-012-Q1-K1-C2



```
292449
Seq. No.
                  LIB3061-012-Q1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141601
BLAST score
                  153
                  5.0e-10
E value
Match length
                  110
% identity
                  41
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
NCBI Description
                  >gi_82657_pir__S03417 19K zein precursor (clone gZ19AB11) -
                  maize >gi 22543 emb CAA29340 (X05911) 19 kd alpha zein (AA
                  1 - 234) [Zea mays]
Seq. No.
                  292450
Seq. ID
                  LIB3061-012-Q1-K1-B12
Method
                  BLASTN
NCBI GI
                  g168665
BLAST score
                  83
                  9.0e-39
E value
Match length
                  87
% identity
                  99
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds
Seq. No.
                  292451
                  LIB3061-012-Q1-K1-B8
Seq. ID
Method
                  BLASTX
                  g141613
NCBI GI
BLAST score
                  179
                   3.0e-20
E value
                  76
Match length
                   79
% identity
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
NCBI Description
                   >gi_72305_pir__ZIZM21 22K zein precursor (clone pZ22.1) -
                  maize >gi 22532 emb CAA24725 (V01478) zein [Zea mays]
Seq. No.
                   292452
                  LIB3061-012-Q1-K1-C1
Seq. ID
Method
                  BLASTX
                  g168701
NCBI GI
BLAST score
                   482
E value
                   1.0e-48
                   116
Match length
                   84
% identity
NCBI Description
                  (M60837) zein [Zea mays]
                   292453
Seq. No.
                   LIB3061-012-Q1-K1-C12
Seq. ID
Method
                  BLASTX
                   g168701
NCBI GI
BLAST score
                   331
                   7.0e-31
E value
Match length
                   113
                   65
% identity
NCBI Description
                  (M60837) zein [Zea mays]
```

Seq. ID Method



```
BLASTX
Method
                   g100940
NCBI GI
BLAST score
                   240
                    3.0e-20
E value
Match length
                    98
% identity
                    51
NCBI Description
                   zein zAl - maize
                   292455
Seq. No.
Seq. ID
                   LIB3061-012-Q1-K1-C7
Method
                    BLASTX
                    g3132476
NCBI GI
BLAST score
                    205
                    4.0e-16
E value
                    120
Match length
% identity
                    42
                   (AC003096) unknown protein [Arabidopsis thaliana]
NCBI Description
                    292456
Seq. No.
                    LIB3061-012-Q1-K1-E12
Seq. ID
                    BLASTX
Method
NCBI GI
                    q1084457
                    146
BLAST score
                    2.0e-09
E value
                    95
Match length
                    44
% identity
                    elongation factor 1-beta - Rice >gi_432368_dbj_BAA04903_
NCBI Description
                    (D23674) elongation factor 1 beta [Oryza sativa]
                    292457
Seq. No.
                    LIB3061-012-Q1-K1-E7
Seq. ID
                    BLASTX
Method
                    g141597
NCBI GI
BLAST score
                    184
                    9.0e-14
E value
Match length
                    77
% identity
                    55
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                    >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                    >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                    [Zea mays]
 Seq. No.
                    292458
                    LIB3061-012-Q1-K1-E8
 Seq. ID
                    BLASTX
 Method
                    g141606
 NCBI GI
                    283
 BLAST score
                    2.0e-25
 E value
                    108
 Match length
                    58
 % identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1)
 NCBI Description
                    >gi_72309_pir__ZIZMD1 19K zein precursor (clone cZ19D1) -
                    \overline{\text{maize}} > \overline{\text{gi}} 168\overline{68}2 \text{ (M12144)} 19 \text{ kDa zein protein [Zea mays]}
                    292459
 Seq. No.
```

40751

LIB3061-012-Q1-K1-E9

BLASTX



```
q2117355
NCBI GI
BLAST score
                  268
E value
                  2.0e-23
Match length
                  104
% identity
                  58
                  mitochondrial processing peptidase (EC 3.4.99.41) alpha-II
NCBI Description
                  chain precursor - potato >gi 587562 emb_CAA56520_ (X80236)
                  mitochondrial processing peptidase [Solanum tuberosum]
                  292460
Seq. No.
Seq. ID
                  LIB3061-012-Q1-K1-F10
Method
                  BLASTX
                  g141608
NCBI GI
BLAST score
                  345
                  1.0e-32
E value
Match length
                  83
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943_pir__S15655
NCBI Description
                   zein, 19K - maize >gi 22446 emb CAA37651 (X53582) 19 kDa
                   zein [Zea mays]
Seq. No.
                  292461
                  LIB3061-012-Q1-K1-F5
Seq. ID
                  BLASTX
Method
                   g141597
NCBI GI
BLAST score
                   319
E value
                   2.0e-29
                   105
Match length
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
Seq. No.
                   292462
                   LIB3061-012-Q1-K1-G11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g22524
BLAST score
                   163
E value
                   1.0e-86
Match length
                   259
% identity
                   91
                   Zea mays mRNA encoding a zein (clone ZG31A)
NCBI Description
                   292463
Seq. No.
                   LIB3061-012-Q1-K1-G3
Seq. ID
                   BLASTX
Method
                   g168699
NCBI GI
                   232
BLAST score
                   2.0e-19
E value
                   65
Match length
                   74
% identity
NCBI Description
                  (M60836) zein [Zea mays]
```

Seq. No. 292464

Seq. ID LIB3061-012-Q1-K1-G4

Method BLASTX



```
NCBI GI
                  q629861
BLAST score
                  146
E value
                  3.0e-09
                  59
Match length
                  53
% identity
NCBI Description zein Zdl, 19K - maize >gi 535020 emb_CAA47639_ (X67203)
                  zein Zd1 (19 kDa zein) [Zea mays]
                  292465
Seq. No.
Seq. ID
                  LIB3061-012-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  q141602
BLAST score
                  318
                  2.0e-29
E value
                  105
Match length
% identity
                  67
NCBI Description
                 ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6)
                  >qi 82658 pir A22831 19K zein precursor (clone M6) - maize
                  >gi 22538 emb CAA26294 (X02450) zein precursor [Zea mays]
Seq. No.
                  292466
                  LIB3061-012-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g72307
BLAST score
                  292
                  2.0e-26
E value
Match length
                  116
                  57
% identity
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686
                  (J01246) 26.99 kd zein protein [Zea mays]
                  292467
Seq. No.
Seq. ID
                  LIB3061-012-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  g16073
BLAST score
                  329
                  9.0e-33
E value
                  132
Match length
% identity
                  64
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
Seq. No.
                  292468
Seq. ID
                  LIB3061-012-Q1-K1-H12
                  BLASTX
Method
NCBI GI
                  q1709619
BLAST score
                  182
E value
                  1.0e-13
Match length
                  84
                  51
% identity
NCBI Description
                  PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) /
                  DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE
                  (GLYCOSYLATION SITE-BINDING CHAIN) (GSBP)
                  >gi 2146814 pir S69181 protein disulfide isomerase (EC
                  5.3.4.1) precursor - maize >gi_625148 (L39014) protein
```

Seq. No. 292469

40753

disulfide isomerase [Zea mays]



```
LIB3061-012-Q1-K1-H2
Seq. ID
                  BLASTX
Method
                  g141609
NCBI GI
                  168
BLAST score
                   8.0e-12
E value
Match length
                   66
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (PMS2) >gi_100944_pir__S15656
NCBI Description
                   zein, 19K - maize >gi_22448_emb_CAA4154\overline{3}_ (X58\overline{7}00) \overline{1}9 kDa
                   zein [Zea mays]
                   292470
Seq. No.
                   LIB3061-012-Q1-K1-H4
Seq. ID
                   BLASTX
Method
                   g2832247
NCBI GI
BLAST score
                   165
E value
                   1.0e-24
Match length
                   114
% identity
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]
                   292471
Seq. No.
                   LIB3061-013-Q1-K1-A2
Seq. ID
                   BLASTX
Method
                   q2832243
NCBI GI
                   448
BLAST score
                   1.0e-44
E value
                   113
Match length
% identity
                   83
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
                   292472
Seq. No.
                   LIB3061-013-Q1-K1-A5
Seq. ID
                   BLASTX
Method
                   g116329
NCBI GI
BLAST score
                   144
                   3.0e-09
E value
Match length
                   29
                   79
% identity
NCBI Description ENDOCHITINASE A PRECURSOR (SEED CHITINASE A) >gi_168441
                   (M84164) chitinase A [Zea mays]
 Seq. No.
                   292473
                   LIB3061-013-Q1-K1-B10
 Seq. ID
                   BLASTX
Method
                   g2244816
NCBI GI
                   176
BLAST score
                   9.0e-13
E value
                   84
Match length
                   58
 % identity
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
                   292474
 Seq. No.
                   LIB3061-013-Q1-K1-B12
 Seq. ID
```

Method BLASTN
NCBI GI g340933
BLAST score 58

```
District States
```

```
E value
                  225
Match length
% identity
                  87
NCBI Description Zea mays 10-kDa zein gene, complete cds
                  292475
Seq. No.
                  LIB3061-013-Q1-K1-B5
Seq. ID
Method
                  BLASTN
                  g168460
NCBI GI
BLAST score
                  191
E value
                  1.0e-103
                  203
Match length
% identity
                  99
NCBI Description Zea mays cyclophilin (CyP) mRNA, complete cds
Seq. No.
                  292476
                  LIB3061-013-Q1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q22514
BLAST score
                  86
E value
                  1.0e-40
Match length
                   336
                  84
% identity
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                  292477
Seq. No.
                  LIB3061-013-Q1-K1-C10
Seq. ID
Method
                  BLASTN
NCBI GI
                   g22445
BLAST score
                   60
                   4.0e-25
E value
Match length
                   220
% identity
                   82
NCBI Description Zea mays ZMPMS1 gene for 19 kDa zein protein
                   292478
Seq. No.
                   LIB3061-013-Q1-K1-D2
Seq. ID
                   BLASTN
Method
                   g170784
NCBI GI
BLAST score
                   34
                   2.0e-09
E value
Match length
                   70
                   87
% identity
NCBI Description Wheat ubiquitin carrier protein (UBC1) mRNA, complete cds
                   292479
Seq. No.
                   LIB3061-013-Q1-K1-D5
Seq. ID
                   BLASTN
Method
                   g168665
NCBI GI
BLAST score
                   288
E value
                   1.0e-161
                   300
Match length
```

Seq. No. 292480

% identity

Seq. ID LIB3061-013-Q1-K1-E2

99

NCBI Description Maize 16-kDa zein-2 mRNA, complete cds



```
BLASTX
Method
                  g3850821
NCBI GI
BLAST score
                  219
                  3.0e-18
E value
                  70
Match length
% identity
                  (Y18350) U2 snRNP auxiliary factor, large subunit
NCBI Description
                  [Nicotiana plumbaginifolia]
                  292481
Seq. No.
                  LIB3061-013-Q1-K1-E6
Seq. ID
                  BLASTN
Method
                  q22288
NCBI GI
                  55
BLAST score
                  3.0e-22
E value
                  107
Match length
% identity
NCBI Description Maize mRNA fragment for endosperm glutelin-2
                  292482
Seq. No.
Seq. ID
                  LIB3061-013-Q1-K1-F2
Method
                  BLASTX
                   g2832246
NCBI GI
                   151
BLAST score
                   2.0e-10
E value
                   53
Match length
% identity
                  (AF031569) 22-kDa alpha zein 8 [Zea mays]
NCBI Description
                   292483
Seq. No.
                   LIB3061-013-Q1-K1-G12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q141597
BLAST score
                   362
                   1.0e-34
E value
Match length
                   119
% identity
                   69
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi 22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
Seq. No.
                   292484
                   LIB3061-013-Q1-K1-G2
Seq. ID
                   BLASTN
Method
                   g22524
NCBI GI
                   65
BLAST score
                   2.0e-28
E value
                   223
Match length
                   84
% identity
NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)
                   292485
Seq. No.
                   LIB3061-013-Q1-K1-H2
Seq. ID
                   BLASTX
Method
```

g141603

381

NCBI GI BLAST score



```
7.0e-37
E value
Match length
                  111
                  75
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                  >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
                  292486
Seq. No.
                  LIB3061-013-Q1-K1-H4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g141608
                  232
BLAST score
                  3.0e-19
E value
                  103
Match length
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_
NCBI Description
                  zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
                  zein [Zea mays]
                  292487
Seq. No.
                  LIB3061-013-Q1-K1-H8
Seq. ID
                  BLASTX
Method
                  g2118425
NCBI GI
                  212
BLAST score
                   6.0e-17
E value
                   61
Match length
% identity
                   subtilisin/chymotrypsin inhibitor - maize
NCBI Description
                   >gi_475253_emb_CAA55588_ (X78988) proteinase inhibitor [Zea
                   mays] >gi 475922 emb CAA49593 (X69972) proteinase
                   inhibitor [Zea mays] > gi_559538_emb_CAA57677_ (X82187)
                   substilin /chymotrypsin-like inhibitor [Zea mays]
                   292488
Seq. No.
                   LIB3061-014-Q1-K1-A1
Seq. ID
                   BLASTX
Method
                   g2662341
NCBI GI
BLAST score
                   501
                   8.0e-51
E value
                   115
Match length
                   83
% identity
                   (D63580) EF-1 alpha [Oryza sativa]
NCBI Description
                   >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza
                   satīva] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha
                   [Oryza sativa]
                   292489
Seq. No.
                   LIB3061-014-Q1-K1-A11
 Seq. ID
                   BLASTX
Method
                   g2150002
NCBI GI
                   367
BLAST score
                   4.0e-35
 E value
                   101
Match length
                   68
 % identity
                   (AF000940) ribonuclease [Hordeum vulgare]
 NCBI Description
```

292490

Seq. No.

% identity

NCBI Description

47



```
LIB3061-014-Q1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q135411
BLAST score
                  608
E value
                  2.0e-63
Match length
                  113
% identity
                  99
NCBI Description
                  TUBULIN ALPHA-2 CHAIN >gi 82732 pir S15772 tubulin alpha-2
                  chain - maize >gi_22148_emb_CAA33733 (X15704)
                  alpha2-tubulin [Zea mays]
                  292491
Seq. No.
Seq. ID
                  LIB3061-014-Q1-K1-C7
Method
                  BLASTN
NCBI GI
                  g4151124
BLAST score
                  43
E value
                  6.0e-15
Match length
                  43
% identity
                  100
NCBI Description Zea mays PDI-like protein mRNA, complete cds
Sea. No.
                  292492
Seq. ID
                  LIB3061-014-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  g141617
BLAST score
                  239
E value
                  4.0e-20
Match length
                  104
% identity
                  50
                  ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                  >gi_100941_pir__S12140_zein_Zc1 - maize
                  >gi 100945_pir B29017 zein 2 - maize
                  >gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                  >gi_168666 (M16460) 16-kDa zein protein [Zea mays]
Seq. No.
                  292493
Seq. ID
                  LIB3061-014-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  q141605
BLAST score
                  516
E value
                  2.0e-54
Match length
                  126
% identity
                  89
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                  292494
Seq. ID
                  LIB3061-014-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g2832246
BLAST score
                  289
                  6.0e-26
E value
Match length
                  148
```

(AF031569) 22-kDa alpha zein 8 [Zea mays]

% identity



```
292495
Seq. No.
                   LIB3061-014-Q1-K1-F11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g141597
BLAST score
                   372
                   1.0e-35
E value
                   109
Match length
% identity
                   70
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi_22545_emb_CAA24728 (V01481) reading frame zein [2]
                   [Zea mays]
                   292496
Seq. No.
                   LIB3061-014-Q1-K1-F5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1037129
BLAST score
                   230
                   1.0e-126
E value
                   409
Match length
                   93 .
% identity
                   (gamma-zeinA) = opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                   Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                   292497
Seq. No.
                   LIB3061-014-Q1-K1-F7
Seq. ID
Method
                   BLASTX
                   q141609
NCBI GI
                   375
BLAST score
E value
                   4.0e-36
                   114
Match length
                   72
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS2) >gi_100944_pir__S15656
NCBI Description
                   zein, 19K - maize >gi_22448_emb_CAA4154\overline{3}_ (X58\overline{7}00) \overline{1}9 kDa
                   zein [Zea mays]
                   292498
Seq. No.
                   LIB3061-014-Q1-K1-G11
Seq. ID
                   BLASTX
Method
                   g232161
NCBI GI
                   195
BLAST score
                    4.0e-15
E value
Match length
                   70
                    66
% identity
                   19 KD GLOBULIN PRECURSOR (ALPHA-GLOBULIN)
NCBI Description
                    >gi 68857_pir__WMRZ19 19K globulin precursor - rice
                    >gi_20159_emb_CAA45400_ (X63990) 19 kDa globulin precursor
                    [Oryza sativa]
                    292499
Seq. No.
                    LIB3061-014-Q1-K1-G4
 Seq. ID
                    BLASTX
Method
                   g168701
NCBI GI
                    259
BLAST score
                    1.0e-22
E value
                    70
Match length
```

BLAST score

E value

267 2.0e-23



NCBI Description

(M60837) zein [Zea mays]

```
292500
Seq. No.
Seq. ID
                  LIB3061-014-Q1-K1-G8
Method
                  BLASTX
                  g141603
NCBI GI
BLAST score
                  330
                  3.0e - 34
E value
                  144
Match length
                  65
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >gi_72311 pir__ZIZM2 19K zein precursor (clone A20) - maize
                  >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
                  292501
Seq. No.
Seq. ID
                  LIB3061-014-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  q141597
                  302
BLAST score
                  1.0e-31
E value
                  131
Match length
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi 72314 pir ZIZM3 19K zein precursor (clone A30) - maize
                   >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
                   [Zea mays]
                   292502
Seq. No.
                   LIB3061-014-Q1-K1-H7
Seq. ID
Method
                   BLASTN
                   q168681
NCBI GI
BLAST score
                   66
                   1.0e-28
E value
Match length
                   122
                   89
% identity
                   Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                   >qi 270686 gb I03333 Sequence 8 from Patent US
                   292503
Seq. No.
                   LIB3061-015-Q1-K1-A7
Seq. ID
Method
                   BLASTX
                   g141597
NCBI GI
BLAST score
                   314
                   3.0e-41
E value
                   138
Match length
                   47
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
                   292504
Seq. No.
                   LIB3061-015-Q1-K1-D2
Seq. ID
                   BLASTX
Method
                   g141597
NCBI GI
```



Match length 129 % identity 48

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)

>gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]

[Zea mays]

Seq. No.

292505

Seq. ID

LIB3061-015-Q1-K1-E4

Method BLASTX
NCBI GI g3461884
BLAST score 225
E value 2.0e-18
Match length 69

% identity
NCBI Description

NCBI Description (AB006082) phosphoribosyl-ATP pyrophosphohydrolase

[Arabidopsis thaliana] >gi_3461886_dbj_BAA32529_ (AB006083)

phosphoribosyl-ATP pyrophosphohydrolase [Arabidopsis

thaliana]

Seq. No. Seq. ID

292506

LIB3061-015-Q1-K1-F7

Method BLASTX
NCBI GI g141597
BLAST score 258
E value 2.0e-22
Match length 76
% identity 70

NCBI Description

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)

>gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]

[Zea mays]

Seq. No.

292507

Seq. ID

LIB3061-016-Q1-K1-A5

Method BLASTX
NCBI GI g224508
BLAST score 150
E value 9.0e-10
Match length 104
% identity 41

NCBI Description

zein A20 [Zea mays]

Seq. No.

292508

Seq. ID

LIB3061-016-Q1-K1-C12

Method BLASTX
NCBI GI g419803
BLAST score 307
E value 4.0e-28
Match length 112
% identity 56

NCBI Description

zein protein - maize >gi_168705 (M72708) zein protein [Zea

mays]

Seq. No.

292509

Seq. ID

LIB3061-016-Q1-K1-D11

Method

BLASTX

```
q141603
NCBI GI
                   506
BLAST score
                   2.0e-51
E value
                   105
Match length
                   97
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                   >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                   >gi_22529_emb_CAA24723 (V01476) zein [Zea mays]
                   292510
Seq. No.
Seq. ID
                   LIB3061-016-Q1-K1-D5
                   BLASTX
Method
                   g100938
NCBI GI
                   149
BLAST score
                   6.0e-10
E value
                   68
Match length
                   60
% identity
                   zein precursor - maize >gi_22442_emb_CAA32513_ (X14335)
NCBI Description
                   zein precursor (AA -21 to 90) [Zea mays]
                   292511
Seq. No.
                   LIB3061-016-Q1-K1-D9
Seq. ID
                   BLASTX
Method
                   q141605
NCBI GI
                   509
BLAST score
                   9.0e-52
E value
                   114
Match length
                    91
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                    >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                   \overline{\text{maize}} > \overline{\text{gi}}_{168680} (M12145) 19 kDa zein protein [Zea mays]
                    292512
Seq. No.
                    LIB3061-016-Q1-K1-E11
Seq. ID
                    BLASTX
Method
                    q1084349
NCBI GI
                    452
BLAST score
E value
                    4.0e-45
                    117
Match length
                    73
 % identity
                    aldehyde dehydrogenase homolog btg-26 - rape
NCBI Description
                    >gi 913941 bbs 164188 (S77096) aldehyde dehydrogenase
                    homolog=btg-26 [Brassica napus, cv. Bridger, Peptide, 494
                    aa] [Brassica napus]
                    292513
 Seq. No.
                    LIB3061-016-Q1-K1-E12
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g1321661
 BLAST score
                    321
                    6.0e-30
 E value
                    83
 Match length
                    77
 % identity
                    (D45423) ascorbate peroxidase [Oryza sativa]
 NCBI Description
```

292514

LIB3061-016-Q1-K1-E3

Seq. No.

Seq. ID



```
Method
                  BLASTX
NCBI GI
                  q2832247
BLAST score
                  199
E value
                  2.0e-19
Match length
                  96
% identity
                  62
                  (AF031569) 22-kDa alpha zein 10 [Zea mays]
NCBI Description
Seq. No.
                  292515
Seq. ID
                  LIB3061-016-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  g629861
BLAST score
                  508
E value
                  1.0e-51
                  120
Match length
                  87
% identity
NCBI Description
                  zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
                  zein Zd1 (19 kDa zein) [Zea mays]
                  292516
Seq. No.
                  LIB3061-016-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3850571
BLAST score
                  188
                  3.0e-14
E value
Match length
                  69
% identity
                   (ACO05278) Similar to gb U85207 snRNP core Sm protein
NCBI Description
                  homolog Sm-X5 from Mus musculus. EST gb_AA612141 comes
                  from this gene. [Arabidopsis thaliana]
                  292517
Seq. No.
                  LIB3061-016-Q1-K1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4185308
BLAST score
                   254
E value
                  2.0e-27
Match length
                  141
% identity
                   55
NCBI Description
                  (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
Seq. No.
                  292518
                  LIB3061-016-Q1-K1-H2
Seq. ID
Method
                  BLASTX
                  g4539303
NCBI GI
BLAST score
                   204
                   4.0e-16
E value
Match length
                  71
                   58
% identity
                  (AL049480) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  292519
                  LIB3061-016-Q1-K1-H5
Seq. ID
```

Method BLASTX NCBI GI q224509 BLAST score 144 E value 4.0e-09



```
Match length
                   43
% identity
NCBI Description zein E19 [Zea mays]
                   292520
Seq. No.
Seq. ID
                   LIB3061-017-Q1-K1-B3
                   BLASTX
Method
                   q141606
NCBI GI
                   264
BLAST score
                   2.0e-23
E value
                   75
Match length
                   73
% identity
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1)
                   >gi_72309_pir__ZIZMD1 19K zein precursor (clone cZ19D1) -
                   \overline{\text{maize}} > \overline{\text{gi}} = 168\overline{682} (M12144) 19 kDa zein protein [Zea mays]
                   292521
Seq. No.
                   LIB3061-017-Q1-K1-C11
Seq. ID
                   BLASTX
Method
                   g141601
NCBI GI
                   209
BLAST score
                   6.0e-17
E value
                   70
Match length
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
NCBI Description
                   >gi_82657_pir__S03417 19K zein precursor (clone gZ19AB11) -
                   maize >gi_22543_emb CAA29340_ (X05911) 19 kd alpha zein (AA
                   1 - 234) [Zea mays]
                    292522
Seq. No.
                   LIB3061-017-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                    q629861
NCBI GI
                    142
BLAST score
                    4.0e-19
E value
                    92
Match length
% identity
                    zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
NCBI Description
                    zein Zd1 (19 kDa zein) [Zea mays]
                    292523
 Seq. No.
                    LIB3061-017-Q1-K1-D11
 Seq. ID
Method
                    BLASTX
 NCBI GI
                    q4455183
                    171
 BLAST score
 E value
                    3.0e-12
                    92
 Match length
                    41
 % identity
                   (AL035521) putative protein [Arabidopsis thaliana]
 NCBI Description
                    292524
 Seq. No.
 Seq. ID
                    LIB3061-017-Q1-K1-E8
 Method
                    BLASTX
 NCBI GI
                    g141602
                    262
 BLAST score
```

3.0e-23

66

E value

Match length



```
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6)
                  >gi 82658 pir A22831 19K zein precursor (clone M6) - maize
                  >gi_22538_emb_CAA26294 (X02450) zein precursor [Zea mays]
                  292525
Seq. No.
Seq. ID
                  LIB3061-017-Q1-K1-G10
                  BLASTN
Method
                  g3821780
NCBI GI
BLAST score
                  37
                  2.0e-11
E value
Match length
                  37
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  292526
Seq. No.
                  LIB3061-017-Q1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3548815
BLAST score
                  161
E value
                  6.0e-11
Match length
                  64
% identity
                  53
NCBI Description
                  (AC005313) similar to axoneme-associated protein mst101
                  [Arabidopsis thaliana]
                  292527
Seq. No.
                  LIB3061-018-Q1-K1-A4
Seq. ID
Method
                  BLASTX
                  g2832247
NCBI GI
BLAST score
                  276
E value
                  2.0e-24
Match length
                  111
% identity
                  57
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]
Seq. No.
                  292528
Seq. ID
                  LIB3061-018-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  g141610
BLAST score
                  144
                  5.0e-09
E value
Match length
                  109
% identity
                  40
NCBI Description ZEIN-ALPHA PRECURSOR (CLONE Z4)
                  292529
Seq. No.
Seq. ID
                  LIB3061-018-Q1-K1-B7
Method
                  BLASTX
```

NCBI GI q141600 BLAST score 144 E value 4.0e-09 Match length 52 % identity 63

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1) NCBI Description

> >gi 72315 pir ZIZMB1 19K zein precursor (clone cZ19B1) maize >gi 168674 (M12143) 19 kDa zein protein [Zea mays]



```
292530
Seq. No.
                  LIB3061-018-Q1-K1-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2462826
BLAST score
                  150
                  1.0e-09
E value
                  138
Match length
% identity
NCBI Description (AF000657) unknown protein [Arabidopsis thaliana]
                  292531
Seq. No.
                  LIB3061-018-Q1-K1-C3
Seq. ID
                  BLASTX
Method
                  g629861
NCBI GI
                  371
BLAST score
                  1.0e-35
E value
                  133
Match length
                  59
% identity
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
                  zein Zdl (19 kDa zein) [Zea mays]
                  292532
Seq. No.
                  LIB3061-018-Q1-K1-C9
Seq. ID
                  BLASTX
Method
                  g629862
NCBI GI
BLAST score
                 433
                   5.0e-44
E value
                  116
Match length
% identity
NCBI Description zein Zdl, 19K - maize >gi_535021_emb_CAA47640_ (X67203)
                   zein Zd1 (19 kDa zein) [Zea mays]
                   292533
Seq. No.
                   LIB3061-018-Q1-K1-D11
Seq. ID
                   BLASTX
Method
                   g224507
NCBI GI
BLAST score
                   511
                   5.0e-52
E value
                   138
Match length
                   78
 % identity
NCBI Description zein Al [Zea mays]
                   292534
 Seq. No.
                   LIB3061-018-Q1-K1-E11
 Seq. ID
                   BLASTX
Method
                   g141604
 NCBI GI
 BLAST score
                   389
                   9.0e-38
 E value
                   125
 Match length
 % identity
                   67
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)
 NCBI Description
                   >gi_72310_pir__ZIZM91 19K zein precursor (clone cZ19C1) -
                   maize >gi_168678 (M12146) 19 kDa zein protein [Zea mays]
```

292535

LIB3061-018-Q1-K1-E3

Seq. No.

Seq. ID

Seq. No.

Seq. ID

292540

LIB3061-018-Q1-K1-G1



```
BLASTX
Method
NCBI GI
                  q141600
BLAST score
                  373
                  1.0e-35
E value
Match length
                  113
% identity
                  73
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
                  >gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) -
                  maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]
                  292536
Seq. No.
                  LIB3061-018-Q1-K1-E4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2895866
                  184
BLAST score
E value
                   3.0e-14
Match length
                   64
% identity
                   (AF045770) methylmalonate semi-aldehyde dehydrogenase
NCBI Description
                   [Oryza sativa]
                   292537
Seq. No.
                  LIB3061-018-Q1-K1-E5
Seq. ID
                   BLASTX
Method
                   g141600
NCBI GI
                   230
BLAST score
E value
                   2.0e-21
                   114
Match length
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
                   >gi 72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) -
                   maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]
                   292538
Seq. No.
                   LIB3061-018-Q1-K1-E8
Seq. ID
Method
                   BLASTN
                   g16072
NCBI GI
BLAST score
                   116
                   1.0e-58
E value
                   263
Match length
                   87
% identity
                  Acetabularia mediterranea zein gene
NCBI Description
                   292539
Seq. No.
                   LIB3061-018-Q1-K1-F6
Seq. ID
                   BLASTX
Method
                   g542182
NCBI GI
                   173
BLAST score
                   6.0e-13
E value
                   40
Match length
                   85
% identity
                   vicilin-like storage protein Glb1-L, embryo - maize
NCBI Description
                   >qi 22284 emb CAA41809 (X59083) vicilin-like embryo
                   storage protein [Zea mays]
```



```
Method
                  BLASTX
                  g224509
NCBI GI
BLAST score
                  175
E value
                  2.0e-13
Match length
                  87
% identity
                  55
NCBI Description zein E19 [Zea mays]
Seq. No.
                  292541
Seq. ID
                  LIB3061-019-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g141615
BLAST score
                  321
E value
                  7.0e-30
                  108
Match length
                  61
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
                  >gi 22536_emb_CAA24727 (V01480) zein protein 3 [Zea mays]
Seq. No.
                  292542
                  LIB3061-019-Q1-K1-G10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168669
BLAST score
                  135
E value
                  7.0e-70
Match length
                  303
% identity
                  86
NCBI Description
                  Maize 19 kDa zein mRNA, clone cZ19A2, partial cds
                  292543
Seq. No.
                  LIB3061-019-Q1-K1-H10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4140643
BLAST score
                  40
                  2.0e-13
E value
Match length
                  60
% identity
                  92
NCBI Description
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
                  complete sequence
Seq. No.
                  292544
Seq. ID
                  LIB3061-020-Q1-K1-A2
Method
                  BLASTN
NCBI GI
                  g22441
BLAST score
                  106
E value
                  1.0e-52
                  278
Match length
                  85
% identity
NCBI Description Maize pML2 gene for zein
                  292545
Seq. No.
Seq. ID
                  LIB3061-020-Q1-K1-B10
Method
                  BLASTX
```

E value 2.0e-23

g1731426

263

Match length 63

NCBI GI

BLAST score



```
% identity
                  ZEAMATIN PRECURSOR >gi_459170 (U06831) unnamed protein
NCBI Description
                  product [Zea mays]
                  292546
Seq. No.
Seq. ID
                  LIB3061-020-Q1-K1-B3
Method
                  BLASTN
NCBI GI
                  q168484
BLAST score
                  68
                  5.0e-30
E value
Match length
                  232
                  82
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
Seq. No.
                  292547
Seq. ID
                  LIB3061-020-Q1-K1-D11
Method
                  BLASTX
                3 g4185308
NCBI GI
BLAST score
                  234
                  2.0e-19
E value
Match length
                  94
                  56
% identity
NCBI Description (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
Seq. No.
                  292548
                  LIB3061-020-Q1-K1-D9
Seq. ID
Method
                  BLASTX
                  g2668742
NCBI GI
BLAST score
                  390
E value
                  5.0e-38
Match length
                  84
% identity
                  89
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]
                  292549
Seq. No.
                  LIB3061-020-Q1-K1-E9
Seq. ID
Method
                  BLASTX
                  q2832246
NCBI GI
BLAST score
                  218
                  7.0e-18
E value
Match length
                  72
                  65
% identity
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]
Seq. No.
                  292550
                  LIB3061-020-Q1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q419803
BLAST score
                  334
E value
                  3.0e-31
Match length
                  112
```

% identity 61

zein protein - maize >gi 168705 (M72708) zein protein [Zea NCBI Description

Seq. No. 292551

LIB3061-020-Q1-K1-G11 Seq. ID

BLAST score

243



```
BLASTX
Method
                   g168693
NCBI GI
BLAST score
                   433
                   7.0e-43
E value
Match length
                   142
% identity
NCBI Description (M29627) zein [Zea mays]
                   292552
Seq. No.
                   LIB3061-020-Q1-K1-G6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g141609
                   450
BLAST score
                   7.0e-45
E value
                   130
Match length
                   72
% identity
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS2) >gi_100944_pir_
                   zein, 19K - maize >gi_22448_emb_CAA4154\overline{3}_ (X58\overline{7}00) \overline{1}9 kDa
                   zein [Zea mays]
                   292553
Seq. No.
                   LIB3061-020-Q1-K1-H10
Seq. ID
                   BLASTX
Method
                   g168701
NCBI GI
BLAST score
                   169
                   7.0e-20
E value
                   105
Match length
% identity
NCBI Description (M60837) zein [Zea mays]
                   292554
Seq. No.
Seq. ID
                   LIB3061-020-Q1-K1-H7
Method
                   BLASTX
                   q82659
NCBI GI
BLAST score
                   174
                    2.0e-12
E value
Match length
                    105
% identity
                    45
NCBI Description 19K zein precursor (clone Z4) - maize
                    >gi 4388702_emb_CAA24719_ (V01472) zein [Zea mays]
                    292555
Seq. No.
                    LIB3061-021-Q1-K1-A3
Seq. ID
                    BLASTX
Method
                    q82660
NCBI GI
                    268
BLAST score
                    2.0e-23
E value
                    100
Match length
                    59
 % identity
                    19K zein precursor (clone ZG31A) - maize (fragment)
 NCBI Description
                    >gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]
                    292556
 Seq. No.
                    LIB3061-021-Q1-K1-A4
 Seq. ID
                    BLASTX
 Method
                    g419803
 NCBI GI
```

% identity

72



```
1.0e-34
E value
                  126
Match length
                  65
% identity
                  zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                  mays]
                  292557
Seq. No.
                  LIB3061-021-Q1-K1-A5
Seq. ID
                  BLASTN
Method
                  q2832242
NCBI GI
                  77
BLAST score
                  3.0e-35
E value
                  201
Match length
                  43
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                  292558
Seq. No.
                  LIB3061-021-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g16073
BLAST score
                  145
E value
                  4.0e-09
                  76
Match length
                  49
% identity
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
                  292559
Seq. No.
                  LIB3061-021-Q1-K1-D6
Seq. ID
Method
                  BLASTN
                   g168700
NCBI GI
BLAST score
                   57
E value
                   3.0e-23
                   264
Match length
                   85
% identity
NCBI Description Z.mays zein mRNA, complete cds
                   292560
Seq. No.
                   LIB3061-021-Q1-K1-D8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g141601
                   216
BLAST score
                   6.0e-21
E value
                   102
Match length
                   63
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
NCBI Description
                   >gi_82657_pir__S03417 19K zein precursor (clone gZ19AB11) -
                   maize >gi_22543_emb_CAA29340_ (X05911) 19 kd alpha zein (AA
                   1 - 234) [Zea mays]
                   292561
Seq. No.
                   LIB3061-021-Q1-K1-F10
Seq. ID
Method
                   BLASTX
                   q224507
NCBI GI
BLAST score
                   481
                   2.0e-48
E value
                   144
Match length
```



NCBI Description zein Al [Zea mays]

```
292562
Seq. No.
                  LIB3061-021-Q1-K1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168663
                  67
BLAST score
                  1.0e-29
E value
                  141
Match length
                  89
% identity
NCBI Description Maize sulfur-rich zein protein of Mr 15,000, complete cds
                  292563
Seq. No.
                  LIB3061-021-Q1-K1-G2
Seq. ID
                  BLASTX
Method
                  q168691
NCBI GI
BLAST score
                  324
                  3.0e-30
E value
Match length
                  87
                   77
% identity
NCBI Description (M29628) zein [Zea mays]
                   292564
Seq. No.
                  LIB3061-021-Q1-K1-G7
Seq. ID
                  BLASTN
Method
                   g1185555
NCBI GI
BLAST score
                   197
                   1.0e-107
E value
                   388
Match length
                   91
% identity
                   Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc4)
NCBI Description
                   gene, partial cds
                   292565
Seq. No.
                   LIB3061-021-Q1-K1-H5
Seq. ID
                   BLASTX
Method
                   g141603
NCBI GI
BLAST score
                   479
E value
                   3.0e-48
Match length
                   118
                   86
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                   >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                   >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
                   292566
Seq. No.
                   LIB3061-021-Q1-K1-H7
Seq. ID
Method
                   BLASTX
                   g141607
NCBI GI
                   308
BLAST score
                   4.0e-28
E value
                   132
Match length
% identity
                   54
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE PZ19.1)
NCBI Description
                   >gi_22521_emb_CAA24718_ (V01471) zein [Zea mays] >gi_168672
```

(J01244) zein 19 kd protein (partial) [Zea mays]



```
292567
Seq. No.
                  LIB3061-022-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                  q468516
NCBI GI
                  209
BLAST score
                  5.0e-17
E value
Match length
                  69
                  67
% identity
NCBI Description (X55724) zein [Zea mays]
                  292568
Seq. No.
                  LIB3061-022-Q1-K1-B4
Seq. ID
                  BLASTX
Method
                  g419803
NCBI GI
                  185
BLAST score
                  5.0e-14
E value
                  81
Match length
                  46
% identity
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea
                  mays]
                  292569
Seq. No.
                  LIB3061-022-Q1-K1-B5
Seq. ID
                  BLASTX
Method
                                          Section 1
                  q1684857
NCBI GI
                   629
BLAST score
                   8.0e-66
E value
                  137
Match length
                   33
% identity
NCBI Description (U77940) polyubiquitin [Phaseolus vulgaris]
                   292570
Seq. No.
                   LIB3061-022-Q1-K1-B8
Seq. ID
                   BLASTX
Method
                   g16073
NCBI GI
BLAST score
                   266
                   2.0e-23
E value
Match length
                   84
% identity
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
                   292571
Seq. No.
                   LIB3061-022-Q1-K1-C8
Seq. ID
                   BLASTN
Method
                   q2832242
NCBI GI
BLAST score
                   65
                   3.0e-28
E value
Match length
                   299
                   13
 % identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                   292572
 Seq. No.
                   LIB3061-022-Q1-K1-D5
 Seq. ID
                   BLASTX
 Method
                   g4185308
 NCBI GI
                   216
 BLAST score
```

1.0e-17

E value



```
Match length
                  93
                  54
% identity
                  (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
NCBI Description
                  292573
Seq. No.
Seq. ID
                  LIB3061-022-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g82696
BLAST score
                  236
                  5.0e-20
E value
                  65
Match length
                  74
% identity
                  glycine-rich protein - maize >gi_22293_emb CAA43431
NCBI Description
                  (X61121) glycine-rich protein [Zea mays]
                  292574
Seq. No.
Seq. ID
                  LIB3061-022-Q1-K1-F1
Method
                  BLASTX
                  q141617
NCBI GI
BLAST score
                  304
E value
                  1.0e-31
Match length
                  101
% identity
                  71
                  ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                  >gi_100941_pir__S12140 zein Zc1 - maize
                  >gi 100945 pir B29017 zein 2 - maize
                  >gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                  >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
Seq. No.
                  292575
                  LIB3061-022-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q16073
BLAST score
                  395
                  2.0e-38
E value
Match length
                  108
                  76
% identity
NCBI Description
                  (X59526) zein protein [Acetabularia mediterranea]
                  292576
Seq. No.
Seq. ID
                  LIB3061-022-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g141608
BLAST score
                  156
E value
                  6.0e-11
                  73
Match length
                  55
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943 pir S15655
NCBI Description
                  zein, 19K - maize >gi 22446 emb CAA37651 (X53582) 19 kDa
                  zein [Zea mays]
```

Seq. No. 292577

LIB3061-022-Q1-K1-G4 Seq. ID

Method BLASTX NCBI GI q141603 BLAST score 600 2.0e-62 E value



```
Match length
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >gi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
                  >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
                  292578
Seq. No.
                  LIB3061-023-Q1-K1-A11
Seq. ID
                  BLASTN
Method
                  g1037129
NCBI GI
BLAST score
                  238
                  1.0e-131
E value
                   401
Match length
% identity
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
                  Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                   292579
Seq. No.
Seq. ID
                  LIB3061-023-Q1-K1-A12
                  BLASTN
Method
                   q22524
NCBI GI
                   83
BLAST score
                   4.0e-39
E value
                   123
Match length
                   92
% identity
NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)
                   292580
Seq. No.
                   LIB3061-023-Q1-K1-A2
Seq. ID
                   BLASTX
Method
                   q3790102
NCBI GI
                   231
BLAST score
                   2.0e-19
E value
Match length
                   102
% identity
                   (AF095521) pyrophosphate-dependent phosphofructokinase
NCBI Description
                   alpha subunit [Citrus X paradisi]
                   292581
Seq. No.
                   LIB3061-023-Q1-K1-A9
Seq. ID
                   BLASTN
Method
NCBI GI
                   g168690
BLAST score
                   34
                   1.0e-09
E value
                   34
Match length
                   100
 % identity
NCBI Description Maize zein mRNA, complete cds, clone ZG124
                   292582
 Seq. No.
                   LIB3061-023-Q1-K1-B1
 Seq. ID
                   BLASTX
 Method
                   g168699
 NCBI GI
 BLAST score
                   269
                   1.0e-23
 E value
                   86
 Match length
                   65
 % identity
```

(M60836) zein [Zea mays]

NCBI Description

```
292583
                   LIB3061-023-Q1-K1-B12
                   BLASTX
                   g100925
BLAST score
                   170
                   1.0e-12
```

59 % identity zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_ NCBI Description (X58197) 27kDa storage protein, zein [Zea mays]

292584 Seq. No. LIB3061-023-Q1-K1-B6 Seq. ID BLASTX Method g141603 NCBI GI

54

412 BLAST score 2.0e-42 E value 142 Match length 66 % identity

Seq. No.

Seq. ID

NCBI GI

E value

Match length

Method

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20) NCBI Description

>gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize

>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

292585 Seq. No. LIB3061-023-Q1-K1-B7 Seq. ID BLASTX Method

g2832247 NCBI GI 199 BLAST score 2.0e-15 E value 117 Match length 41 % identity

NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

292586 Seq. No.

LIB3061-023-Q1-K1-C2 Seq. ID

BLASTX Method NCBI GI q224508 402 BLAST score E value 3.0e-39 101 Match length % identity

NCBI Description zein A20 [Zea mays]

292587 Seq. No.

LIB3061-023-Q1-K1-C9 Seq. ID

BLASTX Method g82659 NCBI GI BLAST score 316 1.0e-35 E value 130 Match length 69 % identity

19K zein precursor (clone Z4) - maize NCBI Description

>gi_4388702_emb_CAA24719_ (V01472) zein [Zea mays]

292588 Seq. No.

LIB3061-023-Q1-K1-D12 Seq. ID



```
Method
                  BLASTX
NCBI GI
                  g141608
BLAST score
                  183
E value
                  1.0e-13
                  38
Match length
                  95
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943 pir S15655
                  zein, 19K - maize >gi 22446 emb CAA37651 (X53582) 19 kDa
                  zein [Zea mays]
                  292589
Seq. No.
Seq. ID
                  LIB3061-023-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  g141614
BLAST score
                  271
E value
                  7.0e-24
Match length
                  103
% identity
                  59
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)
NCBI Description
                  >gi 82662 pir B22831 22K zein precursor (clone M1) - maize
                  >qi 22527 emb CAA24722 (V01475) reading frame zein [Zea
                  mays] >gi 224510 prf 1107201D zein M1 [Zea mays]
Seq. No.
                  292590
Seq. ID
                  LIB3061-023-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g2660677
BLAST score
                  411
                  3.0e-40
E value
Match length
                  124
% identity
                  61
NCBI Description
                  (AC002342) unknown protein [Arabidopsis thaliana]
Seq. No.
                  292591
                  LIB3061-023-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q22216
BLAST score
                  243
E value
                  1.0e-20
                  73
Match length
                  74
% identity
NCBI Description
                  (X55722) 22kD zein [Zea mays]
                  292592
Seq. No.
Seq. ID
                  LIB3061-023-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  g2833385
BLAST score
                  180
E value
                  1.0e-19
Match length
                  114
```

51 % identity

NCBI Description GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR

>qi 1255714 (U23945) granule-bound starch synthase

precursor [Sorghum bicolor]

292593 Seq. No.

Seq. ID LIB3061-023-Q1-K1-E9



```
BLASTX
Method
                  g470340
NCBI GI
BLAST score
                  155
                  3.0e-10
E value
                  119
Match length
% identity
                  35
NCBI Description (U00043) similar to beta-mannosyltransferase
                  [Caenorhabditis elegans]
                  292594
Seq. No.
                  LIB3061-023-Q1-K1-G1
Seq. ID
                  BLASTX
Method
                  q224508
NCBI GI
                  608
BLAST score
                   3.0e-63
E value
                  135
Match length
                   93
% identity
NCBI Description zein A20 [Zea mays]
                   292595
Seq. No.
                  LIB3061-023-Q1-K1-G11
Seq. ID
                  BLASTX
Method
                   q224515
NCBI GI
                   168
BLAST score
                   6.0e-12
E value
                   54
Match length
% identity
NCBI Description zein My2 [Zea mays]
                   292596
Seq. No.
                   LIB3061-023-Q1-K1-G6
Seq. ID
                   BLASTX
Method
                   g141605
NCBI GI
                   541
BLAST score
                   2.0e-55
E value
                   131
Match length
 % identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                   >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                   maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
                   292597
 Seq. No.
                   LIB3061-023-Q1-K1-H12
 Seq. ID
                   BLASTX
 Method
                   g168691
 NCBI GI
                   268
 BLAST score
                   8.0e-24
 E value
 Match length
                   82
 % identity
                   72
                   (M29628) zein [Zea mays]
 NCBI Description
                   292598
 Seq. No.
                   LIB3061-023-Q1-K1-H2
 Seq. ID
                   BLASTN
 Method
                   g168681
 NCBI GI
```

218

1.0e-119

BLAST score

E value



292604

% identity

Seq. No.

```
Match length
                  57
% identity
                  Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                  >gi_270686_gb_I03333_ Sequence 8 from Patent US
                  292599
Seq. No.
Seq. ID
                  LIB3061-023-Q1-K1-H7
                  BLASTN
Method
                  q22445
NCBI GI
                  33
BLAST score
                  2.0e-09
E value
                  49
Match length
                  92
% identity
NCBI Description Zea mays ZMPMS1 gene for 19 kDa zein protein
                  292600
Seq. No.
Seq. ID
                  LIB3061-024-Q1-K1-A8
                  BLASTX
Method
NCBI GI
                  q4406810
                  225
BLAST score
                   8.0e-19
E value
                  87
Match length
                   49
% identity
NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]
                   292601
Seq. No.
                  LIB3061-024-Q1-K1-B8
Seq. ID
                  BLASTX
Method
                   g168691
NCBI GI
                   229
BLAST score
                   3.0e-19
E value
                   81
Match length
                   64
% identity
NCBI Description
                  (M29628) zein [Zea mays]
                   292602
Seq. No.
Seq. ID
                   LIB3061-024-Q1-K1-C1
Method
                   BLASTN
                   g168679
NCBI GI
                   147
BLAST score
                   3.0e-77
E value
Match length
                   246
 % identity
                   90
                   Maize 19 kDa zein mRNA, clone cZ19C2, complete cds.
NCBI Description
                   >gi 270687_gb_I03334_ Sequence 9 from Patent US
                   292603
 Seq. No.
                   LIB3061-024-Q1-K1-C7
 Seq. ID
Method
                   BLASTN
NCBI GI
                   g22445
 BLAST score
                   42
                   9.0e-15
 E value
 Match length
                   46
```

40779

NCBI Description Zea mays ZMPMS1 gene for 19 kDa zein protein

Seq. ID

Method



```
LIB3061-024-Q1-K1-D7
Seq. ID
                  BLASTX
Method
                  q141616
NCBI GI
                  227
BLAST score
                  4.0e-19
E value
Match length
                  50
% identity
NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
                  >gi 168662 (M12147) 15 kDa zein protein [Zea mays]
                  292605
Seq. No.
                  LIB3061-024-Q1-K1-D9
Seq. ID
                  BLASTX
Method
                  q508545
NCBI GI
                  303
BLAST score
                  1.0e-27
E value
                  101
Match length
                   66
% identity
NCBI Description (L34340) zein [Zea mays]
                  292606
Seq. No.
                  LIB3061-024-Q1-K1-E6
Seq. ID
                  BLASTX
Method
                   g3138799
NCBI GI
                   215
BLAST score
                   1.0e-17
E value
                   41
Match length
% identity
NCBI Description (AB014058) beta 6 subunit of 20S proteasome [Oryza sativa]
                   292607
Seq. No.
Seq. ID
                   LIB3061-024-Q1-K1-F5
Method
                   BLASTX
                   q224507
NCBI GI
                   153
BLAST score
                   2.0e-10
E value
                   42
Match length
                   79
% identity
NCBI Description zein Al [Zea mays]
                   292608
Seq. No.
                   LIB3061-024-Q1-K1-F9
Seq. ID
Method
                   BLASTX
                   g2493046
NCBI GI
BLAST score
                   366
                   5.0e-35
E value
                   114
Match length
                   62
 % identity
                   ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                   >gi_82297_pir__A41740 H+-transporting ATP synthase (EC
                   3.6.1.34) delta' chain precursor - sweet potato
                   >gi_217938_dbj_BAA01511_ (D10660) mitochondrial F1-ATPase
                   delta subunit [Ipomoea batatas]
                   292609
 Seq. No.
```

40780

LIB3061-024-Q1-K1-G12

BLASTN



```
q609287
NCBI GI
                    113
BLAST score
                    1.0e-56
E value
Match length
                    165
% identity
                    92
NCBI Description Z.diploperennis Grandel gene
                    292610
Seq. No.
                    LIB3061-024-Q1-K1-G4
Seq. ID
Method
                    BLASTX
                    q168701
NCBI GI
                    289
BLAST score
                    2.0e-26
E value
Match length
                    68
                    85
% identity
NCBI Description (M60837) zein [Zea mays]
                    292611
Seq. No.
                    LIB3061-024-Q1-K1-H4
Seq. ID
Method
                    BLASTN
NCBI GI
                    g2832242
                    80
BLAST score
                    3.0e-37
E value
                    140
Match length
% identity
                    11
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.
                    292612
                    LIB3061-024-Q1-K1-H5
Seq. ID
                    BLASTX
Method
                    q135060
NCBI GI
BLAST score
                    324
                    1.0e-30
E value
                    75
Match length
                    81
% identity.
                    SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
NCBI Description
                    (SHRUNKEN-1) >gi_66570_pir__YUZMS sucrose synthase (EC 2.4.1.13) - maize >gi_22486_emb_CAA26247__(X02400) sucrose
                    synthase [Zea mays] > \overline{gi}_224\overline{8}8 = \overline{mb}_CAA262\overline{2}9 (X02382)
                    sucrose synthase [Zea mays]
                    292613
Seq. No.
                    LIB3061-025-Q1-K1-A10
Seq. ID
                    BLASTX
Method
                    g2501196
NCBI GI
                    271
BLAST score
                    7.0e-24
E value
                     47
Match length
                     98
 % identity
NCBI Description GAMMA-ZEATHIONIN
 Seq. No.
                     292614
                    LIB3061-025-Q1-K1-A5
 Seq. ID
                    BLASTX
 Method
```

g141603

153 1.0e-10

NCBI GI BLAST score

E value



Match length % identity

```
ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >gi 72311 pir_ZIZM2 19K zein precursor (clone A20) - maize
                  >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
                  292615
Seq. No.
                  LIB3061-025-Q1-K1-A6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4185513
BLAST score
                  215
                  2.0e-17
E value
                   60
Match length
% identity
                   (AF102823) actin depolymerizing factor 5 [Arabidopsis
NCBI Description
                   thaliana] >gi_4185517 (AF102825) actin depolymerizing
                   factor 5 [Arabidopsis thaliana]
                   292616
Seq. No.
                  LIB3061-025-Q1-K1-B2
Seq. ID
                  BLASTN
Method
NCBI GI
                   q22544
                   155
BLAST score
                   8.0e-82
E value
                   187
Match length
                   96
% identity
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
                   292617
Seq. No.
                   LIB3061-025-Q1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q629861
BLAST score
                   199
E value
                   2.0e-15
                   119
Match length
% identity
                   46
                   zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
NCBI Description
                   zein Zd1 (19 kDa zein) [Zea mays]
                   292618
Seq. No.
                   LIB3061-025-Q1-K1-C10
Seq. ID
                   BLASTN
Method
NCBI GI
                   g22528
                   68
BLAST score
                   6.0e-30
E value
                   76
Match length
                   60
% identity
                   Zea mays mRNA encoding a zein (clone A20)
NCBI Description
                   292619
Seq. No.
                   LIB3061-025-Q1-K1-C12
Seq. ID
Method
                   BLASTX
                   g629861
NCBI GI
BLAST score
                   380
E value
                   1.0e-36
                   111
Match length
% identity
                   71
```



zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203) NCBI Description zein Zdl (19 kDa zein) [Zea mays]

292620 Seq. No.

Seq. ID LIB3061-025-Q1-K1-C4

Method BLASTX q4587513 NCBI GI 285 BLAST score 9.0e-26 E value 99 Match length % identity

NCBI Description (AC007060) Contains eukaryotic protein kinase domain

PF 00069. [Arabidopsis thaliana]

Seq. No.

292621

Seq. ID LIB3061-025-Q1-K1-C9 Method BLASTX

NCBI GI q113621 447 BLAST score 1.0e-44 E value 105 Match length 87

% identity NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi 295850 emb CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A

cytoplasmic aldolase [Zea mays]

Seq. No. 292622

LIB3061-025-Q1-K1-D6 Seq. ID

BLASTN Method NCBI GI q4185305 216 BLAST score 1.0e-118 E value 386 Match length 90 % identity

Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 NCBI Description

(sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No. 292623

LIB3061-025-Q1-K1-D7 Seq. ID

Method BLASTN g2828011 NCBI GI BLAST score 81 1.0e-37 E value 193 Match length 85 % identity

Zea mays starch synthase I precursor (Ss1) mRNA, nuclear NCBI Description

gene encoding plastid protein, complete cds

292624 Seq. No.

LIB3061-025-Q1-K1-E2 Seq. ID

BLASTN Method g22542 NCBI GI



```
46
BLAST score
                  6.0e-17
E value
                  118
Match length
                  86
% identity
NCBI Description Maize gene for Mr 19000 alpha zein and 5'-flanking region
                  292625
Seq. No.
                  LIB3061-025-Q1-K1-E4
Seq. ID
                  BLASTX
Method
                  g16073
NCBI GI
BLAST score
                  385
                  3.0e-37
E value
                  142
Match length
% identity
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
                   292626
Seq. No.
                   LIB3061-025-Q1-K1-E5
Seq. ID
                   BLASTX
Method
                   q141603
NCBI GI
                   239
BLAST score
                   2.0e-20
E value
                   75
Match length
                   69
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                   >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                   >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
                   292627
Seq. No.
Seq. ID
                   LIB3061-025-Q1-K1-G3
                   BLASTX
Method
                   q1504056
NCBI GI
BLAST score
                   163
                   2.0e-11
E value
                   54
Match length
                   56
% identity
                   (D87045) protein kinase catalytic domain (fragment) [Zea
NCBI Description
                   mays]
                   292628
Seq. No.
                   LIB3061-025-Q1-K1-H6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q224508
BLAST score
                   428
                   3.0e-42
E value
                   131
Match length
 % identity
                   71
NCBI Description
                   zein A20 [Zea mays]
                   292629
 Seq. No.
                   LIB3061-026-Q1-K1-A12
 Seq. ID
                   BLASTX
 Method
                   g2832247
 NCBI GI
                   362
 BLAST score
                   2.0e-34
 E value
                   105
 Match length
```

72

% identity



NCBI Description

```
292630
Seq. No.
                   LIB3061-026-Q1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q141600
                   201
BLAST score
                   1.0e-15
E value
                   109
Match length
% identity
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
                   >gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) -
                   maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]
                   292631
Seq. No.
Seq. ID
                   LIB3061-026-Q1-K1-A5
Method
                   BLASTX
                   q2832247
NCBI GI
                   374
BLAST score
                   6.0e-36
E value
                   140
Match length
                   61
% identity
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]
                   292632
Seq. No.
                   LIB3061-026-Q1-K1-A6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g468516
                   497
BLAST score
                   2.0e-50
E value
                   124
Match length
% identity
NCBI Description (X55724) zein [Zea mays]
                   292633
Seq. No.
                   LIB3061-026-Q1-K1-C11
Seq. ID
                   BLASTX
Method
NCBI GI
                    g141598
BLAST score
                    210
                    6.0e-20
E value
                    116
Match length
% identity
                    59
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE ZG99)
NCBI Description
                    >gi_72313_pir__ZIZM99 19K zein precursor (clone ZG99) -
                    maize >gi_22519_emb_CAA24717_ (V01470) zein [Zea mays]
                    >gi_225\overline{34}_emb_C\overline{A}A24\overline{7}26_ (V01\overline{4}79) zein [Zea mays]
Seq. No.
                    292634
                    LIB3061-026-Q1-K1-C6
 Seq. ID
                    BLASTX
Method
                    g508545
NCBI GI
                    294
 BLAST score
                    2.0e-26
 E value
                    124
Match length
                    52
 % identity
 NCBI Description (L34340) zein [Zea mays]
```

(AF031569) 22-kDa alpha zein 10 [Zea mays]



```
292635
Seq. No.
                  LIB3061-026-Q1-K1-D11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g141603
BLAST score
                  412
E value
                  2.0e-40
                  114
Match length
                  78
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >gi_72311 pir__ZIZM2 19K zein precursor (clone A20) - maize
                  >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
                  292636
Seq. No.
                  LIB3061-026-Q1-K1-D2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2668742
BLAST score
                  353
                  2.0e-33
E value
                  85
Match length
% identity
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]
                   292637
Seq. No.
Seq. ID
                  LIB3061-026-Q1-K1-G2
                   BLASTN
Method
                   g16072
NCBI GI
BLAST score
                   56
                   6.0e-23
E value
                   116
Match length
% identity
                   88
NCBI Description Acetabularia mediterranea zein gene
Seq. No.
                   292638
                   LIB3061-026-Q1-K1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2832247
BLAST score
                   351
E value
                   3.0e-33
Match length
                   109
                   69
% identity
                  (AF031569) 22-kDa alpha zein 10 [Zea mays]
NCBI Description
Seq. No.
                   292639
                   LIB3061-026-Q1-K1-G5
Seq. ID
                   BLASTX
Method
                   g4324597
NCBI GI
                   423
BLAST score
                   1.0e-41
E value
                   145
Match length
                   62
% identity
                   (AF106324) sodium proton exchanger Nhx1 [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. No.

292640

Seq. ID

LIB3061-026-Q1-K1-H1

Method NCBI GI BLASTX g141614



```
BLAST score
                 1.0e-21
E value
Match length
                 75
                 69
% identity
                 ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)
NCBI Description
                 >gi_82662_pir__B22831 22K zein precursor (clone M1) - maize
                 >gi_22527_emb_CAA24722_ (V01475) reading frame zein [Zea
                 292641
Seq. No.
                 LIB3061-026-Q1-K1-H10
Seq. ID
Method
                 BLASTN
NCBI GI
                  g168673
BLAST score
                  43
                  5.0e-15
E value
Match length
                  71
% identity
                  90
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds_
                  292642
Seq. No.
                  LIB3061-026-Q1-K1-H6
Seq. ID
Method
                  BLASTN
                  g535019
NCBI GI
BLAST score
                  195
                  1.0e-106
E value
                  287
Match length
% identity
                  49
NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)
Seq. No.
                  292643
                  LIB3061-026-Q1-K1-H9
Seq. ID
Method
                  BLASTX
                  g141597
NCBI GI
                  415
BLAST score
                  9.0e-41
E value
                  117
Match length
% identity
                  74
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                  >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                  >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                  [Zea mays]
                  292644
Seq. No.
                  LIB3061-027-Q1-K1-A7
Seq. ID
                  BLASTX
Method
                  g322870
NCBI GI
BLAST score
                  166
                  3.0e-22
E value
                  88
Match length
                  69
% identity
                  glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) -
NCBI Description
                  maize (fragment)
                  292645
Seq. No.
                  LIB3061-027-Q1-K1-A9
Seq. ID
```

BLASTX

g135060

Method NCBI GI



```
BLAST score
                  256
                  4.0e-22
E value
                  54
Match length
                  87
% identity
                  SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
NCBI Description
                   (SHRUNKEN-1) >gi 66570 pir YUZMS sucrose synthase (EC
                  2.4.1.13) - maize >gi 22486 emb_CAA26247_ (X02400) sucrose
                  synthase [Zea mays] >gi_22488_emb_CAA262\overline{2}9_ (X02382)
                  sucrose synthase [Zea mays]
                  292646
Seq. No.
Seq. ID
                  LIB3061-027-Q1-K1-B11
                  BLASTN
Method
                  q4185305
NCBI GI
                  132
BLAST score
                   5.0e-68
E value
Match length
                  282
                   87
% identity
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                   (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                   protein, polyprotein, and copia protein genes, complete
                   cds; and unknown genes
                   292647
Seq. No.
Seq. ID
                  LIB3061-027-Q1-K1-C7
Method ...
                  BLASTX
NCBI GI
                   g141603
                   309
BLAST score
                   2.0e-28
E value
Match length
                   110
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                   >gi 72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                   >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
                   292648
Seq. No.
                   LIB3061-027-Q1-K1-D3
Seq. ID
                   BLASTX
Method
                   g141609
NCBI GI
BLAST score
                   421
E value
                   2.0e-41
Match length
                   129
% identity
                   71
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS2) >gi_100944_pir_
NCBI Description
                   zein, 19K - maize >gi_22448 emb_CAA41543_ (X58700) 19 kDa
                   zein [Zea mays]
                   292649
Seq. No.
                   LIB3061-027-Q1-K1-D4
Seq. ID
                   BLASTN
Method
                   g168673
NCBI GI
                   207
```

BLAST score 1.0e-113 E value

215 Match length 99 % identity

NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds

Seq. ID

Method



```
Seq. No.
                  LIB3061-027-Q1-K1-D7
Seq. ID
                  BLASTN
Method
                  q168665
NCBI GI
                  230
BLAST score
                  1.0e-126
E value
Match length
                  362
                  91
% identity
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds
                  292651
Seq. No.
                  LIB3061-027-Q1-K1-D8
Seq. ID
                  BLASTX
Method
                  g2668742
NCBI GI
                  255
BLAST score
                   3.0e-22
E value
                   62
Match length
                   81
% identity
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]
                   292652
Seq. No.
Seq. ID
                   LIB3061-027-Q1-K1-E1
                   BLASTX
Method
                   q141609
NCBI GI
                   223
BLAST score
                   3.0e-18
E value
                   66
Match length
                   71
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS2) >gi_100944_pir_
NCBI Description
                   zein, 19K - maize >gi_22448_emb_CAA41543_ (X58700) 19 kDa
                   zein [Zea mays]
                   292653
Seq. No.
                   LIB3061-027-Q1-K1-E10
Seq. ID
                   BLASTX
Method
                   g2832247
NCBI GI
                   212
BLAST score
E value
                   1.0e-20
                   138
Match length
                   49
% identity
                   (AF031569) 22-kDa alpha zein 10 [Zea mays]
NCBI Description
Seq. No.
                   292654
                   LIB3061-027-Q1-K1-E5
 Seq. ID
                   BLASTX
Method
                   q141603
NCBI GI
BLAST score
                   389
                   1.0e-37
E value
                   136
Match length
                   66
 % identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
 NCBI Description
                   >gi 72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                   >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
                   292655
 Seq. No.
```

40789

LIB3061-027-Q1-K1-F10

BLASTX



```
g4185308
NCBI GI
                  256
BLAST score
                  4.0e-22
E value
                  146
Match length
% identity
NCBI Description (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
                  292656
Seq. No.
                  LIB3061-027-Q1-K1-F5
Seq. ID
                  BLASTX
Method
                  g2832243
NCBI GI
                  310
BLAST score
                  1.0e-37
E value
                  116
Match length
                  72
% identity
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
                  292657
Seq. No.
                  LIB3061-027-Q1-K1-G11
Seq. ID
                  BLASTX
Method
                  q224508
NCBI GI
                  473
BLAST score
                   2.0e-47
E value
                  147
Match length
                   72
% identity
NCBI Description zein A20 [Zea mays]
                   292658
Seq. No.
Seq. ID
                   LIB3061-027-Q1-K1-G5
                   BLASTN
Method
                   g22524
NCBI GI
                   60
BLAST score
                   3.0e-25
E value
                   184
Match length
                   84
% identity
NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)
                   292659
Seq. No.
                   LIB3061-027-Q1-K1-G6
 Seq. ID
                   BLASTN
Method
                   g2832242
NCBI GI
 BLAST score
                   41
E value
                   6.0e-14
Match length
                   137
                   84
 % identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                   292660
 Seq. No.
                   LIB3061-027-Q1-K1-G8
 Seq. ID
                   BLASTX
 Method
                   g141605
 NCBI GI
                   218
 BLAST score
                   7.0e-18
 E value
 Match length
                   64
                   73
 % identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
 NCBI Description
                   >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
```

Seq. ID



```
maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
```

```
292661
Seq. No.
Seq. ID
                  LIB3061-027-Q1-K1-H2
                  BLASTX
Method
NCBI GI
                  g224509
                  262
BLAST score
                  7.0e-23
E value
                  115
Match length
                   54
% identity
NCBI Description zein E19 [Zea mays]
                   292662
Seq. No.
                  LIB3061-027-Q1-K1-H3
Seq. ID
                   BLASTX
Method
                   q3386600
NCBI GI
BLAST score
                   288
                   6.0e-26
E value
Match length
                   84
% identity
                  (AC004665) putative glycoprotein [Arabidopsis thaliana]
NCBI Description
                   292663
Seq. No.
                   LIB3061-027-Q1-K1-H4
Seq. ID
                   BLASTX
Method
                   g451193
NCBI GI
                   244
BLAST score
                   5.0e-21
E value
                   92
Match length
                   57
% identity
                   (L28008) wali7 [Triticum aestivum]
NCBI Description
                   >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]
                   292664
Seq. No.
Seq. ID
                   LIB3061-027-Q1-K1-H7
                   BLASTX
Method
NCBI GI
                   g72307
BLAST score
                   283
                   3.0e-25
E value
                   93
Match length
                   68
% identity
                   22K zein precursor (clone pZ22.3) - maize >gi_168686
NCBI Description
                   (J01246) 26.99 kd zein protein [Zea mays]
                   292665
Seq. No.
Seq. ID
                   LIB3061-027-Q1-K1-H8
                   BLASTX
Method
                   g82660
NCBI GI
BLAST score
                   369
E value
                   2.0e-35
Match length
                   101
                   46
 % identity
                   19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                   >gi 809117_emb_CAA24720_ (V01473) zein [Zea mays]
                   292666
 Seq. No.
```

40791

LIB3061-028-Q1-K1-A11

Method



BLASTX

```
NCBI GI
                  q464705
BLAST score
                  225
E value
                  1.0e-18
Match length
                  63
% identity
                  70
                  40S RIBOSOMAL PROTEIN S13 >gi 419802 pir __S30146 ribosomal
NCBI Description
                  protein S13.e - maize >gi_288059_emb_CAA44311_ (X62455)
                  cytoplasmatic ribosomal protein S13 [Zea mays]
Seq. No.
                  292667
                  LIB3061-028-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141604
BLAST score
                  207
E value
                  1.0e-16
Match length
                  64
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)
NCBI Description
                  >gi_72310_pir__ZIZM91 19K zein precursor (clone cZ19C1) -
                  maize >gi_168678 (M12146) 19 kDa zein protein [Zea mays]
                  292668
Seq. No.
                  LIB3061-028-Q1-K1-B3
Seq. ID
                  BLASTX
Method
                  g1169469
NCBI GI
BLAST score
                   213
                   4.0e-20
E value
                   66
Match length
% identity
                   73
                  EC PROTEIN HOMOLOG (ZINC-METALLOTHIONEIN CLASS II)
NCBI Description
                   >gi 629848_pir__S47158 metallothionein II - maize
                   >gi 506139 (U10696) Ec metallothionein class II protein
                   [Zea mays] >gi_987123_emb_CAA84233_ (Z34469) class II
                   metallothionein with homology to wheat Ec [Zea mays]
                   >gi 1582362_prf__2118343A metallothionein [Zea mays]
                   292669
Seq. No.
                   LIB3061-028-Q1-K1-D4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g168691
                   179
BLAST score
                   3.0e-13
E value
                   92
Match length
                   46
% identity
                   (M29628) zein [Zea mays]
NCBI Description
                   292670
Seq. No.
                   LIB3061-028-Q1-K1-D6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g141605
BLAST score
                   489
                   3.0e-50
E value
                   129
Match length
% identity
                   88
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                   >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
```

Match length

NCBI Description

% identity

123

[Zea mays]

51



```
maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
                  292671
Seq. No.
Seq. ID
                  LIB3061-028-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  q2832247
BLAST score
                  363
                  8.0e-35
E value
                  102
Match length
% identity
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]
Seq. No.
                  292672
                  LIB3061-028-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141597
BLAST score
                   356
                   8.0e-34
E value
                   133
Match length
                   58
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi 72314 pir ZIZM3 19K zein precursor (clone A30) - maize
                   >qi 22545 emb CAA24728 (V01481) reading frame zein [2]
                   [Zea mays]
                   292673
Seq. No.
Seq. ID
                   LIB3061-028-Q1-K1-H12
Method
                   BLASTX
                   q629861
NCBI GI
BLAST score
                   171
                   3.0e-14
E value
                   96
Match length
% identity
                   53
                   zein Zdl, 19K - maize >gi 535020 emb CAA47639 (X67203)
NCBI Description
                   zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                   292674
                   LIB3061-028-Q1-K1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g16073
BLAST score
                   385
E value
                   3.0e-37
Match length
                   137
% identity
                   62
                   (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
                   292675
Seq. No.
Seq. ID
                   LIB3061-029-Q1-K1-A10
Method
                   BLASTX
NCBI GI
                   g2130141
BLAST score
                   224
                   1.0e-24
E value
```

40793

mudrA protein - maize transposon MuDR >gi_540581 (M76978)

mudrA [Zea mays] >gi 595816 (U14597) mudrA gene product



Seq. No.

```
LIB3061-029-Q1-K1-D2
Seq. ID
Method
                  BLASTX
                  q224508
NCBI GI
                  696
BLAST score
                  1.0e-73
E value
                  150
Match length
                  95
% identity
NCBI Description zein A20 [Zea mays]
                  292677
Seq. No.
                  LIB3061-029-Q1-K1-E11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g729470
BLAST score
                  253
E value
                  1.0e-21
Match length
                  101
                  55
% identity
                  MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
NCBI Description
                   (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
                  >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2)
                  precursor, mitochondrial - potato >gi_297798_emb_CAA79702_
                   (Z21493) mitochondrial formate dehydrogenase precursor
                   [Solanum tuberosum]
 ...
Seq. No.
                  292678
                  LIB3061-029-Q1-K1-E4
Seq. ID
Method
                  BLASTX
                  g462195
NCBI GI
                  198
BLAST score
                  2.0e-15
E value
                  47
Match length
                  81
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                   >gi_100682_pir__S21636 GOS2 protein - rice
                   >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                   >gi_3789950 (AF094774) translation initiation factor [Oryza
                   satīva]
                   292679
Seq. No.
                  LIB3061-029-Q1-K1-F4
Seq. ID
                  BLASTX
Method
                  g16073
NCBI GI
                   411
BLAST score
E value
                   3.0e-40
                   130
Match length
                   67
% identity
                  (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
                   292680
Seq. No.
                   LIB3061-030-Q1-K1-A5
Seq. ID
Method
                   BLASTN
                   g22447
NCBI GI
                   176
BLAST score
E value
                   3.0e-94
Match length
                   483
```



```
% identity
NCBI Description Zea mays ZMPMS2 gene for 19 kDa zein protein
                  292681
Seq. No.
                  LIB3061-030-Q1-K1-B6
Seq. ID
Method
                  BLASTX
                  q451193
NCBI GI
                  276
BLAST score
                  2.0e-24
E value
                  75
Match length
                  73
% identity
                  (L28008) wali7 [Triticum aestivum]
NCBI Description
                  >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]
                  292682
Seq. No.
Seq. ID
                  LIB3061-030-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                   q4185308
                   240
BLAST score
                   3.0e-20
E value
                   94
Match length
                   57
% identity
NCBI Description (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
                   292683
Seq. No.
                   LIB3061-030-Q1-K1-D9
Seq. ID
Method
                   BLASTX
                   g2130022
NCBI GI
                   171
BLAST score
E value
                   3.0e-12
Match length
                   33
                   94
% identity
                   aldose reductase homolog - wild oat >gi_1155213 (U21747)
NCBI Description
                   aldose reductase-related protein [Avena fatua]
                   >gi_1587923_prf__2207360A aldose reductase [Avena fatua]
Seq. No.
                   292684
                   LIB3061-030-Q1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4185308
BLAST score
                   339
E value
                   7.0e-32
Match length
                   126
% identity
                   60
                   (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
NCBI Description
                   292685
Seq. No.
                   LIB3061-030-Q1-K1-E6
Seq. ID
                   BLASTX
Method
                   g16073
NCBI GI
                   399
BLAST score
                   7.0e-39
E value
Match length
                   126
% identity
                   69
                   (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
```

292686

Seq. No.



```
LIB3061-030-Q1-K1-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g16072
BLAST score
                  54
E value
                  1.0e-21
Match length
                  90
                   90
% identity
                  Acetabularia mediterranea zein gene
NCBI Description
                  292687
Seq. No.
Seq. ID
                  LIB3061-030-Q1-K1-G3
                  BLASTX
Method
                  g2244988
NCBI GI
                  228
BLAST score
                   8.0e-19
E value
Match length
                   120
% identity
                  (Z97340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   292688
Seq. No.
                   LIB3061-030-Q1-K1-H12
Seq. ID
Method
                   BLASTX
                   q2148017
NCBI GI
                   140
BLAST score
                   4.0e-09
E value
                   38
Match length
% identity
                   63
                   ribonuclease I precursor - Zinnia elegans >gi_642956
NCBI Description
                   (U19923) ribonuclease [Zinnia elegans]
                   292689
Seq. No.
Seq. ID
                   LIB3061-030-Q1-K1-H8
Method
                   BLASTX
                   g4220532
NCBI GI
BLAST score
                   163
                   2.0e-11
E value
Match length
                   54
                   63
% identity
                   (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   292690
                   LIB3061-031-Q1-K1-B6
Seq. ID
Method
                   BLASTX
                   q629861
NCBI GI
                   343
BLAST score
                   3.0e-32
E value
                   136
Match length
% identity
                   57
                   zein Zdl, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
NCBI Description
                   zein Zd1 (19 kDa zein) [Zea mays]
                   292691
Seq. No.
                   LIB3061-031-Q1-K1-E3
 Seq. ID
                   BLASTX
Method
                   g141600
NCBI GI
```

164

2.0e-21

BLAST score E value



```
99
Match length
% identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
                    >gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) -
                   maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]
                    292692
Seq. No.
                   LIB3061-031-Q1-K1-E4
Sea. ID
                   BLASTX
Method
NCBI GI
                    g141605
BLAST score
                    347
                    7.0e-33
E value
                    103
Match length
% identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                    >gi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) -
                    \overline{\text{maize}} > \overline{\text{gi}} = 168\overline{68}0 \text{ (M12145)}  19 kDa zein protein [Zea mays]
                    292693
Seq. No.
                    LIB3061-031-Q1-K1-F5
Seq. ID
                    BLASTX
Method
NCBI GI
                    q141603
BLAST score
                    517
E value
                    1.0e-52
                    126
Match length
                    85
% identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                    >gi 72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                    >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
Seq. No.
                    292694
                    LIB3061-032-Q1-K1-B9
Seq. ID
Method
                    BLASTX
                    g141608
NCBI GI
BLAST score
                    264
                    4.0e-23
E value
Match length
                    64
                    84
% identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655
NCBI Description
                    zein, 19K - maize >gi_22446_emb_CAA3765\overline{1}_ (X53\overline{5}82) \overline{1}9 kDa
                    zein [Zea mays]
Seq. No.
                    292695
                    LIB3061-032-Q1-K1-C12
Seq. ID
                    BLASTX
Method
                    g168701
NCBI GI
BLAST score
                    157
                    9.0e-16
E value
                    104
Match length
                    54
% identity
NCBI Description
                    (M60837) zein [Zea mays]
```

Seq. No. 292696

Seq. ID LIB3061-032-Q1-K1-C8

Method BLASTN NCBI GI g22215 BLAST score 36

BLAST score

E value Match length 142 8.0e-10

103



```
9.0e-11
E value
Match length
                  92
% identity
NCBI Description
                  Z.mays ZSF4C1 gene for zein
Seq. No.
                  292697
Seq. ID
                  LIB3061-032-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  q141601
BLAST score
                  265
E value
                  5.0e-30
                  135
Match length
% identity
                   62
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
NCBI Description
                  >gi 82657 pir S03417 19K zein precursor (clone gZ19AB11) -
                  maize >gi 22543_emb_CAA29340 (X05911) 19 kd alpha zein (AA
                  1 - 234) [Zea mays]
                  292698
Seq. No.
                  LIB3061-032-Q1-K1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q22542
                  89
BLAST score
                   2.0e-42
E value
                   101
Match length
                   97
% identity
NCBI Description Maize gene for Mr 19000 alpha zein and 5'-flanking region
                   292699
Seq. No.
Seq. ID
                  LIB3061-032-Q1-K1-H5
Method
                   BLASTX
NCBI GI
                   q141604
BLAST score
                   214
E value
                   3.0e-17
Match length
                   101
                   50
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)
NCBI Description
                   >gi_72310_pir__ZIZM91 19K zein precursor (clone cZ19C1) -
                   maize >gi_168678 (M12146) 19 kDa zein protein [Zea mays]
Seq. No.
                   292700
                   LIB3061-033-Q1-K1-A1
Seq. ID
Method
                   BLASTX
                   g168699
NCBI GI
BLAST score
                   281
                   2.0e-25
E value
                   69
Match length
% identity
                   80
                  (M60836) zein [Zea mays]
NCBI Description
                   292701
Seq. No.
                   LIB3061-033-Q1-K1-A11
Seq. ID
Method
                   BLASTX
                   g141605
NCBI GI
```



```
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi 72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                  292702
                  LIB3061-033-Q1-K1-A3
Seq. ID
Method
                  BLASTX
                  g224507
NCBI GI
BLAST score
                  178
```

% identity 65 zein Al [Zea mays] NCBI Description

5.0e-13 55

292703 Seq. No. Seq. ID LIB3061-033-Q1-K1-B11

Method BLASTX q224513 NCBI GI BLAST score 314 5.0e-29 E value Match length 104

% identity 62

E value

Match length

zein M6 [Zea mays] NCBI Description

292704 Seq. No.

Seq. ID LIB3061-033-Q1-K1-B3

BLASTX Method q2696229 NCBI GI BLAST score 194 6.0e-15 E value 63 Match length % identity 63

(D55712) chitinase [Oryza sativa] NCBI Description

292705 Seq. No.

Seq. ID LIB3061-033-Q1-K1-B6

Method BLASTX NCBI GI g2832246 BLAST score 209 9.0e-17 E value Match length 70 % identity 63

(AF031569) 22-kDa alpha zein 8 [Zea mays] NCBI Description

292706 Seq. No.

LIB3061-033-Q1-K1-C12 Seq. ID

Method BLASTX g168699 NCBI GI 223 BLAST score 3.0e-18 E value Match length 64 % identity 73

(M60836) zein [Zea mays] NCBI Description

292707 Seq. No.

LIB3061-033-Q1-K1-C4 Seq. ID

```
Method
NCBI GI
                   g419803
BLAST score
                   278
                   7.0e-25
E value
Match length
                   88
% identity
                   59
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea
                   292708
Seq. No.
Seq. ID
                   LIB3061-033-Q1-K1-D4
                   BLASTN
Method
                   g168694
NCBI GI
                   37
BLAST score
                   2.0e-11
E value
Match length
                   85
% identity
                   87
NCBI Description Maize gamma zein mRNA, partial cds
                   292709
Seq. No.
                   LIB3061-033-Q1-K1-E11
Seq. ID
                   BLASTN
Method
NCBI GI
                   q22516
                   318
BLAST score
                   1.0e-179
E value
                   394
Match length
                   95
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                   292710
Seq. No.
                   LIB3061-033-Q1-K1-E2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q141609
BLAST score
                   301
E value
                   5.0e-28
Match length
                   70
                   89
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS2) >gi_100944_pir__S15656
NCBI Description
                   zein, 19K - maize >gi_22448_emb_CAA4154\overline{3}_ (X58\overline{7}00) \overline{1}9 kDa
                   zein [Zea mays]
                   292711
Seq. No.
                   LIB3061-033-Q1-K1-E5
Seq. ID
                   BLASTX
Method
                   q224514
NCBI GI
                   187
BLAST score
                   1.0e-14
E value
Match length
                   48
                   83
% identity
NCBI Description zein M8 [Zea mays]
                   292712
Seq. No.
                   LIB3061-033-Q1-K1-E9
Seq. ID
                   BLASTX
Method
                   g141601
NCBI GI
```

211

7.0e-17

BLAST score E value



```
Match length
% identity
                  50
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
NCBI Description
                  >gi 82657 pir S03417 19K zein precursor (clone gZ19AB11) -
                  maize >gi 22543 emb CAA29340 (X05911) 19 kd alpha zein (AA
                  1 - 234) [Zea mays]
                  292713
Seq. No.
                  LIB3061-033-Q1-K1-F5
Seq. ID
                  BLASTN
Method
NCBI GI
                  q16072
                  65
BLAST score
                  4.0e-28
E value
                  133
Match length
% identity
NCBI Description Acetabularia mediterranea zein gene
                  292714
Seq. No.
                  LIB3061-033-Q1-K1-F9
Seq. ID
Method
                  BLASTX
                  q3294467
NCBI GI
BLAST score
                  208
                  3.0e-29
E value
                  136
Match length
% identity
NCBI Description (U89341) phosphoglucomutase 1 [Zea mays]
                  292715
Seq. No.
                  LIB3061-033-Q1-K1-G5
Seq. ID
Method
                  BLASTX
                  q121205
NCBI GI
BLAST score
                  200
E value
                  1.0e-15
Match length
                  107
                  50
% identity
                  GLOBULIN-1 S ALLELE PRECURSOR (GLB1-S) (7S-LIKE) >gi_168481
NCBI Description
                   (M24845) globulin precursor [Zea mays]
                  292716
Seq. No.
                  LIB3061-033-Q1-K1-H1
Seq. ID
Method
                  BLASTX
                   q136757
NCBI GI
BLAST score
                  377
                  2.0e-36
E value
                  117
Match length
                   67
% identity
                  GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR
NCBI Description
                   >gi 100881 pir S07314 UDPglucose--starch
                   glucosyltransferase (EC 2.4.1.11) precursor - maize
```

glucosyltransferase (EC 2.4.1.11) precursor - maize
>gi_168653 (M24258) amyloplast-specific transit protein
[Zea mays] >gi_1644339_emb_CAA27574 (X03935) glucosyl

transferase [Zea mays]

Seq. No. 292717

Seq. ID LIB3061-033-Q1-K1-H5

Method BLASTX NCBI GI g112994

Method

NCBI GI

BLASTX

g1707019



```
BLAST score
                  410
                  3.0e-40
E value
Match length
                  89
% identity
                  92
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >qi 82685 pir S04536 embryonic abundant protein,
                  glycine-rich - maize >gi 22313 emb CAA31077 (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi 226091_prf__1410284A abscisic acid inducible gene [Zea
                  mays]
                  292718
Seq. No.
                  LIB3061-033-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g224513
BLAST score
                  367
E value
                  2.0e-35
Match length
                  81
                  93
% identity
NCBI Description zein M6 [Zea mays]
Seq. No.
                  292719
                  LIB3061-034-Q1-K1-A5
Seq. ID
Method
                  BLASTX
                  g629862
NCBI GI
BLAST score
                  486
E value
                  5.0e-49
                  140
Match length
                  71
% identity
                  zein Zd1, 19K - maize >gi 535021 emb CAA47640 (X67203)
NCBI Description
                  zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                  292720
                  LIB3061-034-Q1-K1-B10
Seq. ID
Method
                  BLASTX
                  g629861
NCBI GI
BLAST score
                  320
                  1.0e-29
E value
Match length
                  97
                  68
% identity
                  zein Zd1, 19K - maize >gi 535020 emb_CAA47639_ (X67203)
NCBI Description
                  zein Zd1 (19 kDa zein) [Zea mays]
                  292721
Seq. No.
                  LIB3061-034-Q1-K1-B11
Seq. ID
Method
                  BLASTX
                  g168703
NCBI GI
BLAST score
                  178
                  3.0e-13
E value
Match length
                  35
                  97
% identity
NCBI Description
                  (M86591) 22 kDa zein protein [Zea mays]
                  292722
Seq. No.
                  LIB3061-034-Q1-K1-B4
Seq. ID
```

% identity

86



```
BLAST score
                  2.0e-09
E value
                  98
Match length
% identity
NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]
                  292723
Seq. No.
Seq. ID
                  LIB3061-034-Q1-K1-B9
Method
                  BLASTN
                  g168484
NCBI GI
BLAST score
                  170
E value
                  8.0e-91
Match length
                  301
                  89
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
Seq. No.
                  292724
Seq. ID
                  LIB3061-034-Q1-K1-C7
Method
                  BLASTX
                  g141603
NCBI GI
BLAST score
                  476
                  7.0e-48
E value
Match length
                  129
                  78
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >gi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
                  >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
                  292725
Seq. No.
Seq. ID
                  LIB3061-034-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  g2832247
BLAST score
                  309
E value
                  2.0e-28
Match length
                   98
                   65
% identity
NCBI Description
                  (AF031569) 22-kDa alpha zein 10 [Zea mays]
Seq. No.
                  292726
Seq. ID
                  LIB3061-034-Q1-K1-D9
Method
                  BLASTN
NCBI GI
                   q168681
BLAST score
                   139
E value
                   3.0e-72
Match length
                  227
% identity
                   90
                  Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                  >gi_270686_gb_I03333_ Sequence 8 from Patent US
Seq. No.
                  292727
                  LIB3061-034-Q1-K1-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1061304
BLAST score
                   66
                  9.0e-29
E value
Match length
                  165
```

Seq. ID Method



```
NCBI Description Z.mays ZSF4C5 gene for zein
Seq. No.
                  292728
Seq. ID
                  LIB3061-034-Q1-K1-E9
Method
                  BLASTX
                  q16073
NCBI GI
BLAST score
                  181
E value
                  1.0e-13
Match length
                  64
                  64
% identity
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
                  292729
Seq. No.
                  LIB3061-034-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82660
BLAST score
                   268
E value
                   7.0e-24
                   59
Match length
                   92
% identity
                  19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                   >gi 809117 emb CAA24720 (V01473) zein [Zea mays]
Seq. No.
                   292730
                   LIB3061-034-Q1-K1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2832243
BLAST score
                   162
E value
                   7.0e-12
Match length
                   81
                   57
% identity
                  (AF031569) 22-kDa alpha zein 4 [Zea mays]
NCBI Description
                   292731
Seq. No.
                   LIB3061-035-Q1-K1-A2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g16073
                   377
BLAST score
                   3.0e-36
E value
                   103
Match length
% identity
                   75
                   (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
                   292732
Seq. No.
                   LIB3061-035-Q1-K1-A4
Seq. ID
                   BLASTX
Method
                   g451193
NCBI GI
                   257
BLAST score
                   3.0e-22
E value
                   97
Match length
                   81
% identity
                   (L28008) wali7 [Triticum aestivum]
NCBI Description
                   >gi 1090845_prf__2019486B wali7 gene [Triticum aestivum]
                   292733
Seq. No.
```

40804

LIB3061-035-Q1-K1-B1

BLASTX

BLAST score

E value

166

2.0e-11



```
g168691
NCBI GI
                  169
BLAST score
E value
                  5.0e-25
                  133
Match length
% identity
NCBI Description (M29628) zein [Zea mays]
                  292734
Seq. No.
                  LIB3061-035-Q1-K1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22544
BLAST score
                  138
                  1.0e-71
E value
                  318
Match length
                  87
% identity
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
                  292735
Seq. No.
Seq. ID
                  LIB3061-035-Q1-K1-B4
                  {\tt BLASTX}
Method
                  g224509
NCBI GI
BLAST score
                  244
                  9.0e-21
E value
Match length
                  118
                  50
% identity
NCBI Description zein E19 [Zea mays]
                  292736
Seq. No.
Seq. ID
                  LIB3061-035-Q1-K1-B5
                  BLASTX
Method
NCBI GI
                  q141600
BLAST score
                  182
                   3.0e-27
E value
Match length
                  98
                   65
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
                  >gi 72315 pir ZIZMB1 19K zein precursor (clone cZ19B1) -
                  maize >gi 168674 (M12143) 19 kDa zein protein [Zea mays]
                   292737
Seq. No.
                  LIB3061-035-Q1-K1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4206209
BLAST score
                  299
                   3.0e-27
E value
Match length
                  122
% identity
                   52
                   (AF071527) putative glucan synthase component [Arabidopsis
NCBI Description
                   thaliana] >gi 4263042 gb_AAD15311_ (AC005142) putative
                   glucan synthase component [Arabidopsis thaliana]
                   292738
Seq. No.
Seq. ID
                  LIB3061-035-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                   q168691
```

BLAST score

E value

52

2.0e-20



```
Match length
                      78
   % identity
   NCBI Description
                     (M29628) zein [Zea mays]
   Seq. No.
                      292739
   Seq. ID
                      LIB3061-035-Q1-K1-C8
   Method
                      BLASTX
   NCBI GI
                      q141597
BLAST score
                      292
                      1.0e-42
   E value
   Match length
                      136
   % identity
                      76
                      ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
   NCBI Description
                      >gi 72314 pir ZIZM3 19K zein precursor (clone A30) - maize
                      >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
                      [Zea mays]
   Seq. No.
                      292740
                      LIB3061-035-Q1-K1-D1
   Seq. ID
   Method
                      BLASTX
   NCBI GI
                      q728906
   BLAST score
                      274
   E value
                      1.0e-26
   Match length
                      131
                      53
   % identity
   NCBI Description
                      PROBABLE CALCIUM-TRANSPORTING ATPASE 5
                      >gi 1077722 pir S50669 hypothetical protein YER166w -
                      yeast (Saccharomyces cerevisiae) >gi 603407 (U18922)
                      Yer166wp [Saccharomyces cerevisiae]
                      292741
   Seq. No.
                      LIB3061-035-Q1-K1-E3
   Seq. ID
   Method
                      BLASTX
                      g629861
   NCBI GI
   BLAST score
                      457
                      3.0e-48
   E value
   Match length
                      142
   % identity
                      76
                      zein Zd1, 19K - maize >gi_535020_emb_CAA47639 (X67203)
   NCBI Description
                      zein Zd1 (19 kDa zein) [Zea mays]
   Seq. No.
                      292742
   Seq. ID
                      LIB3061-035-Q1-K1-E4
   Method
                      BLASTX
   NCBI GI
                      g2832246
   BLAST score
                      201
   E value
                      1.0e-22
   Match length
                      142
   % identity
                      50
                      (AF031569) 22-kDa alpha zein 8 [Zea mays]
   NCBI Description
                      292743
   Seq. No.
   Seq. ID
                      LIB3061-035-Q1-K1-F10
   Method
                      BLASTN
                      g22528
   NCBI GI
```

```
188
Match length
% identity
                  82
NCBI Description Zea mays mRNA encoding a zein (clone A20)
Seq. No.
                  292744
Seq. ID
                  LIB3061-035-Q1-K1-F11
                  BLASTX
Method
NCBI GI
                  q544421
BLAST score
                  297
                  8.0e-27
E value
Match length
                  62
                  95
% identity
                  GLYCINE-RICH RNA-BINDING PROTEIN 1 >gi 485420_pir__S12311
NCBI Description
                  glycine-rich RNA-binding protein (clone S1) - sorghum
                  (fragment) >gi 21623 emb CAA40863_ (X57663) glycine-rich
                  RNA-binding protein [Sorghum bicolor]
Seq. No.
                  292745
                  LIB3061-035-Q1-K1-F3
Seq. ID
                  BLASTX
Method
                  q4185308
NCBI GI
BLAST score
                  541
                  2.0e-55
E value
Match length
                  121
% identity
NCBI Description (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
                  292746
Seq. No.
                  LIB3061-035-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q419803
BLAST score
                  358
E value
                  4.0e-34
Match length
                  123
                  64
% identity
                  zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                  mays]
                  292747
Seq. No.
                  LIB3061-035-Q1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539005
BLAST score
                  292
                  3.0e-26
E value
                  148
Match length
                  43
% identity
                  (AL049481) putative oxidoreductase [Arabidopsis thaliana]
NCBI Description
                  292748
Seq. No.
                  LIB3061-035-Q1-K1-H7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g629862
```

Match length 93
% identity 63
NCBI Description zein Zd1, 19K - maize >gi_535021_emb_CAA47640_ (X67203)

291

3.0e-26

BLAST score

E value ,



zein Zd1 (19 kDa zein) [Zea mays]

```
Seq. No.
                   292749
Seq. ID
                   LIB3061-036-Q1-K1-A4
Method
                   BLASTX
NCBI GI
                   g2832247
BLAST score
                   191
                   1.0e-14
E value
Match length
                  73
% identity
                   56
                  (AF031569) 22-kDa alpha zein 10 [Zea mays]
NCBI Description
                   292750
Seq. No.
                   LIB3061-036-Q1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2995405
BLAST score
                   506
E value
                   2.0e-51
Match length
                   143
% identity
                   66
                  (Y12432) polyprotein [Ananas comosus]
NCBI Description
Seq. No.
                   292751
                   LIB3061-036-Q1-K1-B9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g168696
BLAST score
                   61
E value
                   1.0e-25
Match length
                   189
% identity
                   84
NCBI Description Z.mays zein mRNA, 3' end
                   292752
Seq. No.
                   LIB3061-036-Q1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g224509
BLAST score
                   230
E value
                   5.0e-19
                  105
Match length
% identity
                   77
NCBI Description zein E19 [Zea mays]
                   292753
Seq. No.
Seq. ID
                   LIB3061-036-Q1-K1-F2
Method
                   BLASTX
NCBI GI
                   g2655098
BLAST score
                   215
E value
                   3.0e-17
Match length
                   138
% identity
                   39
NCBI Description (AF023472) peptide transporter [Hordeum vulgare]
                   292754
Seq. No.
                  LIB3061-036-Q1-K1-F4
Seq. ID
```

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Method BLASTN NCBI GI g168673 BLAST score 192



```
1.0e-104
E value
Match length
                  357
                  89
% identity
                  Maize 19 kDa zein mRNA, clone cZ19B1, complete cds
NCBI Description
Seq. No.
                  292755
                  LIB3061-036-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                  g141600
NCBI GI
                  176
BLAST score
E value
                  5.0e-21
                  133
Match length
                  53
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
                  >gi 72315 pir ZIZMB1 19K zein precursor (clone cZ19B1) -
                  maize >gi 168674 (M12143) 19 kDa zein protein [Zea mays]
                  292756
Seq. No.
                  LIB3061-036-Q1-K1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4185305
BLAST score
                  78
                  9.0e-36
E value
                  219
Match length
                  89
% identity
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                   (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes
                  292757
Seq. No.
Seq. ID
                  LIB3061-036-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  q4432819
BLAST score
                  547
E value
                  3.0e-56
Match length
                  146
% identity
                   69
                   (AC006593) putative kinesin light chain [Arabidopsis
NCBI Description
                  thaliana]
                   292758
Seq. No.
                  LIB3061-036-Q1-K1-H6
Seq. ID
Method
                  BLASTX
                   q168691
NCBI GI
                   239
BLAST score
                   4.0e-20
E value
Match length
                  118
                   51
% identity
NCBI Description
                  (M29628) zein [Zea mays]
```

Seq. No. 292759

Seq. ID LIB3061-037-Q1-K1-B7

Method BLASTX
NCBI GI g141600
BLAST score 143
E value 9.0e-09



```
Match length
                  100
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
                  >gi 72315 pir ZIZMB1 19K zein precursor (clone cZ19B1) -
                  maize >gi 168674 (M12143) 19 kDa zein protein [Zea mays]
Seq. No.
                  292760
                  LIB3061-037-Q1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q175854
BLAST score
                  68
                  8.0e-30
E value
                  76
Match length
                  97
% identity
NCBI Description O.sativa 28S large subunit rRNA, 5' end
Seq. No.
                  292761
Seq. ID
                  LIB3061-037-Q1-K1-C10
Method
                  BLASTN
NCBI GI
                  q168690
BLAST score
                  65
                  3.0e-28
E value
Match length
                  217
                  83
% identity
NCBI Description Maize zein mRNA, complete cds, clone ZG124
                  292762
Seq. No.
                  LIB3061-037-Q1-K1-D2
Seq. ID
                  BLASTX
Method
NCBI GI
                   q141613
BLAST score
                  162
                   4.0e-11
E value
Match length
                   90
% identity
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
NCBI Description
                   >qi 72305 pir ZIZM21 22K zein precursor (clone pZ22.1) -
                  maize >gi 22532 emb CAA24725 (V01478) zein [Zea mays]
Seq. No.
                   292763
                   LIB3061-037-Q1-K1-D5
Seq. ID
Method
                   BLASTX
                   g16073
NCBI GI
BLAST score
                   153
E value
                   1.0e-10
Match length
                   51
% identity
                  (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
Seq. No.
                   292764
                   LIB3061-037-Q1-K1-D6
Seq. ID
Method
                   BLASTX
                   g4185308
NCBI GI
```

Method BLASTX
NCBI GI g4185308
BLAST score 373
E value 8.0e-36
Match length 90
% identity 86

NCBI Description (AF090446) 22-kDa alpha zein protein 21 [Zea mays]

```
292765
Seq. No.
                  LIB3061-037-Q1-K1-E12
Seq. ID
                  BLASTX
Method
NCBI GI
                   q451193
BLAST score
                   313
                   5.0e-29
E value
                   94
Match length
% identity
                   (L28008) wali7 [Triticum aestivum]
NCBI Description
                   >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]
                   292766
Seq. No.
                   LIB3061-037-Q1-K1-E2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q16073
BLAST score
                   149
E value
                   6.0e-10
                   68
Match length
% identity
                   (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
                   292767
Seq. No.
                   LIB3061-037-Q1-K1-E3
Seq. ID
                   BLASTX
Method
                   g16073
NCBI GI
BLAST score
                   361
                   2.0e-34
E value
                   95
Match length
% identity
                   (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
                   292768
Seq. No.
                   LIB3061-037-Q1-K1-E6
Seq. ID
Method
                   BLASTX
                   g72307
NCBI GI
BLAST score
                   270
                   9.0e-24
E value
Match length
                   131
                   50
% identity
                   22K zein precursor (clone pZ22.3) - maize >gi_168686
NCBI Description
                   (J01246) 26.99 kd zein protein [Zea mays]
                   292769
Seq. No.
                   LIB3061-037-Q1-K1-F1
Seq. ID
                   BLASTX
Method
                   g141602
NCBI GI
BLAST score
                   386
                   2.0e-37
E value
                   91
Match length
                   88
 % identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6)
NCBI Description
                   >gi_82658_pir__A22831 19K zein precursor (clone M6) - maize
                   >gi_22538_emb_CAA26294_ (X02450) zein precursor [Zea mays]
                   292770
 Seq. No.
                   LIB3061-037-Q1-K1-F11
 Seq. ID
```

Match length

81

```
Account of the Control of the Contro
```

```
Method
NCBI GI
                  g2673912
BLAST score
                  202
                  9.0e-16
E value
Match length
                   62
% identity
                  61
NCBI Description (AC002561) unknown protein [Arabidopsis thaliana]
                  292771
Seq. No.
                  LIB3061-037-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g16073
BLAST score
                  152
E value
                   6.0e-10
Match length
                  37
                   81
% identity
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
Seq. No.
                  292772
Seq. ID
                  LIB3061-037-Q1-K1-F4
Method
                  BLASTN
NCBI GI
                  g168675
BLAST score
                  195
E value
                   1.0e-105
Match length
                   252
                   97
% identity
NCBI Description Maize mutant zein (zE19) gene, complete cds
Seq. No.
                   292773
Seq. ID
                  LIB3061-037-Q1-K1-F5
Method
                   BLASTX
NCBI GI
                   g16073
BLAST score
                   174
                   8.0e-13
E value
                   52
Match length
                   77
% identity
                  (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
                   292774
Seq. No.
Seq. ID
                   LIB3061-037-Q1-K1-F8
Method
                   BLASTX
NCBI GI
                   q141605
BLAST score
                   580
E value
                   5.0e-60
Match length
                   143
% identity
                   82
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                   >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                   maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                   292775
                   LIB3061-037-Q1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g168693
BLAST score
                   321
                   9.0e-30
E value
```

```
% identity
NCBI Description
                  (M29627) zein [Zea mays]
Seq. No.
                  292776
Seq. ID
                  LIB3061-037-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  q168695
BLAST score
                  345
                  7.0e-33
E value
Match length
                  89
% identity
                  (M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A
NCBI Description
                  zein gamma [Zea mays]
                  292777
Seq. No.
Seq. ID
                  LIB3061-037-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  g141605
BLAST score
                  399
                  7.0e-39
E value
                  105
Match length
% identity
                  80
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi_72312_pir_ ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                  292778
                  LIB3061-037-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g72307
BLAST score
                  321
                  1.0e-29
E value
Match length
                  121
                  59
% identity
                  22K zein precursor (clone pZ22.3) - maize >gi 168686
NCBI Description
                  (J01246) 26.99 kd zein protein [Zea mays]
Seq. No.
                  292779
                  LIB3061-037-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141597
BLAST score
                  242
E value
                  1.0e-20
Match length
                  105
% identity
                  54
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                  >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                  >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
```

[Zea mays]

Seq. No. 292780

LIB3061-037-Q1-K1-H6 Seq. ID

Method BLASTN NCBI GI q22483 BLAST score 40 3.0e-13 E value Match length 60



```
% identity
NCBI Description Z.mays RNA for superoxide dismutase Sod4
                  292781
Seq. No.
Seq. ID
                  LIB3061-037-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  q141600
BLAST score
                  148
E value
                   5.0e-16
Match length
                   100
% identity
                   51
```

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1) NCBI Description >gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) -

maize >gi 168674 (M12143) 19 kDa zein protein [Zea mays]

Seq. No. 292782

Seq. ID LIB3061-038-Q1-K1-A11

Method BLASTN NCBI GI g22447 BLAST score 59 2.0e-24 E value Match length 139 87 % identity

NCBI Description Zea mays ZMPMS2 gene for 19 kDa zein protein

292783 Seq. No.

Seq. ID LIB3061-038-Q1-K1-B7

Method BLASTN NCBI GI g168687 BLAST score 38 E value 6.0e-12 Match length 54 % identity 93

NCBI Description Maize 22 kDa zein mRNA, clone cZ22C2, partial cds

Seq. No. 292784

Seq. ID LIB3061-038-Q1-K1-C10

Method BLASTX NCBI GI g168691 BLAST score 284 E value 2.0e-25 Match length 104 % identity 62

NCBI Description (M29628) zein [Zea mays]

Seq. No. 292785

Seq. ID LIB3061-038-Q1-K1-C11

Method BLASTX NCBI GI g168691 BLAST score 250 E value 2.0e-21 Match length 128 % identity 48

NCBI Description (M29628) zein [Zea mays]

Seq. No. 292786

Seq. ID LIB3061-038-Q1-K1-D1



```
Method
                  BLASTN
NCBI GI
                  g168677
BLAST score
                  50
                  5.0e-19
E value
Match length
                  58
% identity
                  97
NCBI Description Maize 19 kDa zein mRNA, clone cZ19C1, complete cds
Seq. No.
                  292787
Seq. ID
                  LIB3061-038-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g508545
BLAST score
                  231
E value
                  3.0e-19
Match length
                  80
% identity
NCBI Description (L34340) zein [Zea mays]
Seq. No.
                  292788
Seq. ID
                  LIB3061-038-Q1-K1-D12
Method
                  BLASTN
NCBI GI
                  g22525
BLAST score
                  107
E value
                  3.0e-53
                  163
Match length
% identity
                   94
                  Zea mays gene encoding a zein (clone zA1)
NCBI Description
                  292789
Seq. No.
Seq. ID
                  LIB3061-038-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  q2286151
BLAST score
                   439
E value
                   8.0e-49
Match length
                  136
% identity
                  77
NCBI Description
                  (AF007580) translation initiation factor [Zea mays]
Seq. No.
                   292790
                  LIB3061-038-Q1-K1-D6
Seq. ID
Method
                  BLASTX
```

NCBI GI g1170503 BLAST score 237 E value 6.0e - 20Match length 120 50 % identity

NCBI Description EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)

> >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188 (X65052) eukaryotic translation initiation factor 4A-1

[Arabidopsis thaliana]

292791 Seq. No.

LIB3061-038-Q1-K1-E12 Seq. ID

Method BLASTX NCBI GI g224508 BLAST score 382



```
7.0e-37
E value
                  107
Match length
% identity
                  77
NCBI Description zein A20 [Zea mays]
                  292792
Seq. No.
                  LIB3061-038-Q1-K1-E4
Seq. ID
                  BLASTN
Method
NCBI GI
                  q22514
                  142
BLAST score
                   4.0e-74
E value
                  173
Match length
                   97
% identity
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                  292793
Seq. No.
                  LIB3061-038-Q1-K1-E7
Seq. ID
                   BLASTX
Method
                   g82654
NCBI GI
                   217
BLAST score
                   1.0e-17
E value
                   40
Match length
                   100
% identity
                   10K zein precursor - maize >gi_22541_emb_CAA30409_ (X07535)
NCBI Description
                   10kDa zein (AA 1 - 150) [Zea mays]
                   292794
Seq. No.
                   LIB3061-038-Q1-K1-F5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4220532
BLAST score
                   187
                   4.0e-14
E value
Match length
                   100
% identity
                   50
                   (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
                   292795
Seq. No.
                   LIB3061-038-Q1-K1-F7
Seq. ID
                   BLASTN
Method
                   q22514
NCBI GI
BLAST score
                   358
                   0.0e + 00
E value
Match length
                   404
                   98
% identity
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                   292796
Seq. No.
                   LIB3061-038-Q1-K1-G5
 Seq. ID
                   BLASTX
Method
                   g141613
NCBI GI
                   434
BLAST score
                   5.0e-43
 E value
Match length
                   130
                   74
 % identity
                   ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
 NCBI Description
                   >gi_72305_pir__ZIZM21 22K zein precursor (clone pZ22.1) -
```

40816

maize >gi_22532_emb_CAA24725_ (V01478) zein [Zea mays]

% identity

NCBI Description

92



```
292797
Seq. No.
                  LIB3061-038-Q1-K1-G7
Seq. ID
                  BLASTX
Method
                  g3913804
NCBI GI
BLAST score
                  423
E value
                  1.0e-41
                  132
Match length
                  67
% identity
                  HISTONE H2B.3 >gi 577825_emb CAA49584 (X69960) H2B histone
NCBI Description
                  [Zea mays]
                  292798
Seq. No.
                  LIB3061-038-Q1-K1-H8
Seq. ID
                  BLASTX
Method
                  g4580398
NCBI GI
                  233
BLAST score
                  2.0e-30
E value
                  99
Match length
                  71
% identity
                  (AC007171) putative protein kinase APK1A [Arabidopsis
NCBI Description
                  thaliana]
                  292799
Seq. No.
                  LIB3061-039-Q1-K1-A8
Seq. ID
                  BLASTX
Method
                  g141614
NCBI GI
                  177
BLAST score
                  8.0e-14
E value
                   60
Match length
                  75
% identity
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)
NCBI Description
                  >gi 82662 pir B22831 22K zein precursor (clone M1) - maize
                  >gi_22527_emb_CAA24722_ (V01475) reading frame zein [Zea
                  mays] >gi 224510 prf 1107201D zein M1 [Zea mays]
                   292800
Seq. No.
Seq. ID
                  LIB3061-039-Q1-K1-B3
                   BLASTX
Method
                   q1522681
NCBI GI
                   222
BLAST score
                   4.0e-18
E value
                   143
Match length
                   37
% identity
                  (U49240) symplekin [Homo sapiens] >gi_2143262_emb_CAA71861_
NCBI Description
                   (Y10931) symplekin [Homo sapiens]
                   292801
Seq. No.
Seq. ID
                   LIB3061-039-Q1-K1-C2
                   BLASTN
Method
                   g313759
NCBI GI
BLAST score
                   92
                   2.0e-44
E value
Match length
                   140
```

Z.mays hsp 70-1 gene for heat shock protein

Seq. ID Method



```
Seq. No.
                  LIB3061-039-Q1-K1-D12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2832242
BLAST score
                  47
                  1.0e-17
E value
Match length
                  130
                  26
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                  292803
Seq. No.
                  LIB3061-039-Q1-K1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4140643
BLAST score
                  50
E value
                  5.0e-19
Match length
                  118
                  22
% identity
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                  complete sequence
                  292804
Seq. No.
Seq. ID
                  LIB3061-039-Q1-K1-F2
                  BLASTX
Method
                  g629861
NCBI GI
BLAST score
                  170
E value
                  3.0e-25
Match length
                  101
                  62
% identity
NCBI Description
                  zein Zd1, 19K - maize >gi 535020_emb_CAA47639_ (X67203)
                  zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                  292805
Seq. ID
                  LIB3061-039-Q1-K1-F6
Method
                  BLASTN
NCBI GI
                  g22514
BLAST score
                  73
E value
                   4.0e-33
Match length
                  136
                  89
% identity
NCBI Description Maize Zcl gene for Zein Zcl (14 kD zein-2)
Seq. No.
                  292806
                  LIB3061-039-Q1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141600
BLAST score
                  185
E value
                   3.0e-14
                  75
Match length
% identity
                   52
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
                   >gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) -
                  maize >gi 168674 (M12143) 19 kDa zein protein [Zea mays]
                  292807
Seq. No.
```

40818

LIB3061-039-Q1-K1-H2

BLASTX

% identity

94



```
q82660
NCBI GI
                  482
BLAST score
                  2.0e-48
E value
                  136
Match length
% identity
                  19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                  >gi 809117 emb CAA24720 (V01473) zein [Zea mays]
                  292808
Seq. No.
                  LIB3061-040-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1504052
BLAST score
                  361
                  2.0e-47
E value
                  132
Match length
% identity
NCBI Description (D87042) Calcium-dependent protein kinase [Zea mays]
Seq. No.
                  292809
                  LIB3061-040-Q1-K1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2392772
BLAST score
                  157
                  1.0e-10
E value
                  33
Match length
% identity
                  (AC002534) putative chloroplast prephenate dehydratase
NCBI Description
                  [Arabidopsis thaliana]
                  292810
Seq. No.
                  LIB3061-040-Q1-K1-C7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q464986
                  160
BLAST score
                  5.0e-11
E value
                  75
Match length
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                  >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
                  6.3.2.19) UBC9 - Arabidopsis thaliana
                  >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                  enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                  ubiquitin conjugating enzyme [Arabidopsis thaliana]
                  >qi 600391 emb CAA51201 (X72626) ubiquitin conjugating
                  enzyme E2 [Arabidopsis Thaliana]
                  >gi 4455355 emb CAB36765.1 (AL035524) ubiquitin-protein
                  ligase UBC9 [Arabidopsis thaliana]
Seq. No.
                  292811
                  LIB3061-040-Q1-K1-C8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2828011
                  127
BLAST score
                   4.0e-65
E value
Match length
                  171
```



```
NCBI Description
                    Zea mays starch synthase I precursor (Ss1) mRNA, nuclear
                    gene encoding plastid protein, complete cds
                    292812
Seq. No.
Seq. ID
                    LIB3061-040-Q1-K1-E1
Method
                    BLASTX
NCBI GI
                    g629861
BLAST score
                    217
                    2.0e-19
E value
                    77
Match length
                    74
% identity
                    zein Zd1, 19K - maize >gi_535020_emb CAA47639 (X67203)
NCBI Description
                    zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                    292813
Seq. ID
                    LIB3061-040-Q1-K1-E11
Method
                    BLASTX
NCBI GI
                    g133028
BLAST score
                    152
E value
                    6.0e-10
Match length
                    119
                    39
% identity
                    50S RIBOSOMAL PROTEIN L9, CHLOROPLAST PRECURSOR (CL9)
NCBI Description
                    >gi_71257_pir__R5MUL9 ribosomal protein L9 precursor,
chloroplast - Arabidopsis thaliana >gi_16499_emb_CAA77480_
(Z11129) plastid ribosomal protein CL9 [Arabidopsis
                    thaliana] >gi_16501_emb_CAA77594_ (Z11509) Chloroplast
                    ribosomal protein CL9 [Arabidopsis thaliana]
Seq. No.
                    292814
Seq. ID
                    LIB3061-040-Q1-K1-E12
Method
                    BLASTX
NCBI GI
                    g3435196
BLAST score
                    473
                    1.0e-47
E value
                    137
Match length
% identity
                    66
NCBI Description (AF067773) glutamyl-tRNA synthetase [Arabidopsis thaliana]
                    292815
Seq. No.
Seq. ID
                    LIB3061-040-Q1-K1-F6
Method
                    BLASTX
NCBI GI.
                    g141617
BLAST score
                    391
E value
                    3.0e-45
Match length
                    112
% identity
                    84
NCBI Description
                    ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
```

>gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize

>gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
>gi 168666 (MI6460) 16-kDa zein protein [Zea mays]

Seq. No. 292816

Seq. ID LIB3061-040-Q1-K1-F7

Method BLASTX NCBI GI g168691

NCBI Description



```
BLAST score
E value
                   6.0e-23
                   127
Match length
                   41
% identity
NCBI Description
                  (M29628) zein [Zea mays]
Seq. No.
                   292817
                  LIB3061-040-Q1-K1-G11
Seq. ID
Method
                   BLASTN
NCBI GI
                   q725275
BLAST score
                   85
E value
                   1.0e-40
Match length
                   103
                   96
% identity
NCBI Description
                  Zea mays thioredoxin M mRNA, complete cds
Seq. No.
                   292818
Seq. ID
                  LIB3061-040-Q1-K1-G4
Method
                   BLASTX
NCBI GI
                   g2462744
BLAST score
                   278
                   6.0e-25
E value
Match length
                   91
% identity
                   58
NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]
                   292819
Seq. No.
Seq. ID
                   LIB3061-040-Q1-K1-H7
Method
                   BLASTN
NCBI GI
                   g22447
BLAST score
                   46
                   8.0e-17
E value
Match length
                   94
% identity
                   87
                  Zea mays ZMPMS2 gene for 19 kDa zein protein
NCBI Description
                   292820
Seq. No.
Seq. ID
                   LIB3061-041-Q1-K1-A8
Method
                   BLASTX
NCBI GI
                   q2864618
BLAST score
                   438
E value
                   1.0e-43
Match length
                   108
% identity
                   69
NCBI Description
                  (AL021811) putative protein [Arabidopsis thaliana]
Seq. No.
                   292821
Seq. ID
                   LIB3061-041-Q1-K1-B3
Method
                   BLASTX
NCBI GI
                   g141605
BLAST score
                   415
E value
                   7.0e-41
Match length
                   97
% identity
                   91
```

40821

>gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)

Method

BLASTN

```
Seq. No.
                  292822
Seq. ID
                  LIB3061-041-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  g168701
BLAST score
                  441
                  8.0e-44
E value
Match length
                  121
                  79
% identity
NCBI Description (M60837) zein [Zea mays]
                  292823
Seq. No.
Seq. ID
                  LIB3061-041-Q1-K1-F12
Method
                  BLASTN
NCBI GI
                  g22537
BLAST score
                  150
                  8.0e-79
E value
Match length
                  166
% identity
                  69
NCBI Description Maize mRNA for zein polypeptide (clone M6)
Seq. No.
                  292824
                  LIB3061-041-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g629862
                  209
BLAST score
                  6.0e-17
E value
                  72
Match length
                  64
% identity
                  zein Zd1, 19K - maize >gi_535021 emb CAA47640 (X67203)
NCBI Description
                  zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                  292825
                  LIB3061-041-Q1-K1-G2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g141608
BLAST score
                  204
                  4.0e-16
E value
Match length
                  47
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943 pir__S15655
NCBI Description
                  zein, 19K - maize >gi 22446_emb_CAA37651_ (X53582) 19 kDa
                  zein [Zea mays]
Seq. No.
                  292826
                  LIB3061-041-Q1-K1-H4
Seq. ID
Method
                  BLASTN
                  g22099
NCBI GI
BLAST score
                   66
                   1.0e-28
E value
Match length
                  74
                  97
% identity
NCBI Description Z.mays 27kDa zein locus DNA
Seq. No.
                  292827
                  LIB3061-041-Q1-K1-H5
Seq. ID
```

NCBI GI

E value

BLAST score

298

4.0e-29



```
g168665
NCBI GI
                   109
BLAST score
                   2.0e-54
E value
                   317
Match length
                   84
% identity
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds
                   292828
Seq. No.
                   LIB3061-042-Q1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1762142
BLAST score
                   237
                   2.0e-20
E value
                   74
Match length
                   61
% identity
NCBI Description (U48434) putative cytochrome P450 [Solanum chacoense]
Seq. No.
                   292829
                   LIB3061-042-Q1-K1-E1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g141608
BLAST score
                   281
E value
                   4.0e-27
Match length
                   141
                   51
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943 pir_ S15655
NCBI Description
                   zein, 19K - maize >gi_22446_emb_CAA3765\overline{1}_ (X53\overline{5}82) \overline{1}9 kDa
                   zein [Zea mays]
                   292830
Seq. No.
                   LIB3061-042-Q1-K1-E10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g22537
                   121
BLAST score
                   9.0e-62
E value
                   185
Match length
% identity
                   67
NCBI Description Maize mRNA for zein polypeptide (clone M6)
                   292831
Seq. No.
Seq. ID
                   LIB3061-042-Q1-K1-F2
Method
                   BLASTX
NCBI GI
                   q141603
BLAST score
                   302
E value
                   2.0e-27
Match length
                   115
% identity
                   57
NCBI Description
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
                   >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                   >gi 22529_emb_CAA24723 (V01476) zein [Zea mays]
Seq. No.
                   292832
Seq. ID
                   LIB3061-042-Q1-K1-F6
Method
                   BLASTX
                   g468516
```



```
Match length
                  119
                  63
% identity
NCBI Description (X55724) zein [Zea mays]
                  292833
Seq. No.
Seq. ID
                  LIB3061-042-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g169805
                  213
BLAST score
                  3.0e-17
E value
Match length
                  84
                  55
% identity
                  (L12252) [Oryza sativa DNA fragment with a miscellaneous
NCBI Description
                  signal and an open reading frame.], gene product [Oryza
                  sativa]
                  292834
Seq. No.
Seq. ID
                  LIB3061-042-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g82660
BLAST score
                  360
                  3.0e-34
E value
Match length
                  112
% identity
                  68
                  19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                  >qi 809117 emb CAA24720 (V01473) zein [Zea mays]
Seq. No.
                  292835
Seq. ID
                  LIB3061-042-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  g141603
BLAST score
                  278
E value
                  3.0e-35
Match length
                  128
% identity
                  69
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >gi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
                  >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
Seq. No.
                  292836
Seq. ID
                  LIB3061-042-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  g118109
BLAST score
                  285
E value
                  6.0e-34
                  109
Match length
% identity
                  72
NCBI Description
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) (CPH)
```

>gi 68410 pir CSZPA peptidylprolyl isomerase (EC 5.2.1.8)

A - fission yeast (Schizosaccharomyces pombe)

>gi 5016 emb CAA37322 (X53223) cyclophilin (AA 1-162) [Schizosaccharomyces pombe] >gi 1236258 dbj BAA12183

(D83992) peptidyl-prolyl cis-trans isomerase

[Schizosaccharomyces pombe]

292837 Seq. No.

```
LIB3061-042-Q1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g168697
BLAST score
                  361
E value
                  2.0e-34
Match length
                  99
% identity
NCBI Description (M60835) zein [Zea mays]
```

292838 Seq. No. Seq. ID LIB3061-042-Q1-K1-H4 BLASTX Method g168703 NCBI GI 242 BLAST score 8.0e-21 E value

Match length 56 % identity

NCBI Description (M86591) 22 kDa zein protein [Zea mays]

292839 Seq. No.

LIB3061-042-Q1-K1-H6 Seq. ID Method BLASTN

q2341060 NCBI GI 71 BLAST score 4.0e-32 E value 143 Match length % identity 89

Zea mays translational initiation factor eIF-4A (tif-4A3) NCBI Description

mRNA, complete cds

292840 Seq. No.

LIB3061-043-Q1-K1-A6 Seq. ID

Method BLASTX NCBI GI q629861 BLAST score 251 E value 6.0e-22 Match length 62 % identity 81

zein Zd1, 19K - maize >gi 535020 emb CAA47639_ (X67203) NCBI Description

zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 292841

Seq. ID LIB3061-043-Q1-K1-A8

Method BLASTX NCBI GI g141609 BLAST score 146 3.0e-09 E value Match length 93 37 % identity

ZEIN-ALPHA PRECURSOR (19 KD) (PMS2) >gi 100944_pir__S15656 NCBI Description

zein, 19K - maize >gi_22448_emb_CAA4154 $\overline{3}$ _ (X58 $\overline{7}$ 00) $\overline{1}$ 9 kDa

zein [Zea mays]

292842 Seq. No.

LIB3061-043-Q1-K1-B1 Seq. ID

Method BLASTX NCBI GI g224509

BLAST score

E value

212

5.0e-26



```
BLAST score
E value
                  2.0e-31
Match length
                  106
                  68
% identity
NCBI Description
                  zein E19 [Zea mays]
                  292843
Seq. No.
Seq. ID
                  LIB3061-043-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  g168701
BLAST score
                  250
E value
                  1.0e-21
Match length
                  66
                  79
% identity
NCBI Description
                  (M60837) zein [Zea mays]
Seq. No.
                  292844
Seq. ID
                  LIB3061-043-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  g141604
BLAST score
                  207
                  2.0e-16
E value
                  75
Match length
% identity
                  59
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)
                  >gi 72310 pir ZIZM91 19K zein precursor (clone cZ19C1) -
                  maize >gi_168678 (M12146) 19 kDa zein protein [Zea mays]
Seq. No.
                  292845
Seq. ID
                  LIB3061-043-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  q141613
BLAST score
                  419
                  3.0e-41
E value
Match length
                  138
                  67
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
                  >gi_72305_pir__ZIZM21 22K zein precursor (clone pZ22.1) -
                  maize >gi_22532 emb CAA24725 (V01478) zein [Zea mays]
Seq. No.
                  292846
                  LIB3061-043-Q1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q629861
BLAST score
                  350
E value
                  1.0e-43
Match length
                  127
% identity
                  80
NCBI Description
                  zein Zd1, 19K - maize >gi 535020 emb CAA47639 (X67203)
                  zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                  292847
Seq. ID
                  LIB3061-043-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g4185308
```



```
Match length
                  81
% identity
NCBI Description
                  (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
Seq. No.
                  292848
Seq. ID
                  LIB3061-043-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  q468516
BLAST score
                  332
E value
                  5.0e-31
Match length
                  103
% identity
                  68
NCBI Description
                  (X55724) zein [Zea mays]
Seq. No.
                  292849
Seq. ID
                  LIB3061-043-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g141597
BLAST score
                  368
                  3.0e-35
E value
Match length
                  115
                  70
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
                  >gi 72314 pir ZIZM3 19K zein precursor (clone A30) - maize
                  >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
                  [Zea mays]
Seq. No.
                  292850
Seq. ID
                  LIB3061-043-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  g141597
BLAST score
                  220
E value
                  7.0e-18
Match length
                  103
                  50
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
                  >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                  >gi_22545 emb CAA24728 (V01481) reading frame zein [2]
                  [Zea mays]
Seq. No.
                  292851
                  LIB3061-043-Q1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141599
BLAST score
                  418
E value
                  5.0e-41
Match length
                  119
% identity
                  75
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19A2)
                  >gi 72316 pir ZIZMA2 19K zein precursor (clone cZ19A2) -
```

>gi_72316_pir__ZIZMA2 19K zein precursor (clone cZ19A2) maize (fragment) >gi_168670 (M12142) 19 kDa zein protein

[Zea mays]

Seq. No.

292852

Seq. ID

LIB3061-043-Q1-K1-F3

Method -

BLASTX

NCBI GI

q100925



```
BLAST score
                   330
E value
                   7.0e-31
Match length
                   63
                  84
% identity
                  zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_
NCBI Description
                   (X58197) 27kDa storage protein, zein [Zea mays]
Seq. No.
                  292853
Seq. ID
                  LIB3061-043-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  g3915847
BLAST score
                  273
                   5.0e-24
E value
                  75
Match length
                   69
% identity
                  40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative
NCBI Description
                   40S ribosomal protein S2 [Arabidopsis thaliana]
                  292854
Seq. No.
Seq. ID
                  LIB3061-043-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g141604
BLAST score
                  260
E value
                  2.0e-27
Match length
                  84
                   79
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)
NCBI Description
                  >gi 72310 pir ZIZM91 19K zein precursor (clone cZ19C1) -
                  maize >gi 168678 (M12146) 19 kDa zein protein [Zea mays]
Seq. No.
                   292855
Seq. ID
                  LIB3061-043-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                   g16073
BLAST score
                   379
E value
                   1.0e-36
                   107
Match length
% identity
                   75
                  (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
Seq. No.
                   292856
Seq. ID
                  LIB3061-043-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                   q141608
BLAST score
                   322
E value
                   6.0e-30
Match length
                   113
                   63
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943 pir S15655
NCBI Description
                   zein, 19K - maize >gi 22446 emb CAA37651_ (X53582) 19 kDa
                   zein [Zea mays]
()
Seq. No.
                   292857
Seq. ID
                   LIB3061-043-Q1-K1-H2
```

Method BLASTX NCBI GI q4185308 BLAST score 195

BLAST score

E value

41

1.0e-13



```
E value
                     2.0e-21
                     133
  Match length
                     52
  % identity
                     (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
  NCBI Description
                     292858
  Seq. No.
  Seq. ID
                     LIB3061-044-Q1-K1-A6
  Method
                     BLASTX
  NCBI GI
                     g141601
                     184
  BLAST score
                     5.0e-14
  E value
                     80
  Match length
                     50
  % identity
                     ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
  NCBI Description
                     >gi_82657_pir__S03417 19K zein precursor (clone gZ19AB11) -
maize >gi_22543_emb_CAA29340_ (X05911) 19 kd alpha zein (AA
                     1 - 234) [Zea mays]
                     292859
  Seq. No.
                     LIB3061-044-Q1-K1-F6
  Seq. ID
                     BLASTX
  Method
  NCBI GI
                     g141597
                     273
  BLAST score
                     3.0e-24
  E value
  Match length
                     100
  % identity
                      61
                     ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
  NCBI Description
                     >gi 72314 pir ZIZM3 19K zein precursor (clone A30) - maize
                      >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
                      [Zea mays]
                      292860
  Seq. No.
                     LIB3061-044-Q1-K1-H1
  Seq. ID
  Method
                     BLASTX
                      g224508
  NCBI GI
                     195
  BLAST score
                      4.0e-15
  E value
Match length
                      99
  % identity
                      54
  NCBI Description zein A20 [Zea mays]
                      292861
  Seq. No.
  Seq. ID
                     LIB3061-045-Q1-K1-A9
  Method
                      BLASTN
                      q168673
  NCBI GI
  BLAST score
                      265
                      1.0e-147
  E value
                      409
  Match length
                      92
  % identity
  NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds
                      292862
  Seq. No.
                      LIB3061-045-Q1-K1-B10
  Seq. ID
  Method
                      BLASTN
  NCBI GI
                      q168692
```

% identity

NCBI Description

73

```
Match length
                  41
                  100
% identity
NCBI Description Maize zein mRNA, complete cds, clone ZG7
                  292863
Seq. No.
Seq. ID
                  LIB3061-045-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  g141605
BLAST score
                  391
E value
                  6.0e-38
Match length
                  127
                  67
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >qi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
                  292864
Seq. No.
Seq. ID
                  LIB3061-045-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g168424
BLAST score
                  420
E value
                  2.0e-41
Match length
                  113
                  74
% identity
NCBI Description (M59449) polypeptide chain-binding protein [Zea mays]
Seq. No.
                  292865
Seq. ID
                  LIB3061-045-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g16073
BLAST score
                  234
E value
                  1.0e-26
                  98
Match length
% identity
                  70
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
                  292866
Seq. No.
Seq. ID
                  LIB3061-045-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  g141611
BLAST score
                  216
E value
                  1.0e-22
Match length
                  108
% identity
                   63
                  ZEIN-ALPHA (22 KD) (CLONE B49) >gi 72308 pir ZIZM49 22K
NCBI Description
                  zein (clone B49) - maize (fragment)
                  292867
Seq. No.
Seq. ID
                  LIB3061-046-Q1-K1-A6
Method
                  BLASTX
                  g2832246
NCBI GI
BLAST score
                  250
E value
                   2.0e-21
Match length
                  78
```

40830

(AF031569) 22-kDa alpha zein 8 [Zea mays]



```
292868
Seq. No.
                  LIB3061-046-Q1-K1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4151124
BLAST score
                  37
E value
                  2.0e-11
Match length
                  45
                  96
% identity
NCBI Description
                  Zea mays PDI-like protein mRNA, complete cds
Seq. No.
                  292869
Seq. ID
                  LIB3061-046-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g224508
BLAST score
                  387
E value
                  3.0e-44
Match length
                  125
% identity
                  82
NCBI Description zein A20 [Zea mays]
                  292870
Seq. No.
Seq. ID
                  LIB3061-046-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  g141604
BLAST score
                  307
E value
                  2.0e-28
Match length
                  80
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)
                  >gi 72310 pir ZIZM91 19K zein precursor (clone cZ19C1) -
                  maize >gi 168678 (M12146) 19 kDa zein protein [Zea mays]
Seq. No.
                  292871
                  LIB3061-046-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g224508
BLAST score
                  265
E value
                  3.0e-23
Match length
                  114
% identity
                  51
NCBI Description zein A20 [Zea mays]
                  292872
Seq. No.
                  LIB3061-046-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141605
BLAST score
                  189
E value
                  1.0e-14
Match length
                  61
% identity
                   67
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
```

maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 292873

Seq. ID LIB3061-046-Q1-K1-E8

Method BLASTX

BLAST score

E value

8.0e-19



```
g168701
NCBI GI
                  411
BLAST score
                  3.0e-40
E value
                  124
Match length
                  69
% identity
NCBI Description (M60837) zein [Zea mays]
                  292874
Seq. No.
                  LIB3061-046-Q1-K1-F10
Seq. ID
                  BLASTX
Method
                  g72307
NCBI GI
BLAST score
                  424
                  8.0e-42
E value
                  119
Match length
                  76
% identity
                  22K zein precursor (clone pZ22.3) - maize >gi_168686
NCBI Description
                   (J01246) 26.99 kd zein protein [Zea mays]
                  292875
Seq. No.
Seq. ID
                  LIB3061-046-Q1-K1-F2
                  BLASTX
Method
                  g141597
NCBI GI
BLAST score
                  235
                   7.0e-20
E value
                   91
Match length
                   59
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
                   292876
Seq. No.
Seq. ID
                   LIB3061-047-Q1-K1-B11
Method
                   BLASTX
NCBI GI
                   q16073
                   401
BLAST score
                   4.0e-39
E value
Match length
                   132
% identity
                   66
                  (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
                   292877
Seq. No.
Seq. ID
                   LIB3061-047-Q1-K1-B6
Method
                   BLASTN
NCBI GI
                   q902585
                   52
BLAST score
                   3.0e-20
E value
                   76
Match length
% identity
                   92
NCBI Description Zea mays clone MubG9 ubiquitin gene, complete cds
                   292878
Seq. No.
                   LIB3061-047-Q1-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4049351
                   228
```



```
Match length
                  77
% identity
NCBI Description
                  (AL034567) nodulin-like protein [Arabidopsis thaliana]
Seq. No.
                  292879
Seq. ID
                  LIB3061-047-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g82660
BLAST score
                  146
E value
                  3.0e-09
Match length
                  59
% identity
                  58
NCBI Description
                  19K zein precursor (clone ZG31A) - maize (fragment)
                  >gi 809117 emb CAA24720 (V01473) zein [Zea mays]
Seq. No.
                  292880
Seq. ID
                  LIB3061-047-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                  g2832246
BLAST score
                  157
E value
                  7.0e-11
Match length
                  55
% identity
NCBI Description
                  (AF031569) 22-kDa alpha zein 8 [Zea mays]
Seq. No.
                  292881
Seq. ID
                  LIB3061-047-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g141597
BLAST score
                  240
E value
                  3.0e-20
Match length
                  123
% identity
                  47
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                  >gi 72314 pir ZIZM3 19K zein precursor (clone A30) - maize
                  >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
                  [Zea mays]
Seq. No.
                  292882
Seq. ID
                  LIB3061-047-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  g2832246
BLAST score
                  412
E value
                  3.0e-40
Match length
                  119
% identity
                  75
NCBI Description
                  (AF031569) 22-kDa alpha zein 8 [Zea mays]
Seq. No.
                  292883
                  LIB3061-047-Q1-K1-G9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g168673
BLAST score
                  46
                  7.0e-17
E value
Match length
                  150
% identity
                  83
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds
```

```
292884
Seq. No.
                  LIB3061-047-Q1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g419803
BLAST score
                  164
E value
                  6.0e-12
Match length
                  48
% identity
                  67
                  zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                  mays]
Seq. No.
                  292885
Seq. ID
                  LIB3061-047-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  g82660
BLAST score
                  214
E value
                  4.0e-17
Match length
                  115
% identity
                  46
                  19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                  >gi 809117 emb CAA24720 (V01473) zein [Zea mays]
Seq. No.
                  292886
Seq. ID
                  LIB3061-047-Q1-K1-H6
Method
                  BLASTN
NCBI GI
                  g1419369
BLAST score
                  73
E value
                  5.0e-33
Match length
                  149
% identity
                  87
NCBI Description Z.mays ZmABP3 mRNA for actin depolymerizing factor
Seq. No.
                  292887
Seq. ID
                  LIB3061-047-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g82660
BLAST score
                  202
E value
                  9.0e-16
Match length
                  134
% identity
                   41
                  19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                  >gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]
Seq. No.
                  292888
Seq. ID
                  LIB3061-048-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  g141608
BLAST score
                  373
E value
                  8.0e-36
                  125
Match length
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655
NCBI Description
                  zein, 19K - maize >gi 22446 emb CAA37651 (X53582) 19 kDa
                  zein [Zea mays]
```

40834

292889

Seq. No.

```
LIB3061-048-Q1-K1-D9
Seq. ID
                  BLASTX
Method
NCBI GI
                   g141613
                   222
BLAST score
                   4.0e-18
E value
```

54

83 % identity ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1) NCBI Description >gi 72305 pir ZIZM21 22K zein precursor (clone pZ22.1) maize >gi 22532 emb_CAA24725_ (V01478) zein [Zea mays]

Seq. No.

Match length

LIB3061-048-Q1-K1-E10 Seq. ID

Method BLASTN NCBI GI q22531 35 BLAST score E value 4.0e-10 87 Match length % identity 85

Zea mays mRNA encoding a zein (clone pZ22.1) NCBI Description

>gi 270688 gb I03336 Sequence 10 from Patent US 4885357
>gi 270741 gb I03273 Sequence 2 from Patent US

Seq. No. 292891

Seq. ID LIB3061-048-Q1-K1-E11

Method BLASTX NCBI GI q141608 BLAST score 263 4.0e-23 E value Match length 90 67 % identity

ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655 NCBI Description

zein, 19K - maize >gi_22446 emb_CAA37651_ (X53582) 19 kDa

zein [Zea mays]

292892 Seq. No.

LIB3061-048-Q1-K1-F11 Seq. ID

BLASTX Method g168701 NCBI GI BLAST score 212 E value 6.0e-17 109 Match length 47 % identity

NCBI Description (M60837) zein [Zea mays]

292893 Seq. No.

LIB3061-048-Q1-K1-F6 Seq. ID

BLASTX Method q2832246 NCBI GI BLAST score 313 1.0e-28 E value 118 Match length % identity

(AF031569) 22-kDa alpha zein 8 [Zea mays] NCBI Description

292894 Seq. No.

LIB3061-048-Q1-K1-G1 Seq. ID

NCBI Description



```
BLASTX
Method
NCBI GI
                   g141603
                   155
BLAST score
                   7.0e-11
E value
                   55
Match length
                   64
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                   >gi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
                   >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
                   292895
Seq. No.
Seq. ID
                   LIB3061-048-Q1-K1-G10
Method
                   BLASTX
NCBI GI
                   g121472
                   173
BLAST score
                   9.0e-23
E value
                   76
Match length
% identity
                   68
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi 72326 pir ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi 22289 emb CAA26149 (X02230) glutelin-2 precursor
                   [Zea mays] >gi 22517 emb CAA37594 (X53514) zein Zc2 [Zea
                   mays] >gi 1684\overline{8}5 (M1\overline{6}066) glutelin-2 [Zea mays]
                   292896
Seq. No.
                   LIB3061-048-Q1-K1-H11
Seq. ID
                   BLASTX
Method
                   g141605
NCBI GI
                   198
BLAST score
E value
                   1.0e-19
                   87
Match length
% identity
                   67
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                   >qi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) -
                   maize >qi 168680 (M12145) 19 kDa zein protein [Zea mays]
                   292897
Seq. No.
                   LIB3061-048-Q1-K1-H12
Seq. ID
                   BLASTN
Method
NCBI GI
                   g168484
BLAST score
                   36
                   6.0e-11
E value
Match length
                   44
% identity
                   95
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                   292898
Seq. No.
Seq. ID
                   LIB3061-048-Q1-K1-H6
                   BLASTX
Method
                   q141613
NCBI GI
BLAST score
                   149
                   3.0e-18
E value
Match length
                   110
% identity
```

ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)

>qi 72305 pir ZIZM21 22K zein precursor (clone pZ22.1) -



```
maize >gi_22532_emb_CAA24725_ (V01478) zein [Zea mays]
                  292899
Seq. No.
                  LIB3061-049-Q1-K1-A6
Seq. ID
                  BLASTX
Method
                  g16073
NCBI GI
BLAST score
                  319
E value
                  1.0e-29
                  106
Match length
% identity
                   64
                  (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
                   292900
Seq. No.
                  LIB3061-049-Q1-K1-A7
Seq. ID
                  BLASTX
Method
NCBI GI
                   g16073
                   293
BLAST score
                   3.0e-43
E value
Match length
                   113
% identity
                   86
                  (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
                   292901
Seq. No.
                   LIB3061-049-Q1-K1-B1
Seq. ID
Method
                   BLASTX
                   q468516
NCBI GI
BLAST score
                   389
                   1.0e-37
E value
                   106
Match length
                   75
% identity
                  (X55724) zein [Zea mays]
NCBI Description
                   292902
Seq. No.
                   LIB3061-049-Q1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g123620
                   325
BLAST score
                   3.0e-30
E value
                   118
Match length
% identity
                   83
                   HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi_100224_pir__S14950
NCBI Description
                   heat shock cognate protein 70 - tomato
                   >gi_19258_emb_CAA37971_ (X54030) heat shock protein cognate
                   70 [Lycopersicon esculentum]
                   292903
Seq. No.
                   LIB3061-049-Q1-K1-B9
Seq. ID
                   BLASTX
Method
```

Method BLASTX
NCBI GI g16073
BLAST score 508
E value 1.0e-51
Match length 144
% identity 74

NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 292904

Seq. ID LIB3061-049-Q1-K1-C6

Seq. ID

Method

292909

BLASTN

LIB3061-049-Q1-K1-F6

```
Method
                  BLASTX
NCBI GI
                  g2589162
BLAST score
                  584
                  2.0e-60
E value
                  150
Match length
                  73
% identity
NCBI Description (D88451) aldehyde oxidase [Zea mays]
                  292905
Seq. No.
Seq. ID
                  LIB3061-049-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  g3511236
BLAST score
                  208
                  2.0e-21
E value
Match length
                  101
                  59
% identity
NCBI Description (AF072725) starch branching enzyme IIb [Zea mays]
Seq. No.
                  292906
Seq. ID
                  LIB3061-049-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  g141605
BLAST score
                  469
E value
                  5.0e-47
                  130
Match length
                  75
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
                  292907
Seq. No.
Seq. ID
                  LIB3061-049-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g141600
BLAST score
                  153
                   4.0e-10
E value
                  111
Match length
                   46
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
                  >gi 72315 pir ZIZMB1 19K zein precursor (clone cZ19B1) -
                  maize >gi 168674 (M12143) 19 kDa zein protein [Zea mays]
                  292908
Seq. No.
Seq. ID
                  LIB3061-049-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  g141600
BLAST score
                  392
                   5.0e-38
E value
Match length
                  132
                   67
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
                   >gi 72315 pir ZIZMB1 19K zein precursor (clone cZ19B1) -
                  maize >gi 168674 (M12143) 19 kDa zein protein [Zea mays]
```

Seq. ID Method



```
NCBI GI
                  g168700
                  151
BLAST score
E value
                  2.0e-79
                  187
Match length
                  95
% identity
NCBI Description Z.mays zein mRNA, complete cds
Seq. No.
                  292910
Seq. ID
                  LIB3061-049-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  g141603
BLAST score
                  285
E value
                  2.0e-25
                  77
Match length
                  78
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >gi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
                  >gi_22529_emb_CAA24723 (V01476) zein [Zea mays]
Seq. No.
                  292911
                  LIB3061-049-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141602
BLAST score
                  146
E value
                  1.0e-09
                  59
Match length
                  53
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6)
                  >gi 82658 pir A22831 19K zein precursor (clone M6) - maize
                  >gi 22538 emb CAA26294 (X02450) zein precursor [Zea mays]
Seq. No.
                  292912
Seq. ID
                  LIB3061-050-Q1-K1-A1
Method
                  BLASTX
NCBI GI
                  q141613
BLAST score
                  287
E value
                  7.0e-26
Match length
                  103
% identity
                  61
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
NCBI Description
                  >qi 72305 pir ZIZM21 22K zein precursor (clone pZ22.1) -
                  maize >gi_22532 emb CAA24725 (V01478) zein [Zea mays]
Seq. No.
                  292913
Seq. ID
                  LIB3061-050-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  q629862
BLAST score
                  241
E value
                  1.0e-20
Match length
                  64
% identity
                  75
NCBI Description
                  zein Zd1, 19K - maize >gi 535021 emb CAA47640 (X67203)
                  zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                  292914
```

LIB3061-050-Q1-K1-A2

BLASTX

NCBI GI BLAST score

E value Match length



```
NCBI GI
                  g141597
                  221
BLAST score
                  1.0e-22
E value
                  107
Match length
                   60
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                  >gi 72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                  >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
                   [Zea mays]
                  292915
Seq. No.
Seq. ID
                  LIB3061-050-Q1-K1-B11
                  BLASTX
Method
NCBI GI
                  g224507
                  518
BLAST score
                  8.0e-53
E value
Match length
                  139
                   78
% identity
NCBI Description zein Al [Zea mays]
Seq. No.
                   292916
                  LIB3061-050-Q1-K1-B12
Seq. ID
                  BLASTX
Method
NCBI GI
                   g22216
                   147
BLAST score
                   5.0e-20
E value
Match length
                   96
% identity
NCBI Description (X55722) 22kD zein [Zea mays]
Seq. No.
                   292917
                   LIB3061-050-Q1-K1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q468516
                   442
BLAST score
                   7.0e-44
E value
                   109
Match length
% identity
NCBI Description (X55724) zein [Zea mays]
                   292918
Seq. No.
Seq. ID
                   LIB3061-050-Q1-K1-B4
Method
                   BLASTX
NCBI GI
                   q16073
BLAST score
                   421
                   2.0e-41
E value
Match length
                   138
% identity
                   (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
                   292919
Seq. No.
                   LIB3061-050-Q1-K1-C4
Seq. ID
Method
                   BLASTX
```

40840

g141614

392 5.0e-38

Seq. ID

292924

LIB3061-050-Q1-K1-D7

```
% identity
NCBI Description
                   ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)
                   >gi_82662_pir__B22831 22K zein precursor (clone M1) - maize
                   >gi_22527_emb_CAA24722_ (V01475) reading frame zein [Zea
mays] >gi_224510_prf__1107201D zein M1 [Zea mays]
Seq. No.
                   292920
                   LIB3061-050-Q1-K1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g141605
BLAST score
                   418
E value
                   4.0e-41
Match length
                   133
% identity
                   65
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                   >gi 72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                   maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                   292921
                   LIB3061-050-Q1-K1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q141597
BLAST score
                   417
E value
                   6.0e-41
Match length
                   137
                   66
% identity
NCBI Description
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
                   >gi 72314 pir ZIZM3 19K zein precursor (clone A30) - maize
                   >gi 22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
Seq. No.
                   292922
Seq. ID
                   LIB3061-050-Q1-K1-D3
Method
                   BLASTX
NCBI GI
                   g141617
BLAST score
                   429
E value
                   2.0e-42
Match length
                   142
% identity
                   ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                   >gi_100941_pir__S12140 zein Zc1 - maize
                   >gi_100945_pir__B29017 zein 2 - maize
                   >gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                   >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
Seq. No.
                   292923
Sea. ID
                   LIB3061-050-Q1-K1-D5
Method
                   BLASTX
NCBI GI
                   g224513
BLAST score
                   443
E value
                   5.0e-44
Match length
                   130
                   71
% identity
NCBI Description zein M6 [Zea mays]
```



```
Method
                  BLASTX
NCBI GI
                  g141597
BLAST score
                  312
                  7.0e-29
E value
                  92
Match length
                  71
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
                  >gi 72314 pir ZIZM3 19K zein precursor (clone A30) - maize
                  >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
                  [Zea mays]
                  292925
Seq. No.
Seq. ID
                  LIB3061-050-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g629861
BLAST score
                  336
E value
                  2.0e-31
Match length
                  94
                  73
% identity
NCBI Description
                  zein Zd1, 19K - maize >gi_535020 emb CAA47639 (X67203)
                  zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                  292926
Seq. ID
                  LIB3061-050-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  q141599
BLAST score
                  332
E value
                  5.0e-31
Match length
                  87
                  77
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19A2)
                  >gi_72316 pir_ ZIZMA2 19K zein precursor (clone cZ19A2) -
                  maize (fragment) >gi 168670 (M12142) 19 kDa zein protein
                  [Zea mays]
                  292927
Seq. No.
Seq. ID
                  LIB3061-050-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g3688193
BLAST score
                  367
E value
                  5.0e-42
Match length
                  132
% identity
NCBI Description (AJ010091) MAP3K alpha 1 protein kinase [Brassica napus]
Seq. No.
                  292928
Seq. ID
                  LIB3061-050-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  g629861
BLAST score
                  173
E value
                  1.0e-12
Match length
                  62
% identity
                  60
NCBI Description
                  zein Zd1, 19K - maize >gi_535020_emb CAA47639 (X67203)
```

zein Zd1 (19 kDa zein) [Zea mays]



```
LIB3061-050-Q1-K1-F7
Seq. ID
                   BLASTX
Method
                   g168691
NCBI GI
BLAST score
                   210
                   1.0e-16
E value
Match length
                   122
% identity
                   43
NCBI Description
                  (M29628) zein [Zea mays]
                   292930
Seq. No.
Seq. ID
                   LIB3061-050-Q1-K1-G11
Method
                   BLASTX
NCBI GI
                   g141617
BLAST score
                   320
                   5.0e-30
E value
                   102
Match length
                   66
% identity
                   ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                   >gi 100941_pir__S12140 zein Zc1 - maize
                   >gi 100945 pir B29017 zein 2 - maize
                   >qi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                   >qi 168666 (M16460) 16-kDa zein protein [Zea mays]
                   292931
Seq. No.
                   LIB3061-050-Q1-K1-G6
Seq. ID
                   BLASTX
Method
                   g82660
NCBI GI
BLAST score
                   223
E value
                   3.0e-18
                   43
Match length
% identity
                   100
                   19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                   >qi 809117 emb CAA24720 (V01473) zein [Zea mays]
                   292932
Seq. No.
                   LIB3061-050-Q1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g468516
BLAST score
                   336
                   2.0e-31
E value
                   131
Match length
% identity
                   56
NCBI Description
                   (X55724) zein [Zea mays]
                   292933
Seq. No.
Seq. ID
                   LIB3061-050-Q1-K1-G8
Method
                   BLASTX
NCBI GI
                   g141603
BLAST score
                   336
E value
                   1.0e-31
. Match length
                   94
                   77
% identity
NCBI Description
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
                   >qi 72311 pir ZIZM2 19K zein precursor (clone A20) - maize
```

>gi 22529 emb CAA24723 (V01476) zein [Zea mays]



```
LIB3061-050-Q1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82660
BLAST score
                  355
E value
                  3.0e-34
Match length
                  135
% identity
                  67
                  19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                  >gi 809117 emb CAA24720 (V01473) zein [Zea mays]
Seq. No.
                  292935
Seq. ID
                  LIB3061-050-Q1-K1-H6
Method
                  BLASTN
NCBI GI
                  g168704
BLAST score
                  73
E value
                  6.0e-33
Match length
                  255
                  87
% identity
NCBI Description Zea mays zein protein gene, complete cds
Seq. No.
                  292936
                  LIB3061-051-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2144734
                  253
BLAST score
                  4.0e-22
E value
                  84
Match length
                  18
% identity
                  polyubiquitin / ribosomal protein CEP52 - Trypanosoma cruzi
NCBI Description
                  >gi 162337 (J03945) ubiquitin precursor [Trypanosoma cruzi]
Seq. No.
                  292937
Seq. ID
                  LIB3061-051-Q1-K1-C12
Method
                  BLASTN
NCBI GI
                  q22447
BLAST score
                  122
E value
                  2.0e-62
Match length
                  158
% identity
                  95
                  Zea mays ZMPMS2 gene for 19 kDa zein protein
NCBI Description
Seq. No.
                  292938
Seq. ID
                  LIB3061-051-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  q141597
BLAST score
                  277
E value
                  1.0e-24
                  101
Match length
% identity
                  58
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
                  >gi 72314 pir ZIZM3 19K zein precursor (clone A30) - maize
                  >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
                  [Zea mays]
```

Seq. ID LIB3061-051-Q1-K1-D8

Method BLASTX

NCBI GI

q16072



```
q141613
NCBI GI
                  415
BLAST score
E value
                  1.0e-40
Match length
                  142
                   67
% identity
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
NCBI Description
                  >gi 72305 pir _ZIZM21 22K zein precursor (clone pZ22.1) -
                  maize >gi 22532 emb_CAA24725_ (V01478) zein [Zea mays]
Seq. No.
                  292940
                  LIB3061-051-Q1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g141597
BLAST score
                   353
E value
                   2.0e-33
Match length
                   124
% identity
                   65
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
                   [Zea mays]
Seq. No.
                   292941
                   LIB3061-051-Q1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q629861
BLAST score
                   393
E value
                   2.0e-38
                   113
Match length
% identity
                   72
                   zein Zd1, 19K - maize >gi 535020_emb_CAA47639_ (X67203)
NCBI Description
                   zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                   292942
                   LIB3061-051-Q1-K1-E5
Seq. ID
                   BLASTN
Method
                   g168484
NCBI GI
                   93
BLAST score
                   6.0e-45
E value
                   241
Match length
                   85
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                   292943
Seq. No.
                   LIB3061-051-Q1-K1-F2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1931645
BLAST score
                   251
E value
                   1.0e-21
                   62
Match length
% identity
                   (U95973) Fe(II) transporter isolog [Arabidopsis thaliana]
NCBI Description
                   292944
Seq. No.
Seq. ID
                   LIB3061-051-Q1-K1-F8
                   BLASTN
Method
```



```
BLAST score
                  136
E value
                  1.0e-70
                  204
Match length
                  99
% identity
NCBI Description Acetabularia mediterranea zein gene
                  292945
Seq. No.
                  LIB3061-051-Q1-K1-H11
Seq. ID
Method
                  BLASTX
                  g224507
NCBI GI
BLAST score
                  165
                  2.0e-11
E value
                  96
Match length
% identity
                  45
NCBI Description zein Al [Zea mays]
                  292946
Seq. No.
Seq. ID
                  LIB3061-051-Q1-K1-H12
Method
                  BLASTN
NCBI GI
                  g22099
                  212
BLAST score
E value
                  1.0e-116
                  354
Match length
                  98
% identity
NCBI Description Z.mays 27kDa zein locus DNA
Seq. No.
                   292947
                  LIB3061-052-Q1-K1-E9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g168681
BLAST score
                  41
                   9.0e-14
E value
Match length
                  125
% identity
                   83
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
                  >gi_270686_gb_I03333_ Sequence 8 from Patent US
                   292948
Seq. No.
Seq. ID
                  LIB3061-052-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                   g82660
                   396
BLAST score
E value
                   2.0e-38
                   121
Match length
% identity
                   69
                  19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                   >gi 809117 emb CAA24720 (V01473) zein [Zea mays]
                   292949
Seq. No.
                   LIB3061-052-Q1-K1-G1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g168699
BLAST score
                   245
E value
                   5.0e-21
Match length
                   71
% identity
```

40846

(M60836) zein [Zea mays]

NCBI Description

Seq. ID Method

NCBI GI

```
Seq. No.
                  292950
Seq. ID
                  LIB3061-052-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  g141602
BLAST score
                  206
                  1.0e-16
E value
Match length
                  67
% identity
                  61
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6)
                  >gi 82658 pir A22831 19K zein precursor (clone M6) - maize
                  >gi 22538 emb CAA26294 (X02450) zein precursor [Zea mays]
Seq. No.
                  292951
Seq. ID
                  LIB3061-052-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  g3953471
BLAST score
                  363
E value
                  2.0e-37
Match length
                  136
                  57
% identity
NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]
Seq. No.
                  292952
Seq. ID
                  LIB3061-053-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  g468517
BLAST score
                  162
E value
                  2.0e-11
Match length
                  55
% identity
                  67
NCBI Description (X14334) zein [Zea mays]
                  292953
Seq. No.
Seq. ID
                  LIB3061-053-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  g4314370
BLAST score
                  334
E value
                  3.0e-31
Match length
                  116
% identity
NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  292954
Seq. ID
                  LIB3061-053-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  g4204265
BLAST score
                  267
E value
                  2.0e-23
Match length
                  76
% identity
                  64
NCBI Description (AC005223) 45643 [Arabidopsis thaliana]
Seq. No.
                  292955
```

40847

LIB3061-053-Q1-K1-E11

BLASTX

g224508

NCBI GI



```
BLAST score
E value
                   9.0e-48
Match length
                   108
% identity
                   95
NCBI Description
                   zein A20 [Zea mays]
Seq. No.
                   292956
Seq. ID
                   LIB3061-053-Q1-K1-G5
Method
                   BLASTX
NCBI GI
                   g121472
BLAST score
                   149
E value
                   1.0e-09
Match length
                   63
% identity
                   52
NCBI Description
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi 22289 emb CAA26149 (X02230) glutelin-2 precursor
                   [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea mays] >gi_168485 (M16066) glutelin-2 [Zea mays]
Seq. No.
                   292957
Seq. ID
                   LIB3061-053-Q1-K1-H11
Method
                   BLASTN
NCBI GI
                   g168690
BLAST score
                   56
E value
                   1.0e-22
Match length
                   76
% identity
                   95
NCBI Description Maize zein mRNA, complete cds, clone ZG124
Seq. No.
                   292958
Seq. ID
                   LIB3061-054-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   g2832247
BLAST score
                   249
E value
                   2.0e-21
Match length
                   81
% identity
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]
Seq. No.
                   292959
Seq. ID
                   LIB3061-054-Q1-K1-B6
Method
                   BLASTX
NCBI GI
                   q141608
BLAST score
                   220
E value
                   4.0e-18
Match length
                   98
% identity
                   49
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943 pir S15655
NCBI Description
                   zein, 19K - maize >gi_22446_emb_CAA37651 (X53582) 19 kDa
                   zein [Zea mays]
Seq. No.
                   292960
Seq. ID
                   LIB3061-054-Q1-K1-C11
Method
                   BLASTX
```

40848

q2668742

% identity

55



```
BLAST score
                  8.0e-42
E value
Match length
                  86
                  95
% identity
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]
Seq. No.
                  292961
Seq. ID
                · LIB3061-054-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g224509
BLAST score
                  208
E value
                  3.0e-17
Match length
                  136
                  44
% identity
NCBI Description zein E19 [Zea mays]
Seq. No.
                  292962
Seq. ID
                  LIB3061-054-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  g508545
BLAST score
                  181
E value
                  3.0e-13
Match length
                  89
% identity
                  46
NCBI Description (L34340) zein [Zea mays]
Seq. No.
                  292963
Seq. ID
                  LIB3061-054-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g629861
BLAST score
                  177
                  2.0e-24
E value
Match length
                  90
                  72
% identity
                  zein Zd1, 19K - maize >gi 535020 emb CAA47639 (X67203)
NCBI Description
                  zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                  292964
Seq. ID
                  LIB3061-054-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g1825645
BLAST score
                  145
E value
                   2.0e-09
Match length
                  55
% identity
                  55
NCBI Description
                  (U88173) weak similarity to Arabidopsis thaliana
                  ubiquitin-like protein 8 [Caenorhabditis elegans]
Seq. No.
                  292965
Seq. ID
                  LIB3061-054-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g141601
BLAST score
                  188
E value
                  1.0e-18
                  101
Match length
```

40849

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)



>gi 82657 pir S03417 19K zein precursor (clone gZ19AB11) maize >gi_22543_emb_CAA29340 (X05911) 19 kd alpha zein (AA 1 - 234) [Zea mays]

Seq. No. 292966

Seq. ID LIB3061-054-Q1-K1-G12

Method BLASTX NCBI GI g72307 BLAST score 338 E value 1.0e-31 Match length 107 % identity 68

NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi 168686

(J01246) 26.99 kd zein protein [Zea mays]

292967 Seq. No.

Seq. ID LIB3061-054-Q1-K1-H11

Method BLASTX NCBI GI g136647 BLAST score 155 E value 9.0e-11 Match length 45 % identity 62

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-20 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 100813 pir A41547

ubiquitin-conjugating enzyme E2 - wheat

Seq. No. 292968

Seq. ID LIB3061-054-Q1-K1-H12

Method BLASTX NCBI GI g520582 BLAST score 251 E value 2.0e-21 Match length 98 % identity

NCBI Description (D37796) Ids3 [Hordeum vulgare]

Seq. No. 292969

Seq. ID LIB3061-054-Q1-K1-H6

Method BLASTN NCBI GI q3955064 BLAST score 37 E value 3.0e-11 Match length 53 % identity

NCBI Description Zea mays PHYT I gene for acidic phytase

Seq. No. 292970

Seq. ID LIB3061-055-Q1-K1-A11

Method BLASTX NCBI GI g2501555 BLAST score 642 E value 3.0e-67 Match length 131 % identity 92

NCBI Description POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi 549984 (U13148)

```
292971
Seq. No.
Seq. ID
                  LIB3061-055-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g141603
BLAST score
                  295
E value
                  1.0e-27
Match length
                  109
% identity
                  64
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
                  >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize
                  >gi 22529 emb CAA24723 (V01476) zein [Zea mays]
Seq. No.
                  292972
                  LIB3061-055-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1684851
BLAST score
                  203
E value
                  7.0e-16
Match length
                  64
% identity
                  66
NCBI Description
                  (U77935) DnaJ-like protein [Phaseolus vulgaris]
Seq. No.
                  292973
Seq. ID
                  LIB3061-055-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  q141607
BLAST score
                  176
E value
                  5.0e-13
Match length
                  82
                  54
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE PZ19.1)
NCBI Description
                  >gi 22521 emb CAA24718 (V01471) zein [Zea mays] >gi 168672
                  (J01244) zein 19 kd protein (partial) [Zea mays]
Seq. No.
                  292974
                  LIB3061-055-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112994
BLAST score
                  282
E value
                  2.0e-25
                  79
Match length
                  76
% identity
NCBI Description
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
                  >gi 82685 pir S04536 embryonic abundant protein,
                  glycine-rich - maize >gi 22313 emb CAA31077 (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi 226091 prf 1410284A abscisic acid inducible gene [Zea
                  mays]
Seq. No.
                  292975
Seq. ID
                  LIB3061-055-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  g3819699
BLAST score
                  337
E value
                  8.0e-32
Match length
                  79
```

```
% identity
                  (AJ009609) BnMAP4K alpha2 [Brassica napus]
NCBI Description
                  292976
Seq. No.
Seq. ID
                  LIB3061-055-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g322870
BLAST score
                  562
                  5.0e-58
E value
                  123
Match length
% identity
NCBI Description glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) -
                  maize (fragment)
                  292977
Seq. No.
Seq. ID
                  LIB3061-055-Q1-K1-G3
Method
                  BLASTN
                  g168425
NCBI GI
BLAST score
                  96
                  8.0e-47
E value
                  200
Match length
                  88
% identity
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds
                  292978
Seq. No.
Seq. ID
                  LIB3061-055-Q1-K1-H1
                  BLASTX
Method
NCBI GI
                  g141601
                  468
BLAST score
                  6.0e-47
E value
                  117
Match length
                  79
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
NCBI Description
                  >qi 82657 pir S03417 19K zein precursor (clone gZ19AB11) -
                  maize >qi 22543 emb CAA29340 (X05911) 19 kd alpha zein (AA
                  1 - 234) [Zea mays]
Seq. No.
                  292979
                  LIB3061-055-Q1-K1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4506043
BLAST score
                  563
E value
                  4.0e-58
Match length
                  140
                  69
% identity
                  prolyl endopeptidase >gi_1346769_sp_P48147_PPCE HUMAN
NCBI Description
                  PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE)
                  >qi 558596 emb CAA52605 (X74496) prolyl oligopeptidase
```

Seq. ID LIB3061-055-Q1-K1-H3

[Homo sapiens]

Method BLASTX NCBI GI g141605 BLAST score 275 E value 2.0e-24

[Homo sapiens] >gi_1585155 prf _2124300A Pro oligopeptidase



```
Match length
                  107
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                  292981
Sea. ID
                  LIB3061-056-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  g141605
BLAST score
                  254
                  4.0e-22
E value
                  78
Match length
% identity
                  65
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                  292982
Seq. ID
                  LIB3061-056-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g141605
                  259
BLAST score
                  8.0e-23
E value
Match length
                  74
                  72
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
                  >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                  292983
Seq. ID
                  LIB3061-056-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g224508
BLAST score
                  343
E value
                  2.0e-32
Match length
                  86
% identity
                  86
NCBI Description zein A20 [Zea mays]
Seq. No.
                  292984
Seq. ID
                  LIB3061-056-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  g2196466
BLAST score
                  393
E value
                  3.0e-38
Match length
                  123
% identity
                  60
NCBI Description
                   (Y13673) TATA binding protein-associated factor
```

Seq. ID LIB3061-056-Q1-K1-B6

[Arabidopsis thaliana]

Method BLASTX
NCBI GI g4325354
BLAST score 443
E value 4.0e-44



```
Match length
                  115
                  70
% identity
NCBI Description
                  (AF128395) contains similarity to retrovirus-related
                  polyproteins and to CCHC zinc finger protein (Pfam:
                  PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana]
Seq. No.
                  292986
Seq. ID
                  LIB3061-056-Q1-K1-C7
Method
                  BLASTN
NCBI GI
                  q168679
BLAST score
                  112
E value
                  4.0e-56
Match length
                  324
% identity
                  84
                  Maize 19 kDa zein mRNA, clone cZ19C2, complete cds.
NCBI Description
                  >gi_270687_gb_I03334_ Sequence 9 from Patent US
Seq. No.
                  292987
Seq. ID
                  LIB3061-056-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  q3377517
BLAST score
                  280
E value
                  6.0e-29
Match length
                  120
                  57
% identity
NCBI Description (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]
Seq. No.
                  292988
Seq. ID
                  LIB3061-056-Q1-K1-D3
Method
                  BLASTN
NCBI GI
                  g4185305
BLAST score
                  333
E value
                  0.0e + 00
Match length
                  427
                  95
% identity
NCBI Description
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
                  (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes
Seq. No.
                  292989
Seq. ID
                  LIB3061-056-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  q508545
BLAST score
                  268
E value
                  1.0e-23
Match length
                  93
% identity
NCBI Description
                  (L34340) zein [Zea mays]
Seq. No.
                  292990
```

Seq. ID

LIB3061-056-Q1-K1-D5

Method BLASTX NCBI GI g72307 BLAST score 341 E value 4.0e-32 Match length 115

40854

1.06

```
% identity
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686
                  (J01246) 26.99 kd zein protein [Zea mays]
                  292991
Seq. No.
Seq. ID
                  LIB3061-056-Q1-K1-E11
Method
                  BLASTN
                  g168690
NCBI GI
                  170
BLAST score
                  9.0e-91
E value
                  338
Match length
                  88
% identity
NCBI Description Maize zein mRNA, complete cds, clone ZG124
                  292992
Seq. No.
                  LIB3061-056-Q1-K1-E8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g100925
                  257
BLAST score
                  2.0e-22
E value
Match length
                  102
                  50
% identity
NCBI Description zein, 27K - maize (fragment) >gi_22550_emb CAA41175_
                   (X58197) 27kDa storage protein, zein [Zea mays]
                   292993
Seq. No.
                  LIB3061-056-Q1-K1-E9
Seq. ID
                  BLASTX
Method
                  g168699
NCBI GI
                  209
BLAST score
E value
                   2.0e-17
Match length
                  76
                   76
% identity
NCBI Description (M60836) zein [Zea mays]
                   292994
Seq. No.
                   LIB3061-056-Q1-K1-F2
Seq. ID
Method
                   BLASTX
                   q224507
NCBI GI
                   429
BLAST score
                   2.0e-42
E value
Match length
                   133
% identity
                   71
NCBI Description zein A1 [Zea mays]
                   292995
Seq. No.
Seq. ID
                   LIB3061-056-Q1-K1-G4
```

Method BLASTN
NCBI GI g22514
BLAST score 52
E value 2.0e-20
Match length 212
% identity 81

NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 292996

Seq. ID LIB3061-056-Q1-K1-G8



```
Method
                   BLASTX
 NCBI GI
                   g141605
 BLAST score
                   374
                   4.0e-36
 E value
                   101
 Match length
                   79
 % identity
NCBI Description
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
                   >gi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) -
                   maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
                   292997
 Seq. No.
 Seq. ID
                   LIB3061-056-Q1-K1-H3
 Method
                   BLASTN
 NCBI GI
                   q168690
 BLAST score
                   36
 E value
                   7.0e-11
                   40
 Match length
                   97
 % identity
                   Maize zein mRNA, complete cds, clone ZG124
 NCBI Description
 Seq. No.
                   292998
Seq. ID
                   LIB3061-056-Q1-K1-H5
Method
                   BLASTX
 NCBI GI
                   g141617
 BLAST score
                   240
 E value
                   3.0e-20
                   104
 Match length
 % identity
                   50
                   ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
 NCBI Description
                   >gi 100941 pir__S12140 zein Zc1 - maize
                   >gi 100945 pir B29017 zein 2 - maize
                   >gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                   >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
 Seq. No.
                   292999
                   LIB3061-057-Q1-K1-A11
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   g535019
BLAST score
                   39
                   1.0e-12
 E value
                   43
 Match length
 % identity
                   49
 NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)
 Seq. No.
                   293000
 Seq. ID
                   LIB3061-057-Q1-K1-A2
 Method
                   BLASTX
 NCBI GI
                   g3241943
 BLAST score
                   207
 E value
                   2.0e-16
 Match length
                   44
                   82
 % identity
 NCBI Description
                   (AC004625) hypothetical protein [Arabidopsis thaliana]
```

Seq. ID LIB3061-057-Q1-K1-B7

Method BLASTX

NCBI GI

E value

BLAST score

g4185308

6.0e-24

271

```
NCBI GI
                  q22216
BLAST score
                  223
E value
                  1.0e-18
                  68
Match length
% identity
                  65
NCBI Description
                  (X55722) 22kD zein [Zea mays]
Seq. No.
                  293002
Seq. ID
                  LIB3061-057-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  q468516
BLAST score
                  522
E value
                  3.0e-53
Match length
                  128
% identity
                  86
NCBI Description (X55724) zein [Zea mays]
Seq. No.
                  293003
Seq. ID
                  LIB3061-057-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g82660
BLAST score
                  315
E value
                  5.0e-29
                  99
Match length
% identity
                  68
                  19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                  >gi 809117 emb CAA24720 (V01473) zein [Zea mays]
Seq. No.
                  293004
Seq. ID
                  LIB3061-057-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g141614
BLAST score
                  349
                  5.0e-33
E value
Match length
                  114
% identity
                  68
NCBI Description
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)
                  >gi 82662 pir B22831 22K zein precursor (clone M1) - maize
                  >gi_22527_emb_CAA24722_ (V01475) reading frame zein [Zea
                  mays] >gi 224510 prf 1107201D zein M1 [Zea mays]
                  293005
Seq. No.
Seq. ID
                  LIB3061-057-Q1-K1-E4
Method
                  BLASTN
NCBI GI
                  g22526
BLAST score
                  148
E value
                  1.0e-77
Match length
                  344
% identity
                  86
NCBI Description Zea mays mRNA encoding a zein (clone zA1)
                  293006
Seq. No.
Seq. ID
                  LIB3061-057-Q1-K1-E8
Method
                  BLASTX
```

BLAST score

E value Match length 343 2.0e-32

105

```
95
Match length
% identity
                  (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
NCBI Description
                  293007
Seq. No.
Seq. ID
                  LIB3061-057-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  g2832247
                  232
BLAST score
E value
                  2.0e-29
Match length
                  143
% identity
                  53
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]
                  293008
Seq. No.
Seq. ID
                  LIB3061-057-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g468516
BLAST score
                  365
E value
                   6.0e-35
                  132
Match length
% identity
                   63
NCBI Description (X55724) zein [Zea mays]
Seq. No.
                  293009
Seq. ID
                  LIB3061-057-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  g141601
BLAST score
                  295
E value
                   1.0e-34
Match length
                  126
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
                   >qi 82657 pir S03417 19K zein precursor (clone gZ19AB11) -
                  maize >gi 225\overline{43} emb CAA29340 (X05911) 19 kd alpha zein (AA
                   1 - 234) [Zea mays]
Seq. No.
                   293010
Seq. ID
                  LIB3061-057-Q1-K1-G9
Method
                   BLASTX
NCBI GI
                   g141601
BLAST score
                   323
E value
                   3.0e-30
Match length
                   97
% identity
                   70
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
NCBI Description
                   >gi 82657 pir S03417 19K zein precursor (clone gZ19AB11) -
                   maize >gi 22543 emb CAA29340 (X05911) 19 kd alpha zein (AA
                   1 - 234) [Zea mays]
Seq. No.
                   293011
                   LIB3061-057-Q1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2832247
```

NCBI GI

g82660

```
% identity
NCBI Description
                  (AF031569) 22-kDa alpha zein 10 [Zea mays]
                  293012
Seq. No.
                  LIB3061-057-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g232172
BLAST score
                  300
E value
                  2.0e-27
Match length
                  96
% identity
                  68
                  GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT
NCBI Description
                  PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE
                  PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE
                  ADENYL TRANSFERASE) >gi 481816 pir S39504
                  glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) -
                  wheat >gi 21687 emb CAA46879 (X66080) ADP-glucose
                  pyrophosphorylase [Triticum aestivum]
Seq. No.
                  293013
                  LIB3061-057-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g168693
BLAST score
                  404
E value
                  2.0e-39
Match length
                  132
% identity
                  65
NCBI Description
                  (M29627) zein [Zea mays]
Seq. No.
                  293014
Seq. ID
                  LIB3061-058-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  g141617
BLAST score
                  287
E value
                  1.0e-25
Match length
                  130
                  49
% identity
                  ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                  >qi 100941 pir S12140 zein Zc1 - maize
                  >gi 100945 pir B29017 zein 2 - maize
                  >gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                  >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
Seq. No.
                  293015
Seq. ID
                  LIB3061-058-Q1-K1-B5
Method
                  BLASTX
                  g2827661
NCBI GI
BLAST score
                  154
E value
                  4.0e-10
Match length
                  40
% identity
NCBI Description
                  (AL021637) hyuC-like protein [Arabidopsis thaliana]
Seq. No.
                  293016
Seq. ID
                  LIB3061-058-Q1-K1-B7
Method
                  BLASTX
```



```
254
· BLAST score
                    7.0e-22
 E value
 Match length
                    100
 % identity
                    56
                    19K zein precursor (clone ZG31A) - maize (fragment)
 NCBI Description
                    >gi 809117 emb CAA24720 (V01473) zein [Zea mays]
 Seq. No.
                    293017
 Seq. ID
                   LIB3061-058-Q1-K1-C3
 Method
                    BLASTX
 NCBI GI
                    g4185308
 BLAST score
                    407
 E value
                    8.0e-40
 Match length
                    119
 % identity
                    71
                   (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
 NCBI Description
 Seq. No.
                    293018
 Seq. ID
                    LIB3061-058-Q1-K1-C4
 Method
                    BLASTX
 NCBI GI
                    g2832246
 BLAST score
                    226
 E value
                    4.0e-20
                    86
 Match length
 % identity
                    59
                   (AF031569) 22-kDa alpha zein 8 [Zea mays]
 NCBI Description
 Seq. No.
                    293019
                    LIB3061-058-Q1-K1-C5
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g141602
                    271
 BLAST score
                    5.0e-24
 E value
                    82
 Match length
 % identity
                    67
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6)
 NCBI Description
                    >qi 82658 pir A22831 19K zein precursor (clone M6) - maize
                    >gi 22538 emb CAA26294 (X02450) zein precursor [Zea mays]
 Seq. No.
                    293020
 Seq. ID
                    LIB3061-058-Q1-K1-C6
                    BLASTX
 Method
                    g168691
 NCBI GI
 BLAST score
                    312
 E value
                    1.0e-28
 Match length
                    114
                    59
 % identity
 NCBI Description
                   (M29628) zein [Zea mays]
                    293021
 Seq. No.
                    LIB3061-058-Q1-K1-D3
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g3914425
 BLAST score
                    229
 E value
                    5.0e-19
```

40860

99

53

Match length % identity



PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON NCBI Description CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi 2511596 emb_CAA74029.1_ (Y13695) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421117 (AF043536) 20S proteasome beta subunit PBE1 [Arabidopsis thaliana] 293022 Seq. No. LIB3061-058-Q1-K1-D5 Seq. ID BLASTX Method q116333 NCBI GI 145 BLAST score 1.0e-16 E value 91 Match length 57 % identity ENDOCHITINASE B PRECURSOR (SEED CHITINASE B) >gi_168443 NCBI Description (M84165) chitinase B [Zea mays] 293023 Seq. No. LIB3061-058-Q1-K1-D7 Seq. ID BLASTX Method g141613 NCBI GI 168 BLAST score 9.0e-12 E value 108 Match length 42 % identity ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1) NCBI Description >gi_72305_pir__ZIZM21 22K zein precursor (clone pZ22.1) maize >gi_22532_emb_CAA24725_ (V01478) zein [Zea mays] 293024 Seq. No. LIB3061-058-Q1-K1-F11 Seq. ID BLASTX Method q141608 NCBI GI 310 BLAST score 2.0e-28 E value 131 Match length 55 % identity ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655 NCBI Description zein, 19K - maize >gi_22446_emb_CAA3765 $\overline{1}$ _ (X53 $\overline{5}$ 82) $\overline{1}$ 9 kDa zein [Zea mays] 293025 Seq. No. Seq. ID LIB3061-058-Q1-K1-F2 BLASTX Method q468516 NCBI GI 282 BLAST score 3.0e-25E value Match length 114 57 % identity (X55724) zein [Zea mays] NCBI Description 293026 Seq. No.

Seq. ID LIB3061-058-Q1-K1-F7

Method BLASTX NCBI GI g141617 275 BLAST score

Method

NCBI GI

BLAST score

BLASTX

426

g2500047

```
And the state of t
```

```
3.0e-24
E value
Match length
                   67
% identity
                   76
                   ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                   >gi_100941_pir__S12140 zein Zc1 - maize
                   >gi 100945 pir B29017 zein 2 - maize
                   >gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                   >gi^{-}16866\overline{6} (M^{-}6460) 16-kDa zein protein [Zea mays]
Seq. No.
                   293027
                   LIB3061-058-Q1-K1-H11
Seq. ID
Method
                   BLASTN
                   g2668739
NCBI GI
BLAST score
                   68
E value
                   4.0e-30
Match length
                   76
                   97
% identity
                   Zea mays translation initiation factor GOS2 (TIF) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   293028
                   LIB3061-058-Q1-K1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4185308
BLAST score
                   314
E value
                   5.0e-29
Match length
                   105
                   67
% identity
NCBI Description
                   (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
Seq. No.
                   293029
                   LIB3062-001-Q1-K2-F10
Seq. ID
Method
                   BLASTX
                   g82696
NCBI GI
BLAST score
                   405
                   1.0e-39
E value
Match length
                   86
                   93
% identity
                   glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
                   293030
Seq. No.
                   LIB3062-001-Q1-K2-G11
Seq. ID
                   BLASTX
Method
                   q1899025
NCBI GI
BLAST score
                   152
E value
                   3.0e-13
Match length
                   112
% identity
                   47
                   (U28215) hexokinase 2 [Arabidopsis thaliana] >gi_3687232
NCBI Description
                   (AC005169) hexokinase [Arabidopsis thaliana]
                   293031
Seq. No.
Seq. ID
                   LIB3062-001-Q1-K2-H5
```



```
E value 5.0e-42

Match length 111
% identity 73

NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi_534916_emb_CAA85362_ (Z36894) soluble inorganic pyrophosphatase [Solanum tuberosum]

Seq. No. 293032
```

Seq. ID LIB3062-002-Q1-K2-A8 Method BLASTX NCBI GI g729135 BLAST score 170 E value 5.0e-12 Match length 31 % identity 100

NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID

3-O-METHYLTRANSFERASE) (COMT) *gi_283034_pir__S28612 catechol O-methyltransferase (EC 2.1.1.6) - maize >gi_168532 (M73235) O-methyltransferase [Zea mays]

 Seq. No.
 293033

 Seq. ID
 LIB3062-002-Q1-K2-B1

 Method
 BLASTN

 NCBI GI
 g22312

NCBI GI g22312
BLAST score 118
E value 9.0e-60
Match length 158
% identity 94

NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA =

abscisic acid)

Seq. No. 293034

Seq. ID LIB3062-002-Q1-K2-B3

Method BLASTX
NCBI GI g1076646
BLAST score 374
E value 5.0e-36
Match length 117
% identity 65

NCBI Description transcription factor - common tobacco

>gi 431908 emb CAA53782 (X76188) transcription factor

[Nicotiana tabacum]

Seq. No. 293035

Seq. ID LIB3062-002-Q1-K2-D7

Method BLASTX
NCBI GI 9735880
BLAST score 238
E value 2.0e-23
Match length 145
% identity 49

NCBI Description (L40577) geranylgeranyl pyrophosphate synthase-related

protein [Arabidopsis thaliana]

Seq. No. 293036



```
Seq. ID
                  LIB3062-002-Q1-K2-E9
Method
                  BLASTX
                  q2281090
NCBI GI
                  260
BLAST score
E value
                  1.0e-22
Match length
                  125
                  50
% identity
                  (AC002333) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  293037
Seq. No.
                  LIB3062-002-Q1-K2-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g135411
BLAST score
                  330
                  6.0e-31
E value
Match length
                  108
% identity
                  65
                  TUBULIN ALPHA-2 CHAIN >gi 82732 pir S15772 tubulin alpha-2
NCBI Description
                  chain - maize >gi 22148 emb CAA33733 (X15704)
                  alpha2-tubulin [Zea mays]
                  293038
Seq. No.
                  LIB3062-003-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g16073
BLAST score
                  337
E value
                  1.0e-31
Match length
                  136
                  59
% identity
NCBI Description
                  (X59526) zein protein [Acetabularia mediterranea]
                  293039
Seq. No.
                  LIB3062-003-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141600
BLAST score
                  209
E value
                 9.0e-17
Match length
                  64
                  70
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
                  >gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) -
                  maize >gi 168674 (M12143) 19 kDa zein protein [Zea mays]
Seq. No.
                  293040
Seq. ID
                  LIB3062-003-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  g141604
BLAST score
                  346
E value
                  1.0e-32
Match length
                  117
% identity
                  68
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)
                  >gi_72310 pir ZIZM91 19K zein precursor (clone cZ19C1) -
                  maize >gi 168678 (M12146) 19 kDa zein protein [Zea mays]
```

Seq. ID LIB3062-003-Q1-K1-B11

293041

BLAST score

E value

377

1.0e-36



```
Method
                  BLASTX
NCBI GI
                  g16073
BLAST score
                  254
                  6.0e-22
E value
                  114
Match length
                  54
% identity
                  (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
Seq. No.
                  293042
                  LIB3062-003-Q1-K1-C5
Seq. ID
Method
                  BLASTN
                  g4760422
NCBI GI
BLAST score
                  56
                  8.0e-23
E value
Match length
                  220
% identity
                  81
                  Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1)
NCBI Description
                  related locus, complete sequence [Homo sapiens]
Seq. No.
                  293043
                  LIB3062-003-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141605
BLAST score
                  222
                  2.0e-18
E value
Match length
                  73
% identity
                   68
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                  293044
                  LIB3062-003-Q1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2589162
BLAST score
                  248
                   2.0e-34
E value
Match length
                  139
% identity
                   60
                  (D88451) aldehyde oxidase [Zea mays]
NCBI Description
                  293045
Seq. No.
                  LIB3062-003-Q1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g168691
BLAST score
                   323
E value
                   5.0e-30
Match length
                  104
                   67
% identity
NCBI Description
                  (M29628) zein [Zea mays]
                   293046
Seq. No.
                  LIB3062-003-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1657859
```

```
Match length
% identity
                   76
NCBI Description
                   (U73218) chlorophyll a/b-binding protein WCAB precursor
                   [Triticum aestivum]
Seq. No.
                   293047
                   LIB3062-004-Q1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4455350
BLAST score
                   151
E value
                   8.0e-10
Match length
                   34
% identity
                   76
NCBI Description
                  (AL035524) putative protein [Arabidopsis thaliana]
Seq. No.
                   293048
Seq. ID
                  LIB3062-004-Q1-K1-D3
Method
                  BLASTN
                   g1185553
NCBI GI
BLAST score
                   38
E value
                   6.0e-12
Match length
                  54
                  93
% identity
NCBI Description
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2)
                  gene, complete cds
Seq. No.
                  293049
Seq. ID
                  LIB3062-004-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  q2244831
BLAST score
                  200
                  8.0e-16
E value
Match length
                  96
% identity
                   47
NCBI Description
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  293050
                  LIB3062-004-Q1-K1-G6
Seq. ID.
Method
                  BLASTX
NCBI GI
                  q2982434
BLAST score
                  150
E value
                  4.0e-10
Match length
                  48
% identity
                  62
NCBI Description
                  (AL022224) putative protein [Arabidopsis thaliana]
Seq. No.
                  293051
Seq. ID
                  LIB3062-005-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  q4103987
```

Method BLASTX
NCBI GI g4103987
BLAST score 334
E value 3.0e-31
Match length 126
% identity 60

NCBI Description (AF030516) 5,10-methylenetetrahydrofolate

dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase

[Pisum sativum]

```
Seq. No.
                   293052
Seq. ID
                   LIB3062-005-Q1-K1-B7
Method
                   BLASTN
NCBI GI
                   q551482
BLAST score
                   48
E value
                   5.0e-18
Match length
                   72
% identity
                   92
NCBI Description
                   Zea mays ABA- and ripening-inducible-like protein mRNA,
                   complete cds
Seq. No.
                   293053
Seq. ID
                   LIB3062-006-Q1-K1-A5
Method
                   BLASTX
NCBI GI
                   q461451
BLAST score
                   168
E value
                   5.0e-12
Match length
                   45
% identity
                  73
NCBI Description
                  AUXIN-BINDING PROTEIN 4 PRECURSOR (ABP)
                  >gi_418698 pir__B43033 auxin-binding protein 4 precursor -
                  maize >gi 168399 (L08426) auxin-binding protein [Zea mays]
                  >gi 442526_bbs_139535 (S66813) ZmERabp4=auxin-binding
                  protein [Zea mays=corn, seedling, Peptide, 204 aa] [Zea
                  mays]
Seq. No.
                  293054
Seq. ID
                  LIB3062-006-Q1-K1-B1
Method
                  BLASTN
NCBI GI
                  g468055
BLAST score
                  61
E value
                  5.0e-26
Match length
                  129
% identity
                  88
NCBI Description
                  Zea mays B73 QM protein mRNA, complete cds
Seq. No.
                  293055
Seq. ID
                  LIB3062-006-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  q3387349
BLAST score
                  303
E value
                  2.0e-37
Match length
                  150
% identity
NCBI Description
                  (AJ006134) preprotein translocase [Synechococcus PCC7942]
Seq. No.
                  293056
Seq. ID
                  LIB3062-006-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  q114332
BLAST score
                  479
E value
                  3.0e-48
Match length
                  109
% identity
                  84
NCBI Description
                  PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)
                  >gi_482389_pir__A45506 H+-transporting ATPase (EC 3.6.1.35)
```



LHA1 - tomato >gi_170464 (M60166) H+-ATPase [Lycopersicon esculentum] >gi_228405_prf__1803518A H ATPase [Lycopersicon esculentum]

 Seq. No.
 293057

 Seq. ID
 LIB3062-006-Q1-K1-G2

 Method
 BLASTX

 NCBI GI
 g1711615

 BLAST game
 277

BLAST score 277 E value 1.0e-24 Match length 111 % identity 50

NCBI Description HIGH AFFINITY SULPHATE TRANSPORTER 1

>gi_1085847_pir__S51763 high affinity sulphate transporter
- Stylosanthes hamata >gi_607184_emb_CAA57710_ (X82255)
high affinity sulphate transporter [Stylosanthes hamata]

Seq. No. 293058

Seq. ID LIB3062-006-Q1-K1-H1

Method BLASTN
NCBI GI g2431766
BLAST score 58
E value 4.0e-24
Match length 159
% identity 96

NCBI Description Zea mays acidic ribosomal protein P3a (rpp3a) mRNA,

complete cds

Seq. No. 293059

Seq. ID LIB3062-007-Q1-K1-A8

Method BLASTX
NCBI GI g123601
BLAST score 159
E value 3.0e-11
Match length 70
% identity 50

NCBI Description HEAT SHOCK 70 KD PROTEIN >gi_99913_pir__S14992 heat shock

protein, 70K - soybean >gi_18663_emb_CAA44620_ (X62799)

Heat Shock 70kD protein [Glycine max]

Seq. No. 293060

Seq. ID LIB3062-007-Q1-K1-D7

Method BLASTX
NCBI GI g2435522
BLAST score 279
E value 3.0e-25
Match length 81
% identity 62

NCBI Description (AF024504) contains similarity to other AMP-binding enzymes

[Arabidopsis thaliana]

Seq. No. 293061

Seq. ID LIB3062-007-Q1-K1-G7

Method BLASTX
NCBI GI g2462733
BLAST score 432
E value 5.0e-43



```
Match length
                  100
% identity
                  88
NCBI Description
                  (AC002292) Putative enoyl-CoA hydratase/isomerase
                  [Arabidopsis thaliana]
Seq. No.
                  293062
Seq. ID
                  LIB3062-008-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g2688822
BLAST score
                  193
                  4.0e-15
E value
Match length
                  44
% identity
                  82
NCBI Description
                  (U93272) pyrophosphate-dependent phosphofructo-1-kinase
                  [Prunus armeniaca]
Seq. No.
                  293063
Seq. ID
                  LIB3062-008-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  q4538967
BLAST score
                  333
E value
                  4.0e-31
Match length
                  98
                  69
% identity
NCBI Description (AL049488) major intrinsic protein (MIP)-like [Arabidopsis
                  thaliana]
Seq. No.
                  293064
                  LIB3062-008-Q1-K1-D8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g517257
BLAST score
                  61
E value
                  1.0e-25
Match length
                  104
% identity
                  90
NCBI Description Z.mays MNBla mRNA for DNA-binding protein
Seq. No.
                  293065
Seq. ID
                  LIB3062-008-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  q3426039
BLAST score
                  166
E value
                  1.0e-11
Match length
                  45
% identity
                  64
NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]
Seq. No.
                  293066
Seq. ID
                  LIB3062-008-Q1-K1-G2
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2252847
BLAST score 187
E value 5.0e-14
Match length 91
% identity 41

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]



```
Seq. No.
                   293067
Seq. ID
                  LIB3062-008-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                   g4467139
BLAST score
                   230
E value
                   5.0e-29
Match length
                  131
% identity
                   51
NCBI Description
                   (AL035540) putative protein phosphatase-2c [Arabidopsis
                  thaliana]
Seq. No.
                   293068
                  LIB3062-008-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3080401
BLAST score
                  201
E value
                  9.0e-16
Match length
                  59
% identity
                   64
                  (AL022603) putative protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4455265_emb_CAB36801.1 (AL035527) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                  293069
                  LIB3062-008-Q1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3738308
BLAST score
                  313
E value
                  8.0e-29
Match length
                  98
% identity
                  65
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                  293070
Seq. ID
                  LIB3062-009-Q1-K1-B1
Method
                  BLASTN
NCBI GI
                  q4160401
BLAST score
                  189
E value
                  1.0e-102
Match length
                  291
% identity
                  86
NCBI Description Zea mays eIF-5 gene, exons 1-2
Seq. No.
                  293071
Seq. ID
                  LIB3062-009-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  q4262142
BLAST score
                  162
E value
                  5.0e-19
Match length
                  80
% identity
NCBI Description
                  (AC005275) putative alcohol dehydrogenase [Arabidopsis
```

thaliana]

Seq. No.

293072

Seq. ID

LIB3062-009-Q1-K1-E8

Method

BLASTX

Match length

41



```
NCBI GI
                   q1085952
BLAST score
                   177
                   7.0e-21
E value
Match length
                   99
% identity
                   59
NCBI Description
                   hypothetical protein S1 - Phalaris coerulescens
                   >gi_556831_emb_CAA57519_ (X81991) S1 [Phalaris
                   coerulescens] >gi_1103489_emb CAA63108 (X92351)
                   self-incompatibility mutant protein [Phalaris coerulescens]
Seq. No.
                   293073
Seq. ID
                   LIB3062-009-Q1-K1-F12
Method
                   BLASTN
NCBI GI
                   g2196541
BLAST score
                   33
E value
                   3.0e-09
Match length
                   33
% identity
                   100
NCBI Description Oryza sativa glycine-rich protein mRNA, complete cds
Seq. No.
                   293074
Seq. ID
                   LIB3062-009-Q1-K1-G4
Method
                   BLASTX
NCBI GI
                   g4165323
BLAST score
                   159
                   5.0e-16
E value
Match length
                   99
% identity
                   51
NCBI Description
                  (AB022442) p-type H+-ATPase [Vicia faba]
Seq. No.
                   293075
Seq. ID
                   LIB3062-009-Q1-K1-G5
Method
                   BLASTX
NCBI GI
                   g4510383
BLAST score
                   296
E value
                   6.0e-27
Match length
                   85
% identity
                   71
NCBI Description
                  (AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.
                   293076
Seq. ID
                   LIB3062-009-Q1-K1-G9
Method
                   BLASTX
NCBI GI
                   g3201615
BLAST score
                   179
E value
                   7.0e-21
Match length
                  140
% identity
                   47
NCBI Description
                  (AC004669) unknown protein [Arabidopsis thaliana]
Seq. No.
                  293077
Seq. ID
                  LIB3062-009-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g2224915
BLAST score
                  221
E value
                  4.0e-18
```

```
% identity
NCBI Description
                  (U95968) beta-expansin [Oryza sativa]
Seq. No.
                   293078
Seq. ID
                  LIB3062-009-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g452777
BLAST score
                  191
E value
                  2.0e-14
Match length
                   63
% identity
                  57
NCBI Description (X68216) auxin-induced protein [Pisum sativum]
Seq. No.
                  293079
                  LIB3062-010-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3395434
BLAST score
                  193
E value
                  7.0e-15
Match length
                  69
% identity
                  62
NCBI Description
                  (AC004683) peroxidase [Arabidopsis thaliana]
                  >gi_742248_prf__2009327B peroxidase [Arabidopsis thaliana]
Seq. No.
                  293080
                  LIB3062-010-Q1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g541546
BLAST score
                  321
E value
                  4.0e-30
Match length
                  83
% identity
                  17
NCBI Description
                  ubiquitin precursor - Volvox carteri
                  >gi_395295_emb_CAA52290_ (X74214) polyubiquitin [Volvox
                  carteri]
Seq. No.
                  293081
Seq. ID
                  LIB3062-011-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g2506985
BLAST score
                  177
E value
                  7.0e-13
Match length
                  54
% identity
                  65
NCBI Description
```

CDC4-LIKE PROTEIN >gi_1580781 (M83822) beige-like protein [Homo sapiens]

Seq. No. 293082

Seq. ID LIB3062-011-Q1-K1-C7

Method BLASTX NCBI GI q4006867 BLAST score 229 E value 6.0e-19 Match length 119 % identity 41

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

BLAST score

Match length

% identity

E value

245

130

57

4.0e-35

```
Seq. No.
                   293083
                   LIB3062-012-Q1-K1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3193316
BLAST score
                   235
E value
                   1.0e-19
Match length
                   141
% identity
                   49
NCBI Description
                   (AF069299) contains similarity to nucleotide sugar
                   epimerases [Arabidopsis thaliana]
Seq. No.
                   293084
Seq. ID
                   LIB3062-012-Q1-K1-B1
Method
                   BLASTX
NCBI GI
                   q1706130
BLAST score
                   632
E value
                   3.0e-66
Match length
                   141
% identity
                   84
NCBI Description
                  CDPK-RELATED PROTEIN KINASE (PK421) >gi_2129917_pir__$60052
                  calcium-dependent protein kinase homolog - carrot
                  >gi 1103386_emb_CAA58750_ (X83869) CDPK-related protein
                   kinase [Daucus carota]
Seq. No.
                  293085
                  LIB3062-012-Q1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2959358
BLAST score
                  652
E value
                  2.0e-68
Match length
                  129
% identity
                  98
NCBI Description (X96758) clathrin coat assembly protein AP17 [Zea mays]
Seq. No.
                  293086
Seq. ID
                  LIB3062-012-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g112994
BLAST score
                  207
E value
                  2.0e-16
Match length
                  41
% identity
                  100
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi_22313_emb CAA31077 (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi_226091_prf__1410284A abscisic acid inducible gene [Zea
                  mays]
Seq. No.
                  293087
Seq. ID
                  LIB3062-012-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g2765817
```



```
NCBI Description
                   (Z95352) AtMlo-h1 [Arabidopsis thaliana]
                   >gi_3892049_gb_AAC78258.1_AAC78258 (AC002330) AtMlo-h1
                   [Arabidopsis thaliana]
Seq. No.
                   293088
Seq. ID
                   LIB3062-012-Q1-K1-D7
Method
                   BLASTX
NCBI GI
                   g2924777
BLAST score
                   233
E value
                   2.0e-19
Match length
                   100
% identity
                   47
NCBI Description
                   (AC002334) putative receptor protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   293089
Seq. ID
                   LIB3062-012-Q1-K1-F2
Method
                   BLASTN
                   g507770
NCBI GI
BLAST score
                   41
E value
                   1.0e-13
Match length
                  52
% identity
                   96
NCBI Description
                  Zea mays D3L H(+)-transporting ATPase (Mha1) gene, complete
                   293090
Seq. No.
Seq. ID
                  LIB3062-012-Q1-K1-F4
Method
                  BLASTX
                   g3047083
NCBI GI
BLAST score
                   540
E value
                   2.0e-55
                  143
Match length
% identity
                   73
NCBI Description
                  (AF058914) similar to FLAP endonuclease-1 (SW:P39748)
                   [Arabidopsis thaliana]
Seq. No.
                  293091
Seq. ID
                  LIB3062-013-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g4314401
BLAST score
                   214
E value
                   3.0e-17
Match length
                   76
% identity
NCBI Description
                  (AC006232) putative beta-1,3-glucanase [Arabidopsis
                  thaliana]
Seq. No.
                  293092
                  LIB3062-013-Q1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4263825
BLAST score
                  288
E value
                  8.0e-26
Match length
                  152
% identity
                  39
```

NCBI Description (AC006067) hypothetical protein [Arabidopsis thaliana]

Seq. No.

293098

```
Seq. No.
                   293093
Seq. ID
                   LIB3062-013-Q1-K1-B5
Method
                   BLASTX
NCBI GI
                   q3818624
BLAST score
                   196
E value
                   5.0e-15
Match length
                   83
% identity
                   52
NCBI Description
                   (AF095912) actin related protein 2; ARP2 [Arabidopsis
                   thaliana]
Seq. No.
                   293094
Seq. ID
                   LIB3062-013-Q1-K1-C4
Method
                   BLASTX
                   g4098323
NCBI GI
BLAST score
                   396
E value
                   1.0e-38
Match length
                   118
% identity
                   71
NCBI Description (U76746) beta-tubulin 3 [Triticum aestivum]
Seq. No.
                   293095
Seq. ID
                   LIB3062-013-Q1-K1-H5
Method
                   BLASTX
NCBI GI
                   g2773154
BLAST score
                   184
E value
                   1.0e-14
Match length
                   69
% identity
                   58
NCBI Description
                   (AF039573) abscisic acid- and stress-inducible protein
                   [Oryza sativa]
Seq. No.
                   293096
Seq. ID
                   LIB3062-014-Q1-K1-C7
Method
                   BLASTX
NCBI GI
                   g2511531
BLAST score
                   423
E value
                   9.0e-42
Match length
                   88
% identity
                   91
                   (AF008120) alpha tubulin 1 [Eleusine indica]
NCBI Description
                   >gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1
                   [Eleusine indica]
Seq. No.
                   293097
Seq. ID
                   LIB3062-014-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                   q99743
BLAST score
                   155
E value
                   7.0e-11
Match length
                   54
% identity
                   59
NCBI Description
                  2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 2
                   - Arabidopsis thaliana
```



```
LIB3062-014-Q1-K1-F1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1498596
BLAST score
                  54
E value
                  2.0e-21
Match length
                  122
                  86
% identity
NCBI Description Zea mays phospholipid transfer protein mRNA, complete cds
                  293099
Seq. No.
                  LIB3062-014-Q1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1169528
BLAST score
                  369
                  2.0e-35
E value
Match length
                  94
% identity
                  82
NCBI Description
                  ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi 602253 (U17973)
                  enolase [Zea mays]
Seq. No.
                  293100
Seq. ID
                  LIB3062-015-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g283038
BLAST score
                  486
E value
                  4.0e-49
Match length
                  108
% identity
                  88
NCBI Description
                  chlorophyll a/b-binding protein (cab-m7) precursor - maize
                  >gi 22230 emb CAA37474 (X53398) light harvesting
                  chlorophyll a /b binding protein [Zea mays]
Seq. No.
                  293101
Seq. ID
                  LIB3062-015-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g2497539
BLAST score
                  598
E value
                  3.0e-62
Match length
                  138
% identity
                  82
NCBI Description
                  PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >qi 169703
                  (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]
Seq. No.
                  293102
Seq. ID
                  LIB3062-015-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g132147
BLAST score
                  200
E value
                  2.0e-23
Match length
                  91
% identity
                  65
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 68089 pir RKZMS
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
```

precursor - maize >gi_22474 emb CAA29784 (X06535)

ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor



[Zea mays] >gi_217964_dbj_BAA00120_ (D00170) ribulose 1,5-bisphosphate carboxylase small subunit [Zea mays] >gi 359512 prf 1312317A ribulosebisphosphate carboxylase [Zea mays]

293103 Seq. No.

LIB3062-015-Q1-K1-F11 Seq. ID

Method BLASTX NCBI GI q3434975 BLAST score 222 E value 4.0e-18 Match length 64 % identity 66

(AB008107) ethylene responsive element binding factor 5 NCBI Description

[Arabidopsis thaliana]

Seq. No. 293104

LIB3062-015-Q1-K1-F6 Seq. ID

Method BLASTX NCBI GI q3337361 BLAST score 235 E value 9.0e-20 Match length 98 37 % identity

(AC004481) ankyrin-like protein [Arabidopsis thaliana] NCBI Description

Seq. No. 293105

Seq. ID LIB3062-016-Q1-K1-B1

Method BLASTN NCBI GI g3342822 BLAST score 87 E value 2.0e-41 Match length 183

% identity 87

Zea mays eukaryotic translation initiation factor p28 NCBI Description

subunit (eIFiso-4E) mRNA, complete cds

Seq. No. 293106

LIB3062-016-Q1-K1-B3 Seq. ID

Method BLASTX g1706260 NCBI GI BLAST score 163 2.0e-11 E value Match length 35 86 % identity

CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597 NCBI Description

cysteine proteinase 1 precursor - maize

>gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea

mays]

293107 Seq. No.

Seq. ID LIB3062-016-Q1-K1-F11

Method BLASTX q1169238 NCBI GI BLAST score 438 E value 2.0e-43 Match length 123



% identity NCBI Description GLUTAMATE DECARBOXYLASE (GAD) >gi_1076648_pir__A48767 glutamate decarboxylase (EC 4.1.1.15), calmodulin-binding garden petunia >gi_294112 (L16797) glutamate decarboxylase [Petunia hybrida] >gi 309680 (L16977) glutamate decarboxylase [Petunia hybrida] Seq. No. 293108 LIB3062-016-Q1-K1-H10 Seq. ID Method BLASTX NCBI GI g2887459 BLAST score 186 E value 4.0e-14 Match length 53 % identity 74 NCBI Description (AB010922) actin [Cucumis sativus] 293109 Seq. No. LIB3062-016-Q1-K1-H12 Seq. ID Method BLASTX NCBI GI g114420 BLAST score 258 E value 5.0e-29 Match length 78 % identity 90 NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi 100882 pir S11491 H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mitochondrial - maize >gi 22173 emb CAA38140 (X54233) ATPase F1 subunit protein [Zea mays] >gi 897618 (M36087) F-1-ATPase subunit 2 [Zea mays] Seq. No. 293110 Seq. ID LIB3062-017-Q1-K1-A5 BLASTN Method g2773153 NCBI GI BLAST score 84 E value 2.0e-39 Match length 112 94 % identity NCBI Description Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds 293111 Seq. No. Seq. ID LIB3062-017-Q1-K1-D6 Method BLASTX NCBI GI g2262104 BLAST score 182 2.0e-13 E value 75 Match length

% identity 43

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 293112

Seq. ID LIB3062-017-Q1-K1-E2

Method BLASTN NCBI GI g2984708



```
37
BLAST score
E value
                  1.0e-11
Match length
                  85
% identity
                  86
                  Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
NCBI Description
                  293113
Seq. No.
                  LIB3062-017-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4586110
BLAST score
                  237
E value
                  7.0e-20
Match length
                  110
% identity
                   47
                  (AL049638) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  293114
                  LIB3062-017-Q1-K1-H11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168650
BLAST score
                  49
                  5.0e-19
E value
Match length
                  61
% identity
                  95
NCBI Description Zea mays ubiquitin fusion protein (UBF9) gene, complete cds
                  293115
Seq. No.
                  LIB3062-018-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4582787
BLAST score
                  249
                  2.0e-21
E value
Match length
                  50
                  94
% identity
NCBI Description (AJ012281) adenosine kinase [Zea mays]
Seq. No.
                  293116
                  LIB3062-018-Q1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1706260
BLAST score
                   294
                   7.0e-27
E value
                   80
Match length
                   74
% identity
NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597
                   cysteine proteinase 1 precursor - maize
                   >gi 643597 dbj BAA08244 (D45402) cysteine proteinase [Zea
                   mays]
                   293117
Seq. No.
                  LIB3062-018-Q1-K1-D9
Seq. ID
Method
                  BLASTN
```

g22103

57 2.0e-23

NCBI GI BLAST score

E value

Match length

% identity

139

55



```
Match length
                   48
% identity
NCBI Description Zea mays A2 gene
                   293118
Seq. No.
                   LIB3062-018-Q1-K1-F2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g282833
                   424
BLAST score
                   5.0e-42
E value
                   92
Match length
                   89
% identity
NCBI Description phosphoglycerate kinase (EC 2.7.2.3) - spinach (fragment)
                   293119
Seq. No.
                   LIB3062-019-Q1-K1-A1
Seq. ID
                   BLASTX
Method
                   g4544432
NCBI GI
                   155
BLAST score
                   3.0e-10
E value
                   93
Match length
% identity
                   44
                  (AC006955) putative mannose-1-phosphate guanyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   293120
Seq. No.
                   LIB3062-019-Q1-K1-A11
Seq. ID
Method
                   BLASTX
                   g1438881
NCBI GI
BLAST score
                   163
                   3.0e-11
E value
                   60
Match length
                   53
% identity
NCBI Description (U43839) GmCK2p [Glycine max]
                   293121
Seq. No.
                   LIB3062-019-Q1-K1-A6
Seq. ID
Method
                   BLASTX
                   q320618
NCBI GI
BLAST score
                   294
                   1.0e-34
E value
                    140
Match length
                    59
% identity
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                    >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                    [Oryza sativa]
                    293122
Seq. No.
Seq. ID
                    LIB3062-019-Q1-K1-A8
Method
                    BLASTX
NCBI GI
                    q2129552
BLAST score
                    355
E value
                    1.0e-33
```

5.



```
calcium-dependent protein kinase 19 - Arabidopsis thaliana
NCBI Description
                   (fragment)
Seq. No.
                  293123
Seq. ID
                  LIB3062-019-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  g741983
BLAST score
                  335
E value
                  1.0e-31
Match length
                  97
                  68
% identity
NCBI Description sucrose synthase: ISOTYPE=2 [Zea mays]
                  293124
Seq. No.
Seq. ID
                  LIB3062-019-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g2821957
BLAST score
                  454
E value
                  3.0e-45
Match length
                  142
% identity
                  61
NCBI Description
                 (AB006691) spermidine synthase 2 [Hyoscyamus niger]
Seq. No.
                  293125
Seq. ID
                  LIB3062-019-Q1-K1-H7
Method
                  BLASTX
                  g168489
NCBI GI
BLAST score
                  165
                  1.0e-11
E value
Match length
                  88
% identity
                  47
NCBI Description
                  (M16902) glutathione S-transferase I [Zea mays] >gi 168491
                   (M16901) glutathione S-transferase I [Zea mays]
                  >gi_225458_prf__1303351A transferase,glutathione S [Zea
                  mays]
Seq. No.
                  293126
Seq. ID
                  LIB3062-020-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  g2065021
BLAST score
                  186
E value
                  2.0e-14
                  71
Match length
                  54
% identity
NCBI Description (Y12555) alanyl t-RNA synthetase [Arabidopsis thaliana]
Seq. No.
                  293127
Seq. ID
                  LIB3062-020-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g136640
BLAST score
                  179
E value
                  4.0e-13
Match length
                  113
                  39
% identity
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 170785 (M62720)
```

ubiquitin carrier protein [Triticum aestivum]



```
293128
Seq. No.
                  LIB3062-020-Q1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1723511
                  239
BLAST score
                  4.0e-20
E value
                  122
Match length
                  43
% identity
                  PUTATIVE ENDONUCLEASE C1F12.06C >gi_2130239_pir__$67449
NCBI Description
                  hypothetical protein - fission yeast (Schizosaccharomyces
                  pombe) >gi_1217980_emb_CAA93810_ (Z69944) unknown
                  [Schizosaccharomyces pombe]
                  293129
Seq. No.
                  LIB3062-020-Q1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1174846
BLAST score
                  158
                  6.0e-11
E value
                  91
Match length
% identity
                   43
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 3 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 3) (UBIQUITIN CARRIER PROTEIN 3)
                   >gi_1076425_pir__S43782 ubiquitin-conjugating enzyme UBC3 -
                   Arabidopsis thaliana >gi_431262 (L19352) ubiquitin
                   conjugating enzyme [Arabidopsis thaliana]
                   293130
Seq. No.
                   LIB3062-020-Q1-K1-E4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1362009
                   330
BLAST score
                   9.0e-31
E value
                   107
Match length
                   68
% identity
                  ubiquitin-like protein 7 - Arabidopsis thaliana
NCBI Description
                   293131
Seq. No.
                   LIB3062-020-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   g3513746
NCBI GI
                   304
BLAST score
                   5.0e-28
E value
                   99
Match length
                   62
% identity
                   (AF080118) contains similarity to AMP-binding enzymes
NCBI Description
                   (Pfam: AMP-binding.hmm, score: 18.66, 25.90 and 43.55);
                   most similar to acyl-CoA synthetases [Arabidopsis thaliana]
                   293132
Seq. No.
                   LIB3062-020-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   g3915009
NCBI GI
```

259

2.0e-22 115

BLAST score E value

Match length



```
% identity
                  ARGININE DECARBOXYLASE (ARGDC) (ADC) >gi_1163181 (U35367)
NCBI Description
                  arginine decarboxylase [Glycine max]
Seq. No.
                  293133
                  LIB3062-021-Q1-K1-C2
Seq. ID
                  BLASTX
Method
                  q741983
NCBI GI
                  369
BLAST score
                  1.0e-35
E value
                  105
Match length
                  70
% identity
NCBI Description sucrose synthase: ISOTYPE=2 [Zea mays]
                  293134
Seq. No.
                  LIB3062-021-Q1-K1-C7
Seq. ID
Method
                  BLASTX
                  q2497748
NCBI GI
                  183
BLAST score
                  1.0e-13
E value
                  72
Match length
% identity
                   50
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 4 PRECURSOR (LTP 4)
NCBI Description
                   >gi 902058 (U29176) lipid transfer protein precursor [Oryza
                   sativa]
Seq. No.
                   293135
                   LIB3062-021-Q1-K1-D11
Seq. ID
                   BLASTX
Method
                   g1174846
NCBI GI
BLAST score
                   261
                   8.0e-23
E value
Match length
                   95
                   57
% identity
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 3 (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE 3) (UBIQUITIN CARRIER PROTEIN 3)
                   >gi_1076425_pir__S43782 ubiquitin-conjugating enzyme UBC3 -
                   Arabidopsis thaliana >gi_431262 (L19352) ubiquitin
                   conjugating enzyme [Arabidopsis thaliana]
Seq. No.
                   293136
                   LIB3062-021-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   g3451075
NCBI GI
                   311
BLAST score
                   2.0e-28
E value
                   119
Match length
                   50
% identity
                   (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
                   293137
Seq. No.
                   LIB3062-021-Q1-K1-G2
Seq. ID
                   BLASTX
Method
                   q1167953
NCBI GI
```

200

131

2.0e-15

BLAST score

E value Match length



```
% identity
                  (U43496) putative 32.6 kDa jasmonate-induced protein
NCBI Description
                  [Hordeum vulgare] >gi_2465426 (AF021256) 32 kDa protein
                  [Hordeum vulgare]
                  293138
Seq. No.
                  LIB3062-021-Q1-K1-G8
Seq. ID
                  BLASTX
Method
                  g3142289
NCBI GI
BLAST score
                  289
                  4.0e-26
E value
                  95
Match length
                  59
% identity
                   (AC002411) Strong similarity to beta-keto-Coa synthase
NCBI Description
                  gb_U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
                  293139
Seq. No.
                  LIB3062-021-Q1-K1-H7
Seq. ID
Method
                  BLASTX
                   g4240033
NCBI GI
BLAST score
                  195
E value
                   7.0e-15
Match length
                   42
                   83
% identity
                  (AB018587) ZmGRla [Zea mays]
NCBI Description
                   293140
Seq. No.
                   LIB3062-022-Q1-K1-A3
Seq. ID
Method
                   BLASTX
                   g2130107
NCBI GI
                   175
BLAST score
E value
                   1.0e-12
                   115
Match length
                   36
% identity
NCBI Description porin (clone Tavdacl) - wheat
                   293141
Seq. No.
                   LIB3062-022-Q1-K1-A7
Seq. ID
                   BLASTX
Method
                   g4510373
NCBI GI
                   147
BLAST score
                   3.0e-09
E value
                   52
Match length
                   54
% identity
                   (AC007017) putative harpin-induced protein [Arabidopsis
NCBI Description
                   thaliana]
                   293142
Seq. No.
                   LIB3062-022-Q1-K1-B7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2773153
                   93
BLAST score
E value
                   8.0e-45
                   165
Match length
                   89
% identity
                   Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
```

(Asr1) mRNA, complete cds



```
293143
Seq. No.
                  LIB3062-022-Q1-K1-G4
Seq. ID
Method
                  BLASTX
                  g312179
NCBI GI
                  273
BLAST score
                  2.0e-24
E value
                  86
Match length
% identity
                  (X73151) glyceraldehyde 3-phosphate dehydrogenase
NCBI Description
                  (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic
                  glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]
                  >gi_1185554 (U45858) glyceraldehyde-3-phosphate
                  dehydrogenase [Zea mays]
Seq. No.
                  293144
                  LIB3062-022-Q1-K1-H12
Seq. ID
Method
                  BLASTX
                  g3176690
NCBI GI
                  306
BLAST score
                  6.0e-28
E value
                  136
Match length
                  51
% identity
                  (AC003671) Similar to ubiquitin ligase gb_D63905 from S.
NCBI Description
                   cerevisiae. EST gb_R65295 comes from this gene.
                   [Arabidopsis thaliana]
                   293145
Seq. No.
                  LIB3062-022-Q1-K1-H7
Seq. ID
                  BLASTX
Method
                  q2832692
NCBI GI
BLAST score
                   262
                   1.0e-22
E value
                   154
Match length
% identity
                  (AL021713) putative protein [Arabidopsis thaliana]
NCBI Description
                   293146
Seq. No.
                   LIB3062-022-Q1-K1-H8
Seq. ID
                   BLASTX
Method
                   g2501067
NCBI GI
                   495
BLAST score
                   5.0e-50
E value
                   160
Match length
                   56
 % identity
                   VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS)
NCBI Description
                   >gi 1001391_dbj BAA10881_ (D64006) valyl-tRNA synthetase
                   [Synechocystis sp.]
                   293147
 Seq. No.
 Seq. ID
                   LIB3062-022-Q1-K1-H9
Method
                   BLASTX
                   g3608133
 NCBI GI
                   219
 BLAST score
```

9.0e-18

69

55

E value

Match length % identity



```
(AC005314) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  293148
Seq. No.
                  LIB3062-023-Q1-K1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2914706
                  209
BLAST score
                  1.0e-16
E value
                  78
Match length
% identity
NCBI Description (AC003974) putative homeobox protein [Arabidopsis thaliana]
                  293149
Seq. No.
                  LIB3062-023-Q1-K1-G3
Seq. ID
                  BLASTN
Method
                  q22292
NCBI GI
BLAST score
                   63
                   7.0e-27
E value
                   74
Match length
                   96
% identity
NCBI Description Z.mays mRNA for glycine-rich protein
                   293150
Seq. No.
                   LIB3062-024-Q1-K1-D3
Seq. ID
                   BLASTN
Method
                   g169843
NCBI GI
                   37
BLAST score
                   9.0e-12
E value
                   57
Match length
                   91
% identity
                   Saccharum sp. phosphoenolpyruvate carboxylase (SCPEPCD1)
NCBI Description
                   gene, complete cds
                   293151
Seq. No.
                   LIB3062-024-Q1-K1-H7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2130141
 BLAST score
                   214
                   5.0e-22
 E value
                   70
 Match length
                   59
 % identity
                   mudrA protein - maize transposon MuDR >gi 540581 (M76978)
 NCBI Description
                   mudrA [Zea mays] >gi_595816 (U14597) mudrA gene product
                    [Zea mays]
                   293152
 Seq. No.
                   LIB3062-025-Q1-K1-B5
 Seq. ID
 Method
                   BLASTX
                    g3395440
 NCBI GI
                    254
 BLAST score
                    7.0e-22
 E value
                   140
 Match length
 % identity
                   (AC004683) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                    293153
 Seq. No.
                    LIB3062-025-Q1-K1-C6
 Seq. ID
```

BLAST score

E value

211

5.0e-17



```
Method
                  BLASTX
NCBI GI
                  g4559342
BLAST score
                  174
                  2.0e-12
E value
Match length
                  45
                  78
% identity
NCBI Description
                  (AC007087) putative copper methylamine oxidase [Arabidopsis
                  thaliana]
                  293154
Seq. No.
Seq. ID
                  LIB3062-025-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g4538939
BLAST score
                  195
E value
                  6.0e-15
Match length
                  103
% identity
                   42
NCBI Description
                  (AL049483) Col-0 casein kinase I-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  293155
                  LIB3062-025-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g107420
BLAST score
                  143
E value
                  5.0e-09
Match length
                  107
% identity
                  33
NCBI Description X-Pro dipeptidase (EC 3.4.13.9) - human
                  293156
Seq. No.
Seq. ID
                  LIB3062-025-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                  g3114966
BLAST score
                   312
E value
                   3.0e-32
Match length
                   113
% identity
                   60
NCBI Description
                  (Y14996) prolidase [Suberites domuncula]
                  293157
Seq. No.
Seq. ID
                  LIB3062-025-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                   g82696
BLAST score
                   159
                   4.0e-11
È value
Match length
                   40
% identity
                   80
                  glycine-rich protein - maize >gi 22293 emb CAA43431
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
Seq. No.
                   293158
                  LIB3062-026-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885884
```



Match length 85 % identity 60

NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No.

Seq. ID LIB3062-026-Q1-K1-C3

293159

Method BLASTX
NCBI GI g2497748
BLAST score 156
E value 1.0e-10
Match length 52
% identity 58

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 4 PRECURSOR (LTP 4)

>gi 902058 (U29176) lipid transfer protein precursor [Oryza

satīva]

Seq. No. 293160

Seq. ID LIB3062-026-Q1-K1-C9

Method BLASTX
NCBI GI g3540193
BLAST score 145
E value 1.0e-09
Match length 41
% identity 68

NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No. 293161

Seq. ID LIB3062-026-Q1-K1-D5

Method BLASTX
NCBI GI g2058273
BLAST score 208
E value 9.0e-17
Match length 58
% identity 72

NCBI Description (D83527) YK426 [Oryza sativa]

Seq. No. 293162

Seq. ID LIB3062-026-Q1-K1-D6

Method BLASTX
NCBI GI g122771
BLAST score 287
E value 2.0e-27
Match length 102
% identity 68

NCBI Description TRANSCRIPTION FACTOR HBP-1A (HISTONE-SPECIFIC TRANSCRIPTION

FACTOR HBP1) >gi_100808_pir__S15346 transcription factor HBP-1a - wheat >gi_100838_pir__A41349 histone-specific transcription factor HBP1 - wheat >gi_21633_emb_CAA40101_(X56781) HBP-1a [Triticum aestivum] >gi_170749 (M28704)

DNA-binding protein [Triticum aestivum]

>gi 1199790 dbj BAA07289 (D38111) transcription factor

HBP-la(17) [Triticum aestivum]

Seq. No. 293163

Seq. ID LIB3062-026-Q1-K1-F1

Method BLASTX NCBI GI 94538926



```
BLAST score
                  9.0e-18
E value
                  59
Match length
                   68
% identity
                  (AL049483) putative phosphatidylserine decarboxylase
NCBI Description
                   [Arabidopsis thaliana]
                  293164
Seq. No.
                  LIB3062-027-Q1-K1-B6
Seq. ID
                  BLASTX
Method
                  g1272685
NCBI GI
                  294
BLAST score
                   1.0e-26
E value
                   80
Match length
% identity
NCBI Description (Z24449) acetyl CoA carboxylase [Zea mays]
                   293165
Seq. No.
                   LIB3062-027-Q1-K1-C1
Seq. ID
                   BLASTX
Method
                   q2497748
NCBI GI
                   160
BLAST score
                   8.0e-11
E value
                   75
Match length
                   44
% identity
                   NONSPECIFIC LIPID-TRANSFER PROTEIN 4 PRECURSOR (LTP 4)
NCBI Description
                   >gi_902058 (U29176) lipid transfer protein precursor [Oryza
                   satīva]
                   293166
Seq. No.
                   LIB3062-027-Q1-K1-C11
Seq. ID
                   BLASTX
Method
                   q135398
NCBI GI
                   546
BLAST score
                   4.0e-56
E value
                   108
Match length
                   93
 % identity
                   TUBULIN ALPHA-1 CHAIN >gi_82731_pir__S15773 tubulin alpha-1
NCBI Description
                   chain - maize >gi_22147_emb_CAA33734_ (X15704)
                   alphal-tubulin [Zea mays]
                   293167
 Seq. No.
 Seq. ID
                   LIB3062-027-Q1-K1-C6
 Method
                   BLASTN
 NCBI GI
                   a5091496
                   38
 BLAST score
                   4.0e-12
 E value
                   110
 Match length
 % identity
                   Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
 NCBI Description
                   complete sequence
                   293168
 Seq. No.
                   LIB3062-027-Q1-K1-D12
 Seq. ID
 Method
                   BLASTX
                    g3150403
 NCBI GI
```

270

BLAST score

Method

NCBI GI



```
9.0e-24
E value
Match length
                    91
% identity
                   (AC004165) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    293169
Seq. No.
                   LIB3062-027-Q1-K1-D2
Seq. ID
Method
                    BLASTX
                    g2245098
NCBI GI
BLAST score
                    237
E value
                    2.0e-29
                    127
Match length
                    59
% identity
NCBI Description (Z97343) ribosomal protein [Arabidopsis thaliana]
                    293170
Seq. No.
                    LIB3062-027-Q1-K1-D4
Seq. ID
Method
                    BLASTN
NCBI GI
                    g22312
BLAST score
                    63
                    5.0e-27
E value
Match length
                    279
                    87
% identity
NCBI Description Maize ABA-inducible gene for glycine-rich protein ( ABA =
                    abscisic acid)
Seq. No.
                    293171
Seq. ID
                    LIB3062-027-Q1-K1-D6
                    BLASTX
Method
                    g112994
NCBI GI
                    161
BLAST score
                    1.0e-11
 E value
Match length
                    65
                    60
 % identity
                    GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
 NCBI Description
                    >gi_82685_pir__S04536 embryonic abundant protein,
                    glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                    ABA-inducible gene protein [Zea mays]
                    >gi_226091_prf__1410284A abscisic acid inducible gene [Zea
                    mays]
                    293172
 Seq. No.
                    LIB3062-027-Q1-K1-E12
 Seq. ID
                    BLASTX
 Method
                    g122007
 NCBI GI
                    241
 BLAST score
                    2.0e-20
 E value
                    83
 Match length
                     69
 % identity
                    HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley
>gi_20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1
 NCBI Description
                     - 149) [Petroselinum crispum]
                     293173
 Seq. No.
                    LIB3062-027-Q1-K1-E5
 Seq. ID
                    BLASTX
```

40890

g3915826



```
176
BLAST score
                   5.0e-15
E value
                   97
Match length
                   51
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L5
                   293174
Seq. No.
                   LIB3062-027-Q1-K1-E6
Seq. ID
                   BLASTN
Method
                   g296593
NCBI GI
BLAST score
                   56
                   1.0e-22
E value
                   76
Match length
                   93
% identity
NCBI Description H. vulgare pZE40 gene
Seq. No.
                   293175
                   LIB3062-027-Q1-K1-G12
Seq. ID
                   BLASTX
Method
                    q4336747
NCBI GI
                   256
BLAST score
E value
                    4.0e-22
                    142
Match length
% identity
                    49
NCBI Description (AF104924) unconventional myosin heavy chain [Zea mays]
                    293176
Seq. No.
Seq. ID
                    LIB3062-027-Q1-K1-G5
                    BLASTX
Method
NCBI GI
                    g2264373
                    149
BLAST score
                    1.0e-09
E value
Match length
                    40
                    68
% identity
                    (AC002354) putative NAM/no apical meristem protein
NCBI Description
                    [Arabidopsis thaliana]
                    293177
 Seq. No.
                    LIB3062-027-Q1-K1-H2
 Seq. ID
                    BLASTX
Method
                    g1171866
 NCBI GI
                    154
 BLAST score
                    2.0e-10
 E value
                    49
 Match length
                    55
 % identity
                    NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR
 NCBI Description
                    (COMPLEX I-20KD) (CI-20KD) >gi_629601_pir__S48826 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild
                    cabbage >gi_562282_emb_CAA57725_ (X82274) PSST subunit of
                    NADH: ubiquinone oxidoreductase [Brassica oleracea]
                    293178
 Seq. No.
                    LIB3062-028-Q1-K1-A11
 Seq. ID
```

MethodBLASTXNCBI GIg2773154BLAST score266E value2.0e-23

```
Match length
                  104
                   56
% identity
NCBI Description
                   (AF039573) abscisic acid- and stress-inducible protein
                   [Oryza sativa]
Seq. No.
                  293179
Seq. ID
                  LIB3062-028-Q1-K1-C6
Method
                  BLASTN
NCBI GI
                  q498772
BLAST score
                  35
E value
                  3.0e-10
Match length
                  43
                  95
% identity
NCBI Description
                  Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein
Seq. No.
                  293180
Seq. ID
                  LIB3062-028-Q1-K1-E9
Method
                  BLASTN
NCBI GI
                   g2773153
BLAST score
                  58
                   5.0e-24
E value
                  70
Match length
                   96
% identity
                  Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                   (Asr1) mRNA, complete cds
Seq. No.
                  293181
                  LIB3062-028-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2983565
```

BLAST score 164 3.0e-11 E value Match length 122

% identity 32

NCBI Description (AE000722) putative protein [Aquifex aeolicus]

293182 Seq. No. Seq. ID LIB3062-028-Q1-K1-F5 Method BLASTN g3135984 NCBI GI

BLAST score 56 9.0e-23 E value 92 Match length 90 % identity

Homo sapiens DNA sequence from PAC 6802 on chromosome 22. NCBI Description Contains apolipoprotein L, myosin heavy chain, ESTs, CA repeat, STS and GSS, complete sequence [Homo sapiens]

Seq. No. 293183

Seq. ID LIB3062-028-Q1-K1-G6

Method BLASTX NCBI GI g4581109 BLAST score 306 E value 6.0e-28Match length 125 % identity 41

(AC005825) unknown protein [Arabidopsis thaliana] NCBI Description

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293184
Seq. No.
                  LIB3062-029-Q1-K1-E2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4586025
BLAST score
                  210
                  2.0e-17
E value
                  70
Match length
% identity
                  (AC007109) putative succinyl-CoA-ligase beta subunit; 5'
NCBI Description
                  partial [Arabidopsis thaliana]
                   293185
Seq. No.
                  LIB3062-029-Q1-K1-F10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1168537
BLAST score
                   183
                   1.0e-13
E value
                   57
Match length
                   65
% identity
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732
                   aspartic proteinase (EC 3.4.23.-) - rice
                   >gi 218143_dbj_BAA02242_ (D12777) aspartic proteinase
                   [Oryza sativa]
                   293186
Seq. No.
                   LIB3062-029-Q1-K1-F12
Seq. ID
                   BLASTX
Method
                   q2828280
NCBI GI
BLAST score
                   161
                   5.0e-11
E value
                   52
Match length
% identity
                   (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi 2832633 emb CAA16762_ (AL021711) putative protein
                   [Arabidopsis thaliana]
                   293187
Seq. No.
                   LIB3062-029-Q1-K1-F9
Seq. ID
                   BLASTN
Method
                   q22464
NCBI GI
BLAST score
                   58
                   3.0e-24
E value
                   154
Match length
                   84
 % identity
                   Maize rbcS gene for ribulose-1,5-bisphosphate
NCBI Description
                   carboxylase/oxygenase small subunit (EC 4.1.1.39)
                   293188
 Seq. No.
                   LIB3062-029-Q1-K1-G11
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g2499819
                   465
 BLAST score
                   1.0e-46
 E value
                   124
 Match length
                   70
 % identity
```

NCBI Description ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR



>gi_2130068_pir___S66516 aspartic proteinase 1 precursor rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease
[Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic
protease [Oryza sativa]

```
293189
Seq. No.
                  LIB3062-030-Q1-K1-A11
Seq. ID
                  BLASTX
Method
                  g2773154
NCBI GI
                  262
BLAST score
                  7.0e-23
E value
                  111
Match length
% identity
                  (AF039573) abscisic acid- and stress-inducible protein
NCBI Description
                  [Oryza sativa]
Seq. No.
                  293190
                  LIB3062-030-Q1-K1-A2
Seq. ID
                  BLASTX
Method
                  q4559330
NCBI GI
                  181
BLAST score
                  2.0e-13
E value
                  84
Match length
% identity
NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]
Seq. No.
                  293191
                  LIB3062-030-Q1-K1-C9
Seq. ID
                  BLASTX
Method
                  q1362086
NCBI GI
                   188
BLAST score
                   1.0e-14
E value
                   48
Match length
                   79
% identity
                   5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi_2129919_pir__$65957
                   5-methyltetrahydropteroyltriglutamate--homocysteine
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                   [Catharanthus roseus]
```

 Seq. No.
 293192

 Seq. ID
 LIB3062-030-Q1-K1-D10

 Method
 BLASTX

 NCBI GI
 g585452

 BLAST score
 189

BLAST score 189 E value 7.0e-15 Match length 66 % identity 62

NCBI Description

MALATE OXIDOREDUCTASE (NAD), MITOCHONDRIAL 59 KD ISOFORM PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME) (NAD-ME) >gi_1076666_pir__A53318 malate dehydrogenase (decarboxylating) (EC 1.1.1.39) 59K chain precursor, mitochondrial - potato >gi_438131_emb_CAA80547_ (Z23002) precursor of the 59kDa subunit of the mitochondrial NAD+-dependent malic enzyme [Solanum tuberosum]



```
293193
Seq. No.
                  LIB3062-030-Q1-K1-D6
Seq. ID
Method
                  BLASTN
                  g902057
NCBI GI
BLAST score
                  42
                  2.0e-14
E value
Match length
                  54
                  94
% identity
                  Oryza sativa lipid transfer protein precursor, mRNA,
NCBI Description
                  partial cds
                  293194
Seq. No.
Seq. ID
                  LIB3062-030-Q1-K1-E6
Method
                  BLASTN
NCBI GI
                   q4140643
BLAST score
                   36
                   1.0e-10
E value
                   56
Match length
                   91
% identity
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
                   complete sequence
                   293195
Seq. No.
                   LIB3062-030-Q1-K1-F8
Seq. ID
Method
                   BLASTX
                   g520582
NCBI GI
BLAST score
                   177
                   4.0e-13
E value
Match length
                   85
% identity
                   48
                  (D37796) Ids3 [Hordeum vulgare]
NCBI Description
                   293196
Seq. No.
                   LIB3062-030-Q1-K1-H11
Seq. ID
                   BLASTN
Method
                   g396251
NCBI GI
                   34
BLAST score
                   1.0e-09
E value
                   74
Match length
                   86
% identity
                   P.carnea mRNA for 40S ribosomal protein S14
NCBI Description
                   293197
Seq. No.
                   LIB3062-031-Q1-K1-A5
Seq. ID
                   BLASTX
Method
                   g3163946
NCBI GI
                   233
BLAST score
                   2.0e-19
E value
                   72
Match length
                   62
% identity
                   (AJ005599) alpha-tubulin 1 [Eleusine indica]
NCBI Description
                   293198
Seq. No.
                   LIB3062-031-Q1-K1-B3
Seq. ID
```

BLASTX

g1084457

Method

NCBI GI

% identity



```
195
BLAST score
                  4.0e-15
E value
Match length
                  105
                  41
% identity
                  elongation factor 1-beta - Rice >gi_432368_dbj_BAA04903_
NCBI Description
                  (D23674) elongation factor 1 beta [Oryza sativa]
                  293199
Seq. No.
                  LIB3062-031-Q1-K1-C10
Seq. ID
Method
                  BLASTX
                  g2326947
NCBI GI
BLAST score
                  263
                   4.0e-23
E value
                   110
Match length
% identity
                   (Z50801) Chlorophyll a/b-binding protein CP29 precursor
NCBI Description
                   [Zea mays]
                   293200
Seq. No.
                   LIB3062-031-Q1-K1-C2
Seq. ID
Method
                   BLASTX
                   q551288
NCBI GI
BLAST score
                   228
                   2.0e-19
E value
Match length
                   89
                   62
% identity
                  (Z33611) phosphoglycerate mutase [Zea mays]
NCBI Description
Seq. No.
                   293201
                   LIB3062-031-Q1-K1-C4
Seq. ID
                   BLASTX
Method
                   q1841870
NCBI GI
                   137
BLAST score
                   1.0e-08
E value
                   51
Match length
                   63
% identity
                   (U87222) elongation factor 1-beta [Pimpinella brachycarpa]
NCBI Description
                   293202
Seq. No.
                   LIB3062-031-Q1-K1-C6
Seq. ID
                   BLASTN
Method
                   g168587
NCBI GI
BLAST score
                   36
                   4.0e-11
E value
Match length
                   60
                   90
% identity
                   Zea mays cofactor-independent phosphoglycerate mutase mRNA,
NCBI Description
                   complete cds
                   293203
Seq. No.
                   LIB3062-031-Q1-K1-C8
Seq. ID
Method
                   BLASTX
                   q3894214
NCBI GI
                   289
BLAST score
                   6.0e-26
E value
                   79
Match length
                   76
```



```
(D83726) elongation factor 1 beta 2 [Oryza sativa]
NCBI Description
                   >qi 3894216 dbj BAA34599_ (D83727) elongation factor 1 beta
                   2 [Oryza sativa]
                   293204
Seq. No.
                   LIB3062-031-Q1-K1-D4
Seq. ID
                   BLASTX
Method
                   q1835731
NCBI GI
                   152
BLAST score
                   8.0e-14
E value
                   92
Match length
% identity
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                   293205
Seq. No.
Seq. ID
                   LIB3062-031-Q1-K1-D9
Method
                   BLASTX
NCBI GI
                   q2773154
                   179
BLAST score
                    3.0e-13
E value
                    68
Match length
                    51
% identity
                    (AF039573) abscisic acid- and stress-inducible protein
NCBI Description
                    [Oryza sativa]
                    293206
Seq. No.
                    LIB3062-031-Q1-K1-E12
Seq. ID
                    BLASTX
Method
                    q2773154
NCBI GI
BLAST score
                    142
                    3.0e-09
E value
                    55
Match length
% identity
                    (AF039573) abscisic acid- and stress-inducible protein
NCBI Description
                    [Oryza sativa]
                    293207
Seq. No.
                    LIB3062-031-Q1-K1-E5
Seq. ID
Method
                    BLASTX
                    g4056469
NCBI GI
BLAST score
                    343
                    3.0e-32
E value
Match length
                    124
 % identity
                    (AC005990) Strong similarity to gb_M95166 ADP-ribosylation
NCBI Description
                    factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967,
                    gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and
                    gb_{225043} come from t
```

 Seq. No.
 293208

 Seq. ID
 LIB3062-031-Q1-K1-F4

 Method
 BLASTX

 MEDD: GI
 2463363

NCBI GI g463363 BLAST score 199 E value 1.0e-15 Match length 65

```
% identity
                 (U03701) ubiquitin [Stephanodiscus yellowstonensis]
NCBI Description
Seq. No.
                  293209
                  LIB3062-031-Q1-K1-F8
Seq. ID
                  BLASTX
Method
                  q3126967
NCBI GI
                  466
BLAST score
                  1.0e-46
E value
                  134
Match length
                  17
% identity
NCBI Description (AF061807) polyubiquitin [Elaeagnus umbellata]
                  293210
Seq. No.
                  LIB3062-031-Q1-K1-G10
Seq. ID
Method
                  BLASTX
                  g2384760
NCBI GI
                  179
BLAST score
                  2.0e-13
E value
                  92
Match length
                  45
% identity
                  (AF016897) GDP dissociation inhibitor protein OsGDI2 [Oryza
NCBI Description
                  sativa]
                  293211
Seq. No.
                  LIB3062-031-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4567304
BLAST score
                   206
                   3.0e-16
E value
                   127
Match length
% identity
                   42
NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]
                   293212
Seq. No.
                   LIB3062-031-Q1-K1-G9
Seq. ID
                   BLASTX
Method
                   g1052960
NCBI GI
                   194
BLAST score
                   1.0e-16
E value
                   100
Match length
% identity
                   54
NCBI Description (U37437) PNIL34 [Ipomoea nil]
                   293213
Seq. No.
                   LIB3062-032-Q1-K1-A6
Seq. ID
                   BLASTX
Method
                   g2275202
NCBI GI
                   147
BLAST score
                   7.0e-10
E value
Match length
                   72
                   42
 % identity
                   (AC002337) acyl-CoA synthetase isolog [Arabidopsis
 NCBI Description
                   thaliana]
```

293214

LIB3062-032-Q1-K1-B4

Seq. No.

Seq. ID

BLAST score

E value

194 5.0e-19



```
BLASTX
Method
                  g3953471
NCBI GI
                   270
BLAST score
                  8.0e-24
E value
Match length
                  82
                   68
% identity
                   (AC002328) F2202.16 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   293215
                   LIB3062-032-Q1-K1-C6
Seq. ID
                   BLASTX
Method
                   g3860273
NCBI GI
                   291
BLAST score
                   3.0e-26
E value
                   120
Match length
% identity
                   50
                   (AC005824) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4314398_gb_AAD15608_ (AC006232) hypothetical protein
                   [Arabidopsis thaliana]
                   293216
Seq. No.
                   LIB3062-032-Q1-K1-E11
Seq. ID
Method
                   BLASTX
                   g1244716
NCBI GI
BLAST score
                   174
                   4.0e-25
E value
Match length
                   139
                   55
% identity
                   (U42336) ACC synthase [Triticum aestivum]
NCBI Description
                   293217
Seq. No.
                   LIB3062-032-Q1-K1-E2
Seq. ID
                   BLASTX
Method
                   g1808684
NCBI GI
                   148
BLAST score
                   7.0e-10
E value
Match length
                   44
                   68
% identity
                   (Y10782) hypothetical protein [Sporobolus stapfianus]
NCBI Description
                   293218
Seq. No.
                   LIB3062-032-Q1-K1-E4
Seq. ID
                   BLASTX
Method
                   q2924781
NCBI GI
                   196
BLAST score
                   2.0e-15
E value
                   76
Match length
                   55
% identity
                   (AC002334) putative cellulose synthase [Arabidopsis
NCBI Description
                   thaliana]
                   293219
Seq. No.
                   LIB3062-032-Q1-K1-F4
Seq. ID
                   BLASTX
Method
                   g2826786
NCBI GI
```



```
84
Match length
                  62
% identity
                  (Y10905) RAPB protein [Oryza sativa]
NCBI Description
                  293220
Seq. No.
                  LIB3062-032-Q1-K1-F7
Seq. ID
                  BLASTX
Method
                  q1351136
NCBI GI
                  165
BLAST score
                  3.0e-19
E value
                  79
Match length
                  70
% identity
                  SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
NCBI Description
                  >gi_514946 (L22296) UDP-glucose:D-fructose
                  2-glucosyl-transferase [Zea mays] >gi_533252 (L33244)
                  sucrose synthase 2 [Zea mays]
                  293221
Seq. No.
                  LIB3062-032-Q1-K1-G5
Seq. ID
                  BLASTN
Method
NCBI GI
                  g397395
                  134
BLAST score
                  3.0e-69
E value
                  218
Match length
                   90
% identity
                  Z.mays MNB1b mRNA for DNA-binding protein
NCBI Description
Seq. No.
                  293222
                  LIB3062-032-Q1-K1-H1
Seq. ID
                  BLASTX
Method
                   g113965
NCBI GI
                   208
BLAST score
                   2.0e-16
E value
                   129
Match length
                   23
% identity
                  ANNEXIN VII (SYNEXIN) >gi_71775_pir__LUDO7 annexin VII -
NCBI Description
                   slime mold (Dictyostelium discoideum)
                   >gi_829171_emb_CAA42815_ (X60269) annexin 7 [Dictyostelium
                   discoideum]
                   293223
Seq. No.
Seq. ID
                   LIB3062-033-Q1-K1-A2
Method
                   BLASTX
                   g3582335
NCBI GI
BLAST score
                   516
E value
                   1.0e-52
                   148
Match length
                   66
% identity
                  (AC005496) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   293224
                   LIB3062-033-Q1-K1-C5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3928084
BLAST score
                   159
```

1.0e-10

129

E value Match length



```
% identity
                  (AC005770) retrotransposon-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  293225
                  LIB3062-033-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548851
BLAST score
                  185
                  6.0e-14
E value
Match length
                  85
                  47
% identity
                  40S RIBOSOMAL PROTEIN S20 >gi_481226_pir__S38356 ribosomal
NCBI Description
                  protein S20 - rice >gi_391875_dbj_BAA02157_ (D12632) 40S
                  subunit ribosomal protein [Oryza sativa]
Seq. No.
                  293226
Seq. ID
                  LIB3062-033-Q1-K1-E6
                  BLASTX
Method
                  q542157
NCBI GI
BLAST score
                  406
E value
                  1.0e-39
                  92
Match length
                  85
% identity
NCBI Description ribosomal 5S RNA-binding protein - Rice
Seq. No.
                   293227
                  LIB3062-033-Q1-K1-F8
Seq. ID
Method
                  BLASTX
                   g3892709
NCBI GI
BLAST score
                   188
E value
                   1.0e-29
                   119
Match length
                   60
% identity
                  (AL033545) putative protein [Arabidopsis thaliana]
NCBI Description
                   293228
Seq. No.
                   LIB3062-033-Q1-K1-G4
Seq. ID
                   BLASTX
Method
                   g3461820
NCBI GI
                   229
BLAST score
                   5.0e-19
E value
                   73
Match length
                   55
% identity
                  (AC004138) unknown protein [Arabidopsis thaliana]
NCBI Description
                   293229
Seq. No.
                   LIB3062-034-Q1-K1-A12
Seq. ID
                   BLASTN
Method
                   g342663
NCBI GI
BLAST score
                   48
E value
                   3.0e-18
                   140
Match length
% identity
NCBI Description Maize mitochondrial 18S ribosomal RNA gene
```

Seq. No. 293230

Match length

% identity

94 39



```
LIB3062-034-Q1-K1-A8
Seq. ID
                  BLASTX
Method
                  q1174745
NCBI GI
                  313
BLAST score
                  6.0e-29
E value
                  79
Match length
                  78
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)
NCBI Description
                  >gi_1363523_pir__S53761 triose-phosphate isomerase (EC
                  5.3.1.1) precursor, chloroplast - rye
                  >gi_609262_emb_CAA83533_ (Z32521) triosephosphate isomerase
                   [Secale cereale] >gi_1095494_prf__2109226B triosephosphate
                   isomerase [Secale cereale]
                  293231
Seq. No.
                  LIB3062-034-Q1-K1-B4
Seq. ID
                  BLASTX
Method
                   q2914700
NCBI GI
                   230
BLAST score
                   2.0e-19
E value
                   80
Match length
                   60
% identity
                  (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
NCBI Description
                   thaliana]
                   293232
Seq. No.
                   LIB3062-034-Q1-K1-D11
Seq. ID
                   BLASTX
Method
                   g122070
NCBI GI
                   291
BLAST score
                   2.0e-26
E value
                   77
Match length
                   82
% identity
                   HISTONE H3 >gi_82483_pir__A25564 histone H3 - rice
NCBI Description
                   >gi 169793 (M1\overline{5}664) \overline{\text{histone}} 3 [Oryza sativa] >gi_940018
                   (U25664) histone H3 [Oryza sativa]
Seq. No.
                   293233
                   LIB3062-034-Q1-K1-D2
Seq. ID
                   BLASTX
Method
                   g3023522
NCBI GI
                   212
BLAST score
                   1.0e-32
E value
Match length
                   121
% identity
                   COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)
NCBI Description
                   (P102) >gi_2454309 (AF002705) beta prime COP [Rattus
                   norvegicus]
                   293234
Seq. No.
Seq. ID
                   LIB3062-034-Q1-K1-E10
                   BLASTX
Method
                   q1168730
NCBI GI
                   184
BLAST score
                   7.0e-14
E value
```



NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE EL13-2 (CAD) >gi 282866 pir S28043 ELI3-1 protein - Arabidopsis thaliana >gi 16269 emb CAA48026 (X67815) Eli3-2 [Arabidopsis thaliana] >gi_4467105_emb_CAB37539_ (AL035538) cinnamyl-alcohol dehydrogenase ELI3-2 [Arabidopsis thaliana] 293235 Seq. No. Seq. ID LIB3062-034-Q1-K1-E6 Method BLASTX NCBI GI g2832777 276 BLAST score E value 2.0e-24 Match length 130 % identity 43 NCBI Description (AL021086) 1-evidence=predicted by match; 1-match accession=SWISS-PROT:P53624; 1-match description=MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1 (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE).; 1-match species=DROSOPHILA Seq. No. 293236 LIB3062-034-Q1-K1-H9 Seq. ID Method BLASTX NCBI GI g3763927 BLAST score 158 7.0e-11 E value Match length 94 % identity 41 NCBI Description (AC004450) putative carboxyphosphoenolpyruvate mutase [Arabidopsis thaliana] 293237 Seq. No. Seq. ID LIB3062-035-Q1-K1-A12 Method BLASTX NCBI GI g1890575 BLAST score 161 E value 3.0e-11 Match length 65 57 % identity (X93174) xyloglucan endotransglycosylase (XET) [Hordeum NCBI Description vulgare] 293238 Seq. No.

LIB3062-035-Q1-K1-C10 Seq. ID

Method BLASTX NCBI GI q479442 BLAST score 154 E value 4.0e-10 Match length 34 % identity 91

GTP-binding protein - tomato >gi 313029 emb CAA49600 NCBI Description

(X69980) GTP-binding protein [Lycopersicon esculentum]

293239 Seq. No.

LIB3062-035-Q1-K1-C4 Seq. ID

Method BLASTX



```
NCBI GI
                  g1101011
BLAST score
                  209
                  6.0e-17
E value
                  89
Match length
% identity
NCBI Description
                  (U27577) polyubiquitin [Trichomonas vaginalis]
Seq. No.
                  293240
Seq. ID
                  LIB3062-035-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g2499488
BLAST score
                  173
                  1.0e-12
E value
Match length
                  107
% identity
                  36
NCBI Description
                  PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
                  ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                  (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                  (PPI-PFK) >gi 483547 emb CAA83682 (Z32849)
                  pyrophosphate-dependent phosphofructokinase alpha subunit
                  [Ricinus communis]
                  293241
Seq. No.
Seq. ID
                  LIB3062-035-Q1-K1-G4
Method
                  BLASTN
NCBI GI
                  q2196671
BLAST score
                  42
                  1.0e-14
E value
Match length
                  150
                  82
% identity
NCBI Description Z.mays mRNA for HMG protein
Seq. No.
                  293242
                  LIB3062-035-Q1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3236247
BLAST score
                  160
E value
                  8.0e-11
                  123
Match length
                  38
% identity
NCBI Description (AC004684) SCARECROW-like protein [Arabidopsis thaliana]
                  293243
Seq. No.
                  LIB3062-035-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2737973
BLAST score
                  672
E value
                  8.0e-71
Match length
                  129
% identity
                  99
NCBI Description (U83625) protein kinase ZmMEK1 [Zea mays]
```

Seq. No. 293244

LIB3062-035-Q1-K1-H1 Seq. ID

Method BLASTX g3914685 NCBI GI BLAST score 189

Match length

124



```
2.0e-14
E value
Match length
                  78
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L17 >gi_2668748 (AF034948) ribosomal
                  protein L17 [Zea mays]
                  293245
Seq. No.
Seq. ID
                  LIB3062-035-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  g461465
BLAST score
                  602
                  1.0e-62
E value
                  114
Match length
                  97
% identity
NCBI Description ACTIN >gi_322751_pir__S31933 actin - common tobacco
                  >gi 22609 emb CAA45149 (X63603) actin [Nicotiana tabacum]
Seq. No.
                  293246
                  LIB3062-035-Q1-K1-H4
Seq. ID
                  BLASTX
Method
                  q66009
NCBI GI
BLAST score
                  268
                  8.0e-24
E value
                   66
Match length
% identity
                  glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C,
NCBI Description
                  cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH
                   (AA 1-337) [Zea mays]
Seq. No.
                   293247
                  LIB3062-036-Q1-K1-A12
Seq. ID
Method
                  BLASTX
                   g1890575
NCBI GI
BLAST score
                   213
                   5.0e-32
E value
                   120
Match length
% identity
                   63
                   (X93174) xyloglucan endotransglycosylase (XET) [Hordeum
NCBI Description
                   vulgare]
                   293248
Seq. No.
                   LIB3062-036-Q1-K1-A9
Seq. ID
                   BLASTN
Method
                   g19054
NCBI GI
                   49
BLAST score
                   8.0e-19
E value
Match length
                   61
                   95
% identity
NCBI Description H.vulgare myb2 mRNA
                   293249
Seq. No.
                   LIB3062-036-Q1-K1-C6
Seq. ID
Method
                   BLASTX
                   q2224915
NCBI GI
                   231
BLAST score
E value
                   3.0e-19
```

```
% identity
NCBI Description (U95968) beta-expansin [Oryza sativa]
                  293250
Seq. No.
                  LIB3062-036-Q1-K1-F10
Seq. ID
                  BLASTX
Method
                  g2995384
NCBI GI
                  222
BLAST score
                  3.0e-18
E value
                  72
Match length
% identity
NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]
                  293251
Seq. No.
Seq. ID
                  LIB3062-036-Q1-K1-H10
Method
                  BLASTN
                  q3821780
NCBI GI
BLAST score
                  37
                  2.0e-11
E value
                  37
Match length
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  293252
Seq. No.
                  LIB3062-037-Q1-K1-A12
Seq. ID
Method
                  BLASTX
                  g4580461
NCBI GI
BLAST score
                  173
E value
                  2.0e-12
                  103
Match length
% identity
NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]
                  293253
Seq. No.
                  LIB3062-037-Q1-K1-A9
Seq. ID
                  BLASTX
Method
                   g113449
NCBI GI
                   153
BLAST score
                   5.0e-10
E value
                   130
Match length
% identity
                   28
                  PROBABLE ATP-DEPENDENT PERMEASE PRECURSOR
NCBI Description
                   >gi_83202_pir__S19421 ATP-dependent permease ADP1 precursor

    yeast (Saccharomyces cerevisiae)

                   >gi_1907154_emb_CAA42328_ (X59720) YCR011c, len:1049
```

[Saccharomyces cerevisiae]

293254 Seq. No.

LIB3062-037-Q1-K1-B3 Seq. ID

Method BLASTN g4185305 NCBI GI BLAST score 76 1.0e-34 E value

Match length 140 89 % identity

Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 NCBI Description

(sz22-21) gene, complete cds; retrotransposon Opie-2 gag

Seq. ID

```
protein, polyprotein, and copia protein genes, complete cds; and unknown genes
```

```
293255
   Seq. No.
   Seq. ID
                     LIB3062-037-Q1-K1-E5
   Method
                     BLASTX
                     q3163946
   NCBI GI
                     498
   BLAST score
E value
                     2.0e-50
                     97
   Match length
   % identity
   NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]
                     293256
   Seq. No.
                     LIB3062-037-Q1-K1-F4
   Seq. ID
   Method
                     BLASTX
                     q3367591
   NCBI GI
   BLAST score
                     337
                     1.0e-31
   E value
                     108
   Match length
   % identity
   NCBI Description (AL031135) putative protein [Arabidopsis thaliana]
                     293257
   Seq. No.
                     LIB3062-037-Q1-K1-G3
   Seq. ID
                     BLASTX
   Method
   NCBI GI
                      q2673912
   BLAST score
                      164
                      8.0e-16
   E value
   Match length
                      90
   % identity
   NCBI Description (AC002561) unknown protein [Arabidopsis thaliana]
                      293258
   Seq. No.
   Seq. ID
                      LIB3062-037-Q1-K1-H6
   Method
                      BLASTX
   NCBI GI
                      g3927825
   BLAST score
                      261
                      4.0e-23
   E value
   Match length
                      71
   % identity
                      73
                      (AC005727) putative dTDP-glucose 4-6-dehydratase
   NCBI Description
                      [Arabidopsis thaliana]
                      293259
   Seq. No.
                      LIB3062-038-Q1-K1-D7
   Seq. ID
                      BLASTX
   Method
                      g3924596
   NCBI GI
                      259
   BLAST score
                      9.0e-23
   E value
                      87
   Match length
    % identity
                      68
                      (AF069442) putative phospho-ser/thr phosphatase
   NCBI Description
                      [Arabidopsis thaliana]
                      293260
    Seq. No.
```

40907

LIB3062-038-Q1-K1-F1

Seq. ID

Method

NCBI GI



```
BLASTX
Method
                  g3193330
NCBI GI
BLAST score
                  148
                  2.0e-09
                                                                    - 5
E value
                  58
Match length
% identity
                  50
                  (AF069299) contains similarity to Medicago sativa corC
NCBI Description
                  (GB:L22305) [Arabidopsis thaliana]
                  293261
Seq. No.
                  LIB3062-038-Q1-K1-H2
Seq. ID
                  BLASTN
Method
                  g168608
NCBI GI
                  60
BLAST score
                  3.0e-25
E value
                  60
Match length
% identity
                  100
NCBI Description Maize 17S ribosomal RNA gene and flanks
                   293262
Seq. No.
Seq. ID
                  LIB3062-039-Q1-K1-A4
                  BLASTX
Method
                   q3377851
NCBI GI
                   287
BLAST score
                   1.0e-25
E value
                   81
Match length
% identity
                   (AF076274) contains similarity to ATPases associated with
NCBI Description
                   various cellular activities (Pfam: AAA.hmm, score: 155.05)
                   [Arabidopsis thaliana]
                   293263
Seq. No.
                   LIB3062-039-Q1-K1-A6
Seq. ID
                   BLASTX
Method
                   g1361985
NCBI GI
BLAST score
                   154
                   4.0e-10
E value
Match length
                   137
                   31
 % identity
                   disease resistance protein RPM1 - Arabidopsis thaliana
NCBI Description
                   >gi 963017_emb_CAA61131_ (X87851) disease resistance gene
                   [Arabidopsis thaliana]
                   293264
 Seq. No.
                   LIB3062-039-Q1-K1-B4
 Seq. ID
                   BLASTX
 Method
                   g3004552
 NCBI GI
                   149
 BLAST score
                   1.0e-09
 E value
                   68
 Match length
                    41
 % identity
                   (AC003673) unknown protein [Arabidopsis thaliana]
 NCBI Description
                   293265
 Seq. No.
```

40908

LIB3062-039-Q1-K1-D9

BLASTX

g2632252

NCBI Description



```
366
BLAST score
                  5.0e-35
E value
Match length
                  72
                  96
% identity
NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor]
                  293266
Seq. No.
                  LIB3062-039-Q1-K1-E8
Seq. ID
                  BLASTX
Method
                  g3056591
NCBI GI
BLAST score
                  167
                  1.0e-11
E value
                   50
Match length
                   64
% identity
NCBI Description (AC004255) T1F9.12 [Arabidopsis thaliana]
Seq. No.
                   293267
                   LIB3062-039-Q1-K1-F2
Seq. ID
                   BLASTX
Method
                   g2982331
NCBI GI
                   253
BLAST score
E value
                   5.0e-22
                   94
Match length
                   60
% identity
                   (AF051251) TAT-binding protein homolog [Picea mariana]
NCBI Description
                   293268
Seq. No.
                   LIB3062-039-Q1-K1-G10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1438881
BLAST score
                   142
                   1.0e-08
E value
Match length
                   44
% identity
                   61
                   (U43839) GmCK2p [Glycine max]
NCBI Description
                   293269
Seq. No.
                   LIB3062-040-Q1-K1-B2
Seq. ID
                   BLASTX
Method
                   g1076746
NCBI GI
BLAST score
                   257
                   1.0e-22
E value
Match length
                   80
                   71
 % identity
                   heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
                   293270
 Seq. No.
                   LIB3062-040-Q1-K1-B6
 Seq. ID
                   BLASTX
 Method
                   g4580394
 NCBI GI
                   158
 BLAST score
                   1.0e-10
 E value
                   98
 Match length
                   39
 % identity
                   (AC007171) putative fatty acid elongase [Arabidopsis
```



thaliana]

```
293271
Seq. No.
                  LIB3062-040-Q1-K1-E5
Seq. ID
                  BLASTX
Method
                  g2655291
NCBI GI
                  268
BLAST score
                  6.0e-28
E value
                  148
Match length
                  54
% identity
NCBI Description (AF032974) germin-like protein 4 [Oryza sativa]
                  293272
Seq. No.
                  LIB3062-040-Q1-K1-G1
Seq. ID
Method
                  BLASTX
                  g2668742
NCBI GI
                  407
BLAST score
                  1.0e-39
E value
                  85
Match length
                  93
% identity
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]
                  293273
Seq. No.
                  LIB3062-040-Q1-K1-G7
Seq. ID
                  BLASTX
Method
                  g4191778
NCBI GI
                   500
BLAST score
                   5.0e-53
E value
                   139
Match length
                   68
% identity
                  (AC005917) putative nucleosome assembly protein I
NCBI Description
                   [Arabidopsis thaliana]
                   293274
Seq. No.
                   LIB3062-040-Q1-K1-H2
Seq. ID
                   BLASTX
Method
                   g2130091
NCBI GI
BLAST score
                   222
                   3.0e-18
E value
                   102
Match length
                   47
% identity
                   aspartate aminotransferase - proso millet
NCBI Description
                   >gi 633095_dbj BAA08106 (D45076) plastidic aspartate
                   aminotransferase [Panicum miliaceum]
Seq. No.
                   293275
                   LIB3062-041-Q1-K1-A3
Seq. ID
Method
                   BLASTX
                   g2708750
NCBI GI
                   155
BLAST score
E value
                   4.0e-16
Match length
                   128
% identity
                   (AC003952) putative physical impedence protein [Arabidopsis
NCBI Description
                   thaliana]
```

40910

293276

Seq. No.



```
LIB3062-041-Q1-K1-A4
Seq. ID
                  BLASTN
Method
                  g2668739
NCBI GI
BLAST score
                  69
                  2.0e-30
E value
                  69
Match length
                  100
% identity
                  Zea mays translation initiation factor GOS2 (TIF) mRNA,
NCBI Description
                  complete cds
                  293277
Seq. No.
                  LIB3062-041-Q1-K1-B6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g22332
BLAST score
                  270
                  1.0e-150
E value
                  432
Match length
                  91
% identity
NCBI Description Z.mays HRGP gene
                  293278
Seq. No.
                  LIB3062-041-Q1-K1-C12
Seq. ID
                  BLASTX
Method
                  g4056432
NCBI GI
BLAST score
                  295
                  9.0e-39
E value
Match length
                  108
% identity
                  71
                  (AC005990) Similar to gi_2245014 glucosyltransferase
NCBI Description
                  homolog from Arabidopsis thaliana chromosome 4 contig
                  gb Z97341. ESTs gb_T20778 and gb_AA586281 come from this
                  gene. [Arabidopsis thaliana]
                  293279
Seq. No.
Seq. ID
                  LIB3062-041-Q1-K1-D6
Method
                  BLASTN
                  g902200
NCBI GI
BLAST score
                  325
                  0.0e+00
E value
Match length
                  430
% identity
                  93
NCBI Description Z.mays complete chloroplast genome
Seq. No.
                  293280
Seq. ID
                  LIB3062-041-Q1-K1-E10
Method
                  BLASTX
                  g4406815
NCBI GI
                   204
BLAST score
```

Method BLASTX
NCBI GI g4406815
BLAST score 204
E value 4.0e-16
Match length 60
% identity 63

NCBI Description (AC006201) putative peptide methionine sulfoxide reductase

[Arabidopsis thaliana]

Seq. No. 293281

Seq. ID LIB3062-041-Q1-K1-E8

Method BLASTX

```
Transmission of the control of the c
```

```
g2245107
 NCBI GI
                   389
 BLAST score
                   1.0e-37
 E value
                   138
 Match length
% identity
                   35
 NCBI Description (Z97343) thioesterase homolog [Arabidopsis thaliana]
                   293282
 Seq. No.
                   LIB3062-041-Q1-K1-F10
 Seq. ID
                   BLASTX
 Method
                   g1197461
 NCBI GI
                   209
 BLAST score
                   1.0e-16
 E value
                   74
 Match length
 % identity
                    57
 NCBI Description (X78819) casein kinase I [Arabidopsis thaliana]
                   293283
 Seq. No.
                   LIB3062-041-Q1-K1-F12
 Seq. ID
                   BLASTX
 Method
                   g3450889
 NCBI GI
                    344
 BLAST score
                    2.0e-32
 E value
                    139
 Match length
 % identity
                    55
                   (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    293284
                    LIB3062-041-Q1-K1-H10
 Seq. ID
                    BLASTX
 Method
                    g2980782
 NCBI GI
                    272
 BLAST score
                    5.0e-24
 E value
                    101
 Match length
                    57
 % identity
                   (AL022198) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                    293285
 Seq. No.
                    LIB3062-041-Q1-K1-H3
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g3036796
                    510
 BLAST score
                    7.0e-52
 E value
                    138
 Match length
                    73
 % identity
                    (AL022373) putative protein [Arabidopsis thaliana]
 NCBI Description
                    >gi_3805858_emb_CAA21478_ (AL031986) putative protein
                    [Arabidopsis thaliana]
                    293286
 Seq. No.
 Seq. ID
                    LIB3062-042-Q1-K1-C7
                    BLASTX
 Method
                    q2252632
 NCBI GI
 BLAST score
                    272
                    3.0e-24
 E value
 Match length
                    96
                    57
 % identity
```

Seq. No.

Seq. ID



```
(U95973) Barley Mlo protein isolog [Arabidopsis thaliana]
NCBI Description
                  293287
Seq. No.
                  LIB3062-042-Q1-K1-E2
Seq. ID
                  BLASTX
Method
                  g2429087
NCBI GI
                   243
BLAST score
                  9.0e-21
E value
                  103
Match length
% identity
                   48
                  (L37358) lipoxygenase 2 [Hordeum vulgare]
NCBI Description
                   293288
Seq. No.
                   LIB3062-042-Q1-K1-G6
Seq. ID
Method
                   BLASTX
                   q1076580
NCBI GI
BLAST score
                   192
                   9.0e-15
E value
                   76
Match length
% identity
                   46
                   alcohol dehydrogenase homolog ADH3b - tomato
NCBI Description
                   >qi 913446 bbs 160508 (S75487) alcohol dehydrogenase ADH
                   \{EC 1.1.1.\overline{1}\}\ [\overline{L}ycopersicon esculentum=tomatoes, cv. red
                   cherry, Peptide, 390 aa] [Lycopersicon esculentum]
Seq. No.
                   293289
                   LIB3062-042-Q1-K1-G8
Seq. ID
Method
                   BLASTX
                   g1944573
NCBI GI
                   301
BLAST score
                   2.0e-27
E value
Match length
                   130
                   57
% identity
                   (249146) phenylalanine ammonia-lyase [Hordeum vulgare]
NCBI Description
                   293290
Seq. No.
                   LIB3062-043-Q1-K1-A1
Seq. ID
                   BLASTN
Method
                   g287834
NCBI GI
BLAST score
                   60
                   5.0e-25
E value
Match length
                   118
                   97
% identity
NCBI Description Z.mays yptm2 cDNA
Seq. No.
                   293291
                   LIB3062-043-Q1-K1-A12
Seq. ID
                   BLASTX
Method
                   q2462822
NCBI GI
                   206
BLAST score
E value
                   3.0e-16
Match length
                   71
                   49
% identity
                   (AF000657) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   293292
```

40913

LIB3062-043-Q1-K1-A5

```
BLASTX
Method
                   g2980798
NCBI GI
                   261
BLAST score
                   4.0e-25
E value
                   94
Match length
                   61
% identity
                  (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
                   293293
Seq. No.
                   LIB3062-043-Q1-K1-B1
Seq. ID
                   BLASTX
Method
```

q4335739 NCBI GI 222 BLAST score 5.0e-18 E value Match length 93 % identity 47

NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No. LIB3062-043-Q1-K1-B10 Seq. ID Method BLASTX NCBI GI q4432866 BLAST score 348 6.0e-33 E value Match length 127

50 % identity

(AC006300) putative reverse transcriptase [Arabidopsis NCBI Description

thaliana]

293294

293295 Seq. No.

LIB3062-043-Q1-K1-B11 Seq. ID

Method BLASTX q3335363 NCBI GI 334 BLAST score 2.0e-31 E value 112 Match length 33 % identity

(AC003028) hypothetical protein [Arabidopsis thaliana] NCBI Description

293296 Seq. No.

LIB3062-043-Q1-K1-C10 Seq. ID

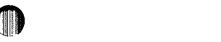
BLASTX Method g2342724 NCBI GI 288 BLAST score 6.0e-26 E value 123 Match length % identity 62

(AC002341) unknown protein [Arabidopsis thaliana] NCBI Description

293297 Seq. No.

LIB3062-043-Q1-K1-C11 Seq. ID

BLASTX Method g3158376 NCBI GI 411 BLAST score 2.0e-40 E value Match length 114 74 % identity



(AF035385) unknown [Arabidopsis thaliana] NCBI Description 293298 Seq. No. LIB3062-043-Q1-K1-C2 Seq. ID BLASTX Method q133361 NCBI GI

522 BLAST score 3.0e-53 E value 139 Match length 71 % identity

DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (RNA NCBI Description

POLYMERASE III SUBUNIT 2) >gi_66988_pir_ RNFF32

DNA-directed RNA polymerase (EC 2.7.7.6) III second-largest

chain - fruit fly (Drosophila melanogaster)

>gi_10963_emb_CAA41631_ (X58826) RNA polymerase III
second-largest subunit [Drosophila melanogaster]

293299 Seq. No.

LIB3062-043-Q1-K1-C9 Seq. ID

BLASTX Method g1401268 NCBI GI 199 BLAST score 2.0e-15 E value 59 Match length 61 % identity

(U59812) ornithine decarboxylase [Nicotiana tabacum] NCBI Description

293300 Seq. No.

LIB3062-043-Q1-K1-D10 Seq. ID

Method BLASTX g3176687 NCBI GI BLAST score 484 7.0e-49E value Match length 125 % identity 73

(AC003671) Strong similarity to trehalose-6-phosphate NCBI Description

synthase homolog from A. thaliana chromosome 4 contig gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and gb R64855 come from this gene. [Arabidopsis thaliana]

293301 Seq. No.

LIB3062-043-Q1-K1-D11 Seq. ID

BLASTX Method g2369766 NCBI GI BLAST score 396 1.0e-38 E value 107 Match length % identity

(AJ001304) hypothetical protein [Citrus x paradisi] NCBI Description

Seq. No. 293302

LIB3062-043-Q1-K1-D12 Seq. ID

Method BLASTX NCBI GI g4510400 BLAST score 244 1.0e-20 E value Match length 60



```
% identity
                  (AC006587) putative vacuolar-type H(+)-ATPase [Arabidopsis
NCBI Description
                  thaliana]
                  293303
Seq. No.
                  LIB3062-043-Q1-K1-D9
Seq. ID
                  BLASTX
Method
                  g1572819
NCBI GI
                  236
BLAST score
                  8.0e-20
E value
                  98
Match length
                   49
% identity
                  (U70855) similar to the RAS gene family [Caenorhabditis
NCBI Description
                  elegans]
Seq. No.
                   293304
                  LIB3062-043-Q1-K1-E9
Seq. ID
Method
                  BLASTX
                   g2231034
NCBI GI
                   298
BLAST score
E value
                   4.0e-27
Match length
                   91
% identity
                   67
                  (Y12785) MAP kinase I [Petroselinum crispum]
NCBI Description
Seq. No.
                   293305
                   LIB3062-043-Q1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2576361
                   349
BLAST score
                   4.0e-33
E value
                   94
Match length
                   67
% identity
                   (U39782) lysine and histidine specific transporter
NCBI Description
                   [Arabidopsis thaliana]
                   293306
Seq. No.
                   LIB3062-043-Q1-K1-F11
Seq. ID
Method
                   BLASTX
                   g1657374
NCBI GI
BLAST score
                   462
                   3.0e-46
E value
                   100
Match length
                   85
% identity
                   (X96853) endo-beta-1,4-glucanase [Prunus persica]
NCBI Description
                   >gi 1657380 emb_CAA65600_ (X96856) endo-beta-1,4-glucanase
                   [Prunus persica]
                   293307
Seq. No.
                   LIB3062-043-Q1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2832623
                   477
BLAST score
```

E value 4.0e-48
Match length 125
% identity 73

NCBI Description (AL021711) protein kinase - like protein [Arabidopsis



thaliana]

```
293308
Seq. No.
Seq. ID
                  LIB3062-043-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  q3319457
BLAST score
                  144
                  5.0e-09
E value
                  79
Match length
                  39
% identity
NCBI Description (AF077542) contains similarity to O-linked GlcNAc
                  transferases [Caenorhabditis elegans]
                  293309
Seq. No.
                  LIB3062-043-Q1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2443878
BLAST score
                  380
                  1.0e-36
E value
                  126
Match length
% identity
                  62
NCBI Description (AC002294) Unknown protein [Arabidopsis thaliana]
                  293310
Seq. No.
                  LIB3062-043-Q1-K1-H9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2258418
                  287
BLAST score
                  8.0e-26
E value
Match length
                  84
% identity
                  (AF007875) dolichol monophosphate mannose synthase [Homo
NCBI Description
                  sapiens]
Seq. No.
                  293311
                  LIB3062-044-Q1-K1-B8
Seq. ID
Method
                  BLASTX
                  g3850581
NCBI GI
BLAST score
                  341
                  5.0e-32
E value
Match length
                  108
% identity
                   61
                  (AC005278) EST qb N96383 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                   293312
Seq. No.
                  LIB3062-044-Q1-K1-D12
Seq. ID
Method
                  BLASTX
                   g2191135
NCBI GI
                   256
BLAST score
                   5.0e-22
E value
Match length
                   105
% identity
                   48
                  (AF007269) A IG002N01.14 gene product [Arabidopsis
NCBI Description
```

Seq. No. 293313

thaliana]

BLAST score

E value

2.0e-26



```
LIB3062-044-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2668742
BLAST score
                  195
E value
                  3.0e-15
Match length
                   63
% identity
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                  293314
Seq. No.
                  LIB3062-044-Q1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462749
BLAST score
                   420
E value
                   2.0e-41
Match length
                   108
% identity
                   75
                   (AC002292) Putative Serine/Threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   293315
Seq. ID
                   LIB3062-044-Q1-K1-F7
Method
                   BLASTX
NCBI GI
                   g2340108
BLAST score
                   367
                   4.0e-35
E value
Match length
                   126
                   57
% identity
NCBI Description (U65948) starch branching enzyme IIa [Zea mays]
Seq. No.
                   293316
                   LIB3062-044-Q1-K1-F9
Seq. ID
Method
                   BLASTX
                   g4099090
NCBI GI
                   310
BLAST score
                   2.0e-28
E value
Match length
                   71
                   80
% identity
                   (U83178) unknown [Arabidopsis thaliana]
NCBI Description
                   293317
Seq. No.
                   LIB3062-044-Q1-K1-G3
Seq. ID
Method
                   BLASTX
                   q4587987
NCBI GI
BLAST score
                   165
                   2.0e-11
E value
                   40
Match length
                   80
% identity
                   (AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   293318
                   LIB3062-045-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   g3319342
NCBI GI
                   292
```



```
100
Match length
                  60
% identity
                  (AF077407) similar to mitochondrial carrier proteins (Pfam:
NCBI Description
                  mit carr.hmm, score: 79.74 and 42.50) [Arabidopsis
                  thaliana]
                  293319
Seq. No.
Seq. ID
                  LIB3062-045-Q1-K1-H1
                  BLASTX
Method
                  g1800147
NCBI GI
BLAST score
                  165
                  8.0e-12
E value
                  45
Match length
                  76
% identity
NCBI Description (U83655) membrane associated protein [Arabidopsis thaliana]
Seq. No.
                  293320
Seq. ID
                  LIB3062-045-Q1-K1-H5
                  BLASTX
Method
                  g4164149
NCBI GI
                  229
BLAST score
                  1.0e-22
E value
Match length
                  68
                  81
% identity
NCBI Description (AB014056) iron-superoxide dismutase [Oryza sativa]
                   293321
Seq. No.
Seq. ID
                  LIB3062-045-Q1-K1-H6
                   BLASTX
Method
                   g120670
NCBI GI
                   191
BLAST score
                   5.0e-27
E value
Match length
                   107
                   70
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_100879_pir__S06879 glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) C - maize
                   >gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]
                   293322
Seq. No.
                   LIB3062-046-Q1-K1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4587373
BLAST score
                   164
                   2.0e-11
E value
                   53
Match length
                   60
 % identity
                   (AB024575) ethylene responsive element binding factor
NCBI Description
                   [Nicotiana tabacum]
                   293323
 Seq. No.
                   LIB3062-046-Q1-K1-G6
 Seq. ID
```

Method BLASTX
NCBI GI g1085973
BLAST score 195
E value 1.0e-15
Match length 56

E value

Match length

2.0e-18



```
% identity
                   isopentyl pyrophosphate isomerase - Clarkia breweri
(fragment) >gi_572635_emb_CAA57947_ (X82627) isopentenyl
NCBI Description
                   pyrophosphate isomerase [Clarkia breweri]
                   293324
Seq. No.
                   LIB3062-047-Q1-K1-A3
Seq. ID
                   BLASTX
Method
                   g1737492
NCBI GI
BLAST score
                   222
                   3.0e-18
E value
Match length
                   111
% identity
                   (U81318) poly(A)-binding protein [Triticum aestivum]
NCBI Description
                   293325
Seq. No.
                   LIB3062-047-Q1-K1-C6
Seq. ID
                   BLASTX
Method
                   g3242071
NCBI GI
BLAST score
                   485
E value
                   3.0e-49
Match length
                   94
% identity
NCBI Description (AJ007289) myb-like protein [Arabidopsis thaliana]
                   293326
Seq. No.
                   LIB3062-047-Q1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g66615
BLAST score
                   245
                   4.0e-21
E value
                   94
Match length
                   76
% identity
                   glutathione transferase (EC 2.5.1.18) I - maize
NCBI Description
                   293327
Seq. No.
                   LIB3062-047-Q1-K1-F1
Seq. ID
                   BLASTX
Method
                   g118926
NCBI GI
BLAST score
                   220
                   5.0e-18
E value
                   80
Match length
% identity
                   53
                   DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
NCBI Description
                   >qi 320600 pir E45509 desiccation-related protein (clone
                   PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991)
                   dessication-related protein [Craterostigma plantagineum]
                   >gi_227781_prf__1710351E abscisic acid responsive protein E
                    [Craterostigma plantagineum]
                   293328
Seq. No.
                   LIB3062-047-Q1-K1-F4
Seq. ID
Method
                   BLASTN
                   g3821794
NCBI GI
BLAST score
                   49
```



```
% identity
                  Zea mays gene encoding protein kinase CK2 alpha subunit
NCBI Description
Seq. No.
                  293329
                  LIB3062-047-Q1-K1-G1
Seq. ID
                  BLASTX
Method
                  g4371292
NCBI GI
                  227
BLAST score
                  1.0e-18
E value
Match length
                  120
% identity
                  39
                  (AC006260) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  293330
Seq. ID
                  LIB3062-048-Q1-K1-G2
Method
                  BLASTN
                  g722325
NCBI GI
BLAST score
                  48
                  3.0e-18
E value
Match length
                  166
                  85
% identity
                  Zea mays clone Zm-Rab2-A GTP binding protein (rab2) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  293331
Seq. ID
                  LIB3062-048-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g3176691
BLAST score
                  171
                  1.0e-13
E value
Match length
                  70
% identity
                  61
                  (AC003671) Contains homology to serine/threonine protein
NCBI Description
                  kinase gb_X99618 from Mycobacterium tuberculosis. ESTs
                  gb_F14403, gb_F14404, and gb_N96730 come from this gene.
                   [Arabidopsis thaliana]
                  293332
Seq. No.
                  LIB3062-049-Q1-K1-B2
Seq. ID
Method
                  BLASTX
                  g741983
NCBI GI
BLAST score
                  160
                  2.0e-11
E value
                  48
Match length
                  69
% identity
                  sucrose synthase:ISOTYPE=2 [Zea mays]
NCBI Description
                  293333
Seq. No.
                  LIB3062-049-Q1-K1-B9
Seq. ID
Method
                  BLASTN
```

Method BLASTN
NCBI GI g22379
BLAST score 35
E value 4.0e-10
Match length 35
% identity 100

NCBI Description Z.mays mRNA for CAAT-box DNA binding protein subunit B

(NF-YB)

% identity

Seq. No.

NCBI Description

293339

```
Seq. No.
                  293334
                  LIB3062-049-Q1-K1-C4
Seq. ID
Method
                  BLASTN
                  g452340
NCBI GI
                  85
BLAST score
                  2.0e-40
E value
                  113
Match length
                   95
% identity
                  Z.mays mRNA for type II light-harvesting chlorophyll
NCBI Description
                  a/b-binding protein
                   293335
Seq. No.
                  LIB3062-049-Q1-K1-F1
Seq. ID
Method
                   BLASTX
                   g100487
NCBI GI
                   176
BLAST score
                   9.0e-13
E value
                   105
Match length
% identity
                   40
                   TNP1 protein - garden snapdragon >gi_16057_emb_CAA40554_
NCBI Description
                   (X57297) TNP1 [Antirrhinum majus]
                   293336
Seq. No.
                   LIB3062-049-Q1-K1-F7
Seq. ID
Method
                   BLASTX
                   g1946355
NCBI GI
BLAST score
                   269
E value
                   1.0e-23
                   125
Match length
                   40
% identity
                   (U93215) maize transposon MuDR mudrA protein isolog
NCBI Description
                   [Arabidopsis thaliana] >gi 2880040 (AC002340) maize
                   transposon MuDR mudrA-like protein [Arabidopsis thaliana]
Seq. No.
                   293337
                   LIB3062-049-Q1-K1-G1
Seq. ID
Method
                   BLASTX
                   g2773154
NCBI GI
                   175
BLAST score
E value
                   1.0e-12
                   58
Match length
                   55
% identity
                   (AF039573) abscisic acid- and stress-inducible protein
NCBI Description
                   [Oryza sativa]
                   293338
Seq. No.
                   LIB3062-049-Q1-K1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4531444
BLAST score
                   246
E value
                   5.0e-21
                   121
Match length
```

40922

(AC006224) putative protein kinase [Arabidopsis thaliana]

NCBI Description



LIB3062-049-Q1-K1-H7 Seq. ID BLASTX Method NCBI GI q129915 BLAST score 421 E value 5.0e-57 Match length 142 80 % identity PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR NCBI Description >gi_66912_pir__TVWTGC phosphoglycerate kinase (EC 2.7.2.3) precursor, chloroplast - wheat >gi_21833_emb_CAA33303_ (X15233) phosphoglycerate kinase (AA 1 - 480) [Triticum aestivum] >gi 3293043 emb CAA51931 (X73528) phosphoglycerate kinase [Triticum aestivum] 293340 Seq. No. Seq. ID LIB3062-050-Q1-K1-B11 Method BLASTX q4191791 NCBI GI BLAST score 499 E value 1.0e-50 Match length 127 % identity 71 (AC005917) putative sf21 {Helianthus annuus} protein NCBI Description [Arabidopsis thaliana] 293341 Seq. No. LIB3062-050-Q1-K1-F12 Seq. ID Method BLASTX NCBI GI q2065531 BLAST score 468 6.0e-47 E value Match length 143 62 % identity (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum] NCBI Description 293342 Seq. No. LIB3062-050-Q1-K1-F8 Seq. ID BLASTX Method g4512660 NCBI GI 313 BLAST score 8.0e-29 E value 102 Match length 58 % identity (AC006931) hypothetical protein [Arabidopsis thaliana] NCBI Description >gi 4544467 gb AAD22374.1_AC006580_6 (AC006580) hypothetical protein [Arabidopsis thaliana] 293343 Seq. No. LIB3062-050-Q1-K1-H8 Seq. ID Method BLASTX NCBI GI q2244996 BLAST score 211 4.0e-17 E value Match length 92 46 % identity

40923

protein [Arabidopsis thaliana]

(Z97341) similarity to a membrane-associated salt-inducible

BLAST score

231

```
293344
Seq. No.
                  LIB3062-051-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3668088
BLAST score
                  417
                  5.0e-41
E value
                  121
Match length
% identity
                  (AC004667) G9a-like protein [Arabidopsis thaliana]
NCBI Description
                  293345
Seq. No.
                  LIB3062-051-Q1-K1-A9
Seq. ID
                  BLASTX
Method
                   g3201631
NCBI GI
BLAST score
                  294
E value
                   1.0e-26
Match length
                   73
                   71
% identity
                   (AC004669) putative GTP-binding protein, 5' partial
NCBI Description
                   [Arabidopsis thaliana]
                   293346
Seq. No.
                   LIB3062-051-Q1-K1-D10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4510381
BLAST score
                   176
                   8.0e-13
E value
Match length
                   73
% identity
                   55
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
                   293347
Seq. No.
                   LIB3062-051-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   g4239692
NCBI GI
BLAST score
                   206
                   2.0e-16
E value
                   87
Match length
                   49
% identity
                   (AJ132745) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   293348
Seq. No.
                   LIB3062-051-Q1-K1-H6
Seq. ID
                   BLASTX
Method
                   g3935170
NCBI GI
BLAST score
                   153
                   2.0e-10
E value
                   86
Match length
% identity
                   37
                  (AC004557) F17L21.13 [Arabidopsis thaliana]
NCBI Description
                   293349
Seq. No.
                   LIB3062-052-Q1-K1-A2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4582787
```

Seq. No.

293355



```
8.0e-20
E value
Match length
                  65
                  74
% identity
                  (AJ012281) adenosine kinase [Zea mays]
NCBI Description
                  293350
Seq. No.
                  LIB3062-052-Q1-K1-A6
Seq. ID
                  BLASTX
Method
                  g4091117
NCBI GI
BLAST score
                  309
                  2.0e-28
E value
                  73
Match length
                  81
% identity
                  (AF047428) nucleic acid binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  293351
                  LIB3062-052-Q1-K1-D9
Seq. ID
Method
                  BLASTX
                   g4585871
NCBI GI
                   290
BLAST score
                   3.0e-26
E value
                   87
Match length
                   62
% identity
                  (AC005850) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   293352
                   LIB3062-052-Q1-K1-G10
Seq. ID
Method
                   BLASTX
                   g1173027
NCBI GI
BLAST score
                   206
                   3.0e-16
E value
                   65
Match length
                   65
% identity
                   60S RIBOSOMAL PROTEIN L31 >gi_915313 (U23784) ribosomal
NCBI Description
                   protein L31 [Nicotiana glutinosa]
                   293353
Seq. No.
                   LIB3062-052-Q1-K1-G2
Seq. ID
Method
                   BLASTX
                   g3763932
NCBI GI
BLAST score
                   322
                   3.0e - 30
E value
                   88
Match length
                   77
% identity
                  (AC004450) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   293354
Seq. No.
                   LIB3062-052-Q1-K1-H8
Seq. ID
Method
                   BLASTX
                   g3288113
NCBI GI
BLAST score
                   190
                   2.0e-28
E value
                   81
Match length
% identity
                   83
                  (Z97067) elongation factor 1-beta [Beta vulgaris]
NCBI Description
```

NCBI GI BLAST score

E value

191

1.0e-14



```
LIB3062-053-Q1-K1-A9
Seq. ID
                  BLASTX
Method
                  g2668742
NCBI GI
BLAST score
                  153
                  3.0e-10
E value
                  66
Match length
                  56
% identity
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
Seq. No.
                  293356
                  LIB3062-053-Q1-K1-D12
Seq. ID
                  BLASTX
Method
                  g2668742
NCBI GI
BLAST score
                  371
E value
                  8.0e-36
Match length
                  85
% identity
                   87
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                   293357
Seq. No.
                  LIB3062-053-Q1-K1-H10
Seq. ID
                   BLASTX
Method
                   g693918
NCBI GI
                   200
BLAST score
                   9.0e-16
E value
Match length
                   86
% identity
                   52
                  (U21112) chlorophyll a/b binding protein [Solanum
NCBI Description
                   tuberosum]
Seq. No.
                   293358
                   LIB3062-053-Q1-K1-H5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2459445
BLAST score
                   223
                   2.0e-18
E value
Match length
                   102
                   44
% identity
                  (AC002332) putative ribonucleoprotein [Arabidopsis
NCBI Description
                   thaliana]
                   293359
Seq. No.
                   LIB3062-056-Q1-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2500215
BLAST score
                   185
                   3.0e-14
E value
                   63
Match length
                   56
% identity
                  60S ACIDIC RIBOSOMAL PROTEIN PO (L10E)
NCBI Description
                   293360
Seq. No.
                   LIB3062-056-Q1-K1-B10
Seq. ID
Method
                   BLASTX
                   g1172810
```



Match length 38 95 % identity 60S RIBOSOMAL PROTEIN L10 (QM PROTEIN HOMOLOG) NCBI Description >gi 543339 pir JC2013 ribosomal protein L10, cytosolic mouse >gi_2143959_pir__JC4911 ribosomal protein L10 - rat >gi_407466_emb_CAA53061_ (X75312) QM protein [Mus musculus]
>gi_410742 (M93980) 24.6 kda protein [Mus musculus] >qi 1854567 emb CAA60587 (X87106) ribosomal protein L10 [Rattus norvegicus] Seq. No. 293361 LIB3062-056-Q1-K1-C10 Seq. ID BLASTX Method

Seq. ID LIB3062-056-Q1-K1-C10
Method BLASTX
NCBI GI g35053
BLAST score 333
E value 3.0e-31
Match length 103
% identity 68

NCBI Description (X53778) uracil DNA glycosylase [Homo sapiens]

 Seq. No.
 293362

 Seq. ID
 LIB3062-056-Q1-K1-C11

 Method
 BLASTX

 NCBI GI
 g120649

 BLAST score
 142

 E value
 6.0e-09

 Match length
 90

% identity 41

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER >qi 625203 pir DEHUG3 glyceraldehyde-3-phosphate

dehydrogenase (EC 1.2.1.12) - human >gi_182861 (M17851) glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]

>gi_182863 (J02642) glyceraldehyde 3-phosphate

dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi_182977
(M33197) glyceraldehyde-3-phosphate dehydrogenase (EC

1.2.1.12) [Homo sapiens] >gi_182981 (J04038)

glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]

>gi 224880_prf__1203217A

dehydrogenase, glyceraldehydephosphate [Homo sapiens]

Seq. No. 293363

Seq. ID LIB3062-056-Q1-K1-C12

Method BLASTX
NCBI GI g181519
BLAST score 455
E value 2.0e-45
Match length 84
% identity 100

NCBI Description (L01131) decorin [Homo sapiens]

Seq. No. 293364

Seq. ID LIB3062-056-Q1-K1-D10

Method BLASTX
NCBI GI g1322019
BLAST score 660
E value 2.0e-69
Match length 125



% identity NCBI Description

(U30787) uroporphyrinogen decarboxylase [Homo sapiens] >gi 1418944 emb CAA61540 (X89267) uroporphyrinogen decarboxylase [Homo sapiens] >gi 4151813 (AF104421) uroporphyrinogen decarboxylase [Homo sapiens] >gi_4151815 (AF104422) uroporphyrinogen decarboxylase [Homo sapiens] >gi 4151817 (AF104423) uroporphyrinogen decarboxylase [Homo sapiens] >gi 4151819 (AF104424) uroporphyrinogen decarboxylase [Homo sapiens] >gi_4151821 (AF104425) uroporphyrinogen decarboxylase [Homo sapiens] >gi_4151823 (AF104426) uroporphyrinogen decarboxylase [Homo sapiens] >gi_4151825 (AF104427) uroporphyrinogen decarboxylase [Homo sapiens] >gi_4151827 (AF104428) uroporphyrinogen decarboxylase [Homo sapiens] >gi_4151829 (AF104429) uroporphyrinogen decarboxylase [Homo sapiens] >gi_4151831 (AF104430) uroporphyrinogen decarboxylase [Homo sapiens] >gi_4151833 (AF104431) uroporphyrinogen decarboxylase [Homo sapiens] >gi_4151835 (AF104432) uroporphyrinogen decarboxylase [Homo sapiens] >gi 4151837 (AF104433) uroporphyrinogen decarboxylase $[\overline{\text{H}}\text{omo} \text{ sapiens}] > \text{gi} 4151839$ (AF104434) uroporphyrinogen decarboxylase [Homo sapiens] >gi_4151841 (AF104435) uroporphyrinogen decarboxylase [Homo sapiens] >gi_4151843 (AF104436) uroporphyrinogen decarboxylase [Homo sapiens] >gi_4151845 (AF104437) uroporphyrinogen decarboxylase [Homo sapiens] >gi_4151847 (AF104438) uroporphyrinogen decarboxylase [Homo sapiens] >gi 4151849 (AF104439) uroporphyrinogen decarboxylase [Homo sapiens] >gi_4151851 (AF104440) uroporphyrinogen decarboxylase [Homo sapiens]

Seq. No. 293365 LIB3062-056-Q1-K1-D11 Seq. ID Method BLASTN NCBI GI g1737211 BLAST score 417 E value 0.0e+00Match length 417 % identity 100

NCBI Description

Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds

 Seq. No.
 293366

 Seq. ID
 LIB3062-056-Q1-K1-D9

 Method
 BLASTN

 NCBI GI
 g4503684

 BLAST score
 96

 E value
 1.0e-46

 Match length
 100

% identity 99
NCBI Description Homo sapiens farmesyl diphosphate synthase (farmesyl pyrophosphate synthetase, dimethylallyltranstransferase,

geranyltranstransferase) (FDPS) mRNA

>gi_285964_dbj_D14697_HUMORF14 Human mRNA for KIAA0003

gene, complete cds

```
293367
Seq. No.
                   LIB3062-056-Q1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2982114
BLAST score
                   721
                   1.0e-76
E value
                   137
Match length
                   93
% identity
                   Crystal Structure Of Human Recombinant Procathepsin B At
NCBI Description
                   3.2 Angstrom Resolution >gi_2982144_pdb_2PBH_ Crystal
                   Structure Of Human Procathepsin B At 3.3 Angstrom
                   Resolution >gi_2982152_pdb_3PBH_ Refined Crystal Structure
                   Of Human Procathepsin B At 2.5 Angstrom Resolution
Seq. No.
                   293368
Seq. ID
                   LIB3062-056-Q1-K1-F9
Method
                   BLASTX
                   q4507645
NCBI GI
BLAST score
                   470
E value
                   3.0e-47
Match length
                   117
% identity
                   80
                   {\tt triosephosphate~isomerase~1~gi\_136060\_sp\_P00938\_TPIS\_HUMAN}
NCBI Description
                   TRIOSEPHOSPHATE ISOMERASE (TIM) >gi_68420 pir__ISCZT1
                   triose-phosphate isomerase (EC 5.3.1.1) 1 - chimpanzee
                   >gi 2144541 pir ISHUT triose-phosphate isomerase (EC
                   5.3.1.1) - human >gi_37247_emb_CAA49379 (X69723) triosephosphate isomerase [Homo sapiens] >gi_176960
                   (M57946) triose-phosphate isomerase [Pan troglodytes]
                   >gi 339841 (M10036) triosephosphate isomerase (EC 5.3.1.1)
                   [Homo sapiens] >gi_1200507 (U47924) triosephosphate
                   isomerase [Homo sapiens]
                   293369
Seq. No.
```

LIB3062-056-Q1-K1-G11 Seq. ID Method BLASTX g4506179 NCBI GI BLAST score 541 1.0e-55 E value Match length 108 97 % identity

proteasome (prosome, macropain) subunit, alpha type, 1 NCBI Description >gi 130848 sp P25786 PRC2 HUMAN PROTEASOME COMPONENT C2

(MACROPAIN SUBUNIT CZ) (PROTEASOME NU CHAIN)

(MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C2) (30 KD

PROSOMAL PROTEIN) (PROS-30) >gi_220022_dbj_BAA00656_

(D00759) proteasome subunit C2 [Homo sapiens]

>gi_296738_emb_CAA43961_ (X61969) macropaine subunit nu

[Homo sapiens]

Seq. No.

LIB3062-056-Q1-K1-H12 Seq. ID

293370

Method BLASTN g4501864 NCBI GI 354 BLAST score E value 0.0e+00Match length 416



```
% identity
                  Homo sapiens ATP citrate lyase (ACLY) mRNA
NCBI Description
                  >gi 28934 emb_X64330_HSATPCITL H.sapiens mRNA for
                  ATP-citrate lyase
                  293371
Seq. No.
                  LIB3062-056-Q1-K1-H9
Seq. ID
                  BLASTN
Method
                  g2339976
NCBI GI
BLAST score
                  55
                  4.0e-22
E value
Match length
                  63
                  10
% identity
                  Homo sapiens chromosome 16 BAC clone CIT987SK-381E11
NCBI Description
                  complete sequence [Homo sapiens]
                  293372
Seq. No.
                  LIB3062-057-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4585976
BLAST score
                  341
E value
                  4.0e-32
Match length
                  117
                  62
% identity
                  (AC005287) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  293373
Seq. No.
                  LIB3062-057-Q1-K1-A9
Seq. ID
Method
                  BLASTX
                  g3337361
NCBI GI
BLAST score
                  255
E value
                  5.0e-22
Match length
                   67
                   69
% identity
                  (AC004481) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
                   293374
Seq. No.
                  LIB3062-057-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1514530
                   292
BLAST score
                   2.0e-26
E value
                   110
Match length
                   25
% identity
                  (X97187) ABC-C transporter [Homo sapiens]
NCBI Description
                   293375
Seq. No.
                   LIB3062-057-Q1-K1-C6
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3982617
```

Method BLASTN
NCBI GI g398261
BLAST score 153
E value 1.0e-80
Match length 388
% identity 96

NCBI Description Zea mays disease resistance gene analog PIC13 (pic13) gene,

partial cds



```
293376
Seq. No.
Seq. ID
                  LIB3062-057-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g1903364
BLAST score
                  156
                  2.0e-10
E value
Match length
                  54
                  57
% identity
                  (AC000104) EST gb_T45093 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  293377
Seq. No.
                  LIB3062-057-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4325345
BLAST score
                  181
                  2.0e-13
E value
Match length
                  68
% identity
                  18
                  (AF128393) similar to thioredoxin-like proteins (Pfam:
NCBI Description
                  PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity
                  to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42,
                  N=1) [Arabidopsis thaliana]
Seq. No.
                  293378
                  LIB3062-057-Q1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132147
BLAST score
                  275
E value
                  3.0e-31
Match length
                  117
% identity
                  62
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 68089 pir RKZMS
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - maize >gi 22474 emb CAA29784 (X06535)
                  ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor
                  [Zea mays] >gi_217964_dbj_BAA00120_ (D00170) ribulose
                  1,5-bisphosphate carboxylase small subunit [Zea mays]
                  >gi 359512 prf 1312317A ribulosebisphosphate carboxylase
                  [Zea mays]
                  293379
Seq. No.
                  LIB3062-057-Q1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3135543
BLAST score
                  452
E value
                  3.0e-45
Match length
                  108
% identity
                  83
NCBI Description
                  (AF062393) aquaporin [Oryza sativa]
```

293380

Seq. No. LIB3062-058-Q1-K1-B9 Seq. ID

Method BLASTX NCBI GI g1352200

BLAST score 226



E value 1.0e-18 Match length 87 % identity 54

CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT) NCBI Description

>gi 480909 pir S37497 triose

phosphate/3-phosphoglycerate/phosphate translocator - maize

>gi 405635 emb CAA81349 (Z26595) triose phosphate/phosphate translocator [Zea mays]

293381 Seq. No.

LIB3062-058-Q1-K1-C2 Seq. ID

Method BLASTX NCBI GI g119928 BLAST score 216 8.0e-18 E value 76 Match length 63 % identity

FERREDOXIN I PRECURSOR (FD I) >gi_168469 (M73829) NCBI Description

ferredoxin [Zea mays] >gi 168471 (M73830) ferredoxin [Zea mays] >qi 444685 prf 1907324B ferredoxin:ISOTYPE=I [Zea

mays]

293382 Seq. No.

LIB3062-058-Q1-K1-F12 Seq. ID

Method BLASTX g1706260 NCBI GI BLAST score 191 1.0e-14 E value Match length 84 49 % identity

NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir S59597

cysteine proteinase 1 precursor - maize

>gi 643597 dbj BAA08244 (D45402) cysteine proteinase [Zea

mays]

Seq. No. 293383

Seq. ID LIB3062-058-Q1-K1-F6

Method BLASTX NCBI GI q3850568 BLAST score 531 2.0e-54E value Match length 124 % identity 79

(AC005278) Similar to hypothetical protein SPAC2F7.14c NCBI Description

gi 1052797 from Schizosaccharomyces pombe cosmid gb_Z50142.

[Arabidopsis thaliana]

Seq. No. 293384

Seq. ID LIB3062-059-Q1-K1-B7

Method BLASTX NCBI GI q4467147 BLAST score 588 E value 5.0e-61 Match length 140 % identity

NCBI Description (AL035540) putative protein [Arabidopsis thaliana]



```
293385
Seq. No.
Seq. ID
                  LIB3062-059-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  g4115925
BLAST score
                  233
                  5.0e-27
E value
Match length
                  102
                  67
% identity
                  (AF118222) contains similarity to RNA recognition motifs
NCBI Description
                   (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
                  >gi 4539439 emb CAB40027.1 (AL049523) RNA-binding protein
                  [Arabidopsis thaliana]
                  293386
Seq. No.
Seq. ID
                  LIB3062-059-Q1-K1-D5
Method
                  BLASTX
                  g3334320
NCBI GI
BLAST score
                  225
                  4.0e-19
E value
Match length
                  69
% identity
                  67
                  40S RIBOSOMAL PROTEIN SA (P40) >qi 2444420 (AF020553)
NCBI Description
                  ribosome-associated protein p40 [Glycine max]
                  293387
Seq. No.
Seq. ID
                  LIB3062-059-Q1-K1-D6
Method
                  BLASTX
                  g3551245
NCBI GI
BLAST score
                  184
                  5.0e-14
E value
Match length
                  82
% identity
                  51
                  (AB012702) P40-like protein [Daucus carota]
NCBI Description
                  293388
Seq. No.
                  LIB3062-059-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g548770
BLAST score
                  214
                  2.0e-26
E value
Match length
                  88
                  73
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi 481228 pir S38359 ribosomal
NCBI Description
                  protein L3 - rice >gi 303853 dbj BAA02155 (D12630)
                  ribosomal protein L3 [Oryza sativa]
                  293389
Seq. No.
```

Seq. ID LIB3066-001-Q1-K1-A10 Method BLASTN

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 6.0e-11
Match length 48
% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 293390

E value

Match length

2.0e-30

127



```
LIB3066-001-Q1-K1-C5
Seq. ID
Method
                  BLASTX
                  g1708191
NCBI GI
BLAST score
                  263
                  6.0e-23
E value
                  126
Match length
                  42
% identity
                  HEXOSE CARRIER PROTEIN HEX6 >gi 467319 (L08188) hexose
NCBI Description
                  carrier protein [Ricinus communis]
                  293391
Seq. No.
                  LIB3066-001-Q1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3337361
BLAST score
                  523
E value
                  2.0e-53
Match length
                  122
                  77
% identity
                  (AC004481) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  293392
                  LIB3066-001-Q1-K1-D9
Seq. ID
                  BLASTN
Method
                  g293901
NCBI GI
BLAST score
                  58
E value
                  6.0e-24
Match length
                  74
% identity
                  96
                  Zea mays Zea mI gene, complete cds
NCBI Description
                  293393
Seq. No.
                  LIB3066-002-Q1-K1-B4
Seq. ID
                  BLASTN
Method
                  g3885491
NCBI GI
BLAST score
                  218
                  1.0e-119
E value
                  316
Match length
                   94
% identity
NCBI Description Zea mays tapetum specific protein mRNA, complete cds
                   293394
Seq. No.
                  LIB3066-002-Q1-K1-B5
Seq. ID
                  BLASTX
Method
NCBI GI
                   g639722
BLAST score
                   237
E value
                   4.0e-20
                   56
Match length
                   80
% identity
                  (L27484) calcium-dependent protein kinase [Zea mays]
NCBI Description
Seq. No.
                   293395
                  LIB3066-002-Q1-K1-B7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4454051
BLAST score
                   326
```



```
% identity
                  (AL035394) putative polygalacturonase [Arabidopsis
NCBI Description
                  thaliana]
                  293396
Seq. No.
                  LIB3066-002-Q1-K1-C3
Seq. ID
Method
                  BLASTN
                  g3821780
NCBI GI
BLAST score
                  36
                  9.0e-11
E value
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  293397
Seq. No.
                  LIB3066-002-Q1-K1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1620371
                  172
BLAST score
                  3.0e-12
E value
                  53
Match length
                  58
% identity
                  (Y08782) peroxidase ATP23a [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  293398
                  LIB3066-002-Q1-K1-D7
Seq. ID
Method
                  BLASTX
                  g3264767
NCBI GI
                  179
BLAST score
                  2.0e-13
E value
Match length
                  44
                  73
% identity
                  (AF071893) AP2 domain containing protein [Prunus armeniaca]
NCBI Description
                  293399
Seq. No.
                  LIB3066-002-Q1-K1-E2
Seq. ID
Method
                  BLASTN
                   g3821780
NCBI GI
BLAST score
                   36
E value
                   1.0e-10
Match length
                   36
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   293400
Seq. ID
                   LIB3066-002-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                   q1351856
BLAST score
                   535
E value
                   8.0e-55
Match length
                   134
                   74
% identity
                  ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
```

NCBI Description

(ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase

[Cucurbita sp.]

Seq. No.



```
LIB3066-002-Q1-K1-E6
Seq. ID
                   BLASTX
Method
                   g2344890
NCBI GI
BLAST score
                   221
                   5.0e-18
E value
Match length
                   78
% identity
                   (AC002388) TINY transcription factor isolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   293402
                   LIB3066-002-Q1-K1-F3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g532622
BLAST score
                   82
E value
                   3.0e-38
Match length
                   224
% identity
                   89
NCBI Description Zea mays lipase (LIP) mRNA, complete cds
Seq. No.
                   293403
                   LIB3066-002-Q1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4587513
BLAST score
                   394
E value
                   3.0e-38
Match length
                   136
                   57
% identity
NCBI Description
                   (AC007060) Contains eukaryotic protein kinase domain
                   PF 00069. [Arabidopsis thaliana]
Seq. No.
                   293404
                   LIB3066-003-Q1-K1-A11
Seq. ID
                   BLASTX
Method
                   q3236249
NCBI GI
BLAST score
                   241
                   2.0e-20
E value
Match length
                   54
                   78
% identity
                   (AC004684) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   293405
                   LIB3066-003-Q1-K1-A3
Seq. ID
Method
                   BLASTX
                   g1502430
NCBI GI
BLAST score
                   250
                   8.0e-22
E value
Match length
                   62
                   74
% identity
                   (U62331) phosphate transporter [Arabidopsis thaliana]
NCBI Description
                   >gi_2564661 (AF022872) phosphate transporter [Arabidopsis
                   thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770)
                   phosphate transporter, AtPT2 [Arabidopsis thaliana]
```

Seq. No. 293406

Seq. ID LIB3066-003-Q1-K1-A8

BLAST score

E value

37

2.0e-11



```
Method
                  BLASTN
                  g1666078
NCBI GI
BLAST score
                  34
                  2.0e-09
E value
Match length
                  50
                  92
% identity
NCBI Description H.vulgare mRNA for glutamyl-tRNA reductase (2nd isoform)
                  293407
Seq. No.
                  LIB3066-003-Q1-K1-B2
Seq. ID
Method
                  BLASTX
                  g3335060
NCBI GI
BLAST score
                  504
                  3.0e-51
E value
Match length
                  127
% identity
                  80
                  (AF025842) plasma membrane-type calcium ATPase [Arabidopsis
NCBI Description
                  thaliana] >gi 4468989 emb CAB38303 (AL035605) plasma
                  membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]
Seq. No.
                  293408
                  LIB3066-003-Q1-K1-B9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g22136
BLAST score
                  45
                  3.0e-16
E value
                  49
Match length
% identity
                  98
NCBI Description Maize Adh2-N mRNA for alcohol dehydrogenase
                  293409
Seq. No.
                  LIB3066-003-Q1-K1-C1
Seq. ID
Method
                  BLASTX
                  g4585966
NCBI GI
BLAST score
                  146
                   3.0e-09
E value
                   51
Match length
% identity
                   57
                   (AC005287) Putative dihyrdolipoamide acetyltransferase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   293410
                  LIB3066-003-Q1-K1-D5
Seq. ID
Method
                  BLASTN
NCBI GI
                   g248336
BLAST score
                   45
                   4.0e-16
E value
Match length
                   53
% identity
                   98
                  polyubiquitin [maize, Genomic, 3841 nt]
NCBI Description
Seq. No.
                   293411
Seq. ID
                  LIB3066-003-01-K1-E4
Method
                  BLASTN
NCBI GI
                   q1532072
```

NCBI Description



```
65
Match length
                  89
% identity
NCBI Description
                  Z.mays mRNA for S-adenosylmethionine decarboxylase
Seq. No.
                  293412
                  LIB3066-004-Q1-K1-A7
Seq. ID
                  BLASTX
Method
                  q322854
NCBI GI
BLAST score
                  246
                  6.0e-21
E value
                  98
Match length
                  53
% identity
                  pollen-specific protein - rice >gi 20310 emb CAA78897_
NCBI Description
                  (Z16402) pollen specific gene [Oryza sativa]
Seq. No.
                  293413
                  LIB3066-004-Q1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3928519
BLAST score
                  254
E value
                  7.0e-22
Match length
                  122
% identity
                  48
                  (AB011670) wpk4 protein kinase [Triticum aestivum]
NCBI Description
Seq. No.
                  293414
                  LIB3066-004-Q1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2586082
BLAST score
                  415
E value
                  9.0e-41
                  139
Match length
% identity
                  63
                  (U72725) retrofit [Oryza longistaminata]
NCBI Description
                  293415
Seq. No.
                  LIB3066-004-Q1-K1-C3
Seq. ID
Method
                  BLASTX
                  g481432
NCBI GI
BLAST score
                  201
E value
                  9.0e-16
                  82
Match length
% identity
                  56
                  allergen Phl pI - common timothy >gi 1582250 prf 2118271A
NCBI Description
                  allergen PhI p I [Phleum pratense]
Seq. No.
                  293416
                  LIB3066-004-Q1-K1-F4
Seq. ID
Method
                  BLASTX
                  g1705567
NCBI GI
BLAST score
                  199
                  2.0e-15
E value
Match length
                  92
                  49
% identity
```

calmodulin [Naegleria gruberi]

CALMODULIN, FLAGELLAR (CAM-1) >qi 458232 (U04381) flagellar

BLAST score

E value

88

9.0e-42



```
293417
Seq. No.
                  LIB3066-004-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2618691
BLAST score
                  239
                  2.0e-20
E value
                  108
Match length
                  48
% identity
NCBI Description (AC002510) putative chloroplast envelope Ca2+-ATPase
                  [Arabidopsis thaliana]
                  293418
Seq. No.
                  LIB3066-004-Q1-K1-G10
Seq. ID
                  BLASTN
Method
NCBI GI
                  g22458
BLAST score
                  83
                  6.0e-39
E value
Match length
                  187
% identity
                  86
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)
                  293419
Seq. No.
                  LIB3066-004-Q1-K1-G3
Seq. ID
                  BLASTN
Method
                  q3821780
NCBI GI
BLAST score
                  36
                  1.0e-10
E value
Match length
                  48
% identity
                  67
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  293420
Seq. No.
                  LIB3066-004-Q1-K1-H5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  36
                  4.0e-11
E value
Match length
                  46
% identity
                  66
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  293421
Seq. No.
                  LIB3066-004-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4531444
BLAST score
                  242
E value
                  2.0e-20
Match length
                  101
                  48
% identity
                  (AC006224) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  293422
                  LIB3066-004-Q1-K1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2340107
```



Match length 94 % identity Zea mays starch branching enzyme IIa (Sbe2a) mRNA, partial NCBI Description 293423 Seq. No. LIB3066-005-Q1-K1-A5 Seq. ID Method BLASTX NCBI GI g3335341 BLAST score 219 9.0e-18 E value Match length 71 66 % identity (AC004512) T8F5.10 [Arabidopsis thaliana] NCBI Description 293424 Seq. No. LIB3066-005-Q1-K1-B1 Seq. ID Method BLASTX NCBI GI g4325339 BLAST score 390 8.0e-38 E value 109 Match length 65 % identity NCBI Description (AF128392) No definition line found [Arabidopsis thaliana] 293425 Seq. No. LIB3066-005-Q1-K1-B7 Seq. ID Method BLASTX NCBI GI g118104 BLAST score 245 8.0e-21 E value 56 Match length % identity 86 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) NCBI Description (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) maize >gi_168461 (M55021) cyclophilin [Zea mays] >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays] Seq. No. 293426 Seq. ID LIB3066-005-Q1-K1-B8 Method BLASTX NCBI GI g4544438 188 BLAST score E value 4.0e-14 Match length 146 % identity 36 (AC006592) hypothetical protein [Arabidopsis thaliana] NCBI Description 293427 Seq. No. LIB3066-005-Q1-K1-D5 Seq. ID Method BLASTX

NCBI GI q2586127 BLAST score 197 E value 4.0e-15 Match length 155 36 % identity



(U89510) b-keto acyl reductase [Hordeum vulgare] NCBI Description 293428 Seq. No. Seq. ID LIB3066-005-Q1-K1-E12 Method BLASTX NCBI GI q4587519 BLAST score 479 E value 3.0e-48 Match length 122 75 % identity (AC007060) Strong similarity to F19I3.7 gi_3033380 putative NCBI Description coatomer epsilon subunit from Arabidopsis thaliana BAC gb AC004238. ESTs gb Z17908, gb_AA728673, gb_N96555, gb H76335, gb AA712463, gb W43247, gb T45611, g Seq. No. 293429 LIB3066-005-Q1-K1-F5 Seq. ID Method BLASTX q2934902 NCBI GI BLAST score 488 3.0e-49 E value Match length 138 % identity 75 (AF039304) cpSecY [Zea mays] NCBI Description 293430 Seq. No. Seq. ID LIB3066-005-Q1-K1-F7 BLASTX Method NCBI GI q3367593 BLAST score 295 1.0e-26 E value Match length 123 % identity 45 (AL031135) putative protein [Arabidopsis thaliana] NCBI Description >qi 3805841 emb CAA21461 (AL031986) putative protein [Arabidopsis thaliana] Seq. No. 293431 LIB3066-005-Q1-K1-H5 Seq. ID Method BLASTN NCBI GI g3821780 BLAST score 36 E value 1.0e-10 Match length 36 100 % identity Xenopus laevis cDNA clone 27A6-1 NCBI Description 293432 Seq. No. LIB3066-006-Q1-K1-B5 Seq. ID

BLASTX Method g2270994 NCBI GI BLAST score 276 E value 1.0e-24 91 Match length 54 % identity

(AF004809) Ca+2-binding EF hand protein [Glycine max] NCBI Description

NCBI GI

BLAST score

g3805844

212



```
293433
Seq. No.
                   LIB3066-006-Q1-K1-C2
Seq. ID
Method
                   BLASTX
                   g100489
NCBI GI
BLAST score
                   168
                   7.0e-12
E value
                   115
Match length
% identity
                   33
                  transposase Tam3 - garden snapdragon transposon Tam3
NCBI Description
                   >gi_16064_emb_CAA38906_ (X55078) Tam3-transposase
[Antirrhinum majus] >gi_3219237_dbj_BAA28817.1_ (AB013982)
                   transposase [Antirrhinum majus] >gi_3219239_dbj_BAA28818.1_
                   (AB013983) transposase [Antirrhinum majus]
                   >qi 3219241 dbj BAA28819.1 (AB013984) transposase
                   [Antirrhinum majus] >gi_3219244_dbj_BAA28820.1_ (AB013986)
                   transposase [Antirrhinum majus] >gi_3219249_dbj_BAA28821.1_
                   (AB013990) transposase [Antirrhinum majus]
                   >qi 3219251 dbj BAA28822.1 (AB013991) transposase
                   [Antirrhinum majus] >gi 3219256_dbj_BAA28823.1_ (AB013995)
                   transposase [Antirrhinum majus] >gi_3219259_dbj_BAA28824.1_
                   (AB013997) transposase [Antirrhinum majus]
                   293434
Seq. No.
                   LIB3066-006-Q1-K1-E1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2347195
                   170
BLAST score
                   4.0e-12
E value
Match length
                   64
                   53
% identity
                  (AC002338) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   293435
Seq. No.
                   LIB3066-006-Q1-K1-E8
Seq. ID
Method
                   BLASTX
                   g2270994
NCBI GI
BLAST score
                   231
E value
                   3.0e-19
Match length
                   101
% identity
                   48
NCBI Description (AF004809) Ca+2-binding EF hand protein [Glycine max]
                   293436
Seq. No.
                   LIB3066-006-Q1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3063465
BLAST score
                   168
                   7.0e-12
E value
Match length
                   97
% identity
                   40
NCBI Description (AC003981) F22013.27 [Arabidopsis thaliana]
                   293437
Seq. No.
                   LIB3066-006-Q1-K1-G8
Seq. ID
Method
                   BLASTX
```

```
6.0e-17
E value
Match length
                  81
% identity
                  46
                  (AL031986) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  293438
Seq. No.
                  LIB3066-007-Q1-K1-B11
Seq. ID
Method
                  BLASTX
                  g2222798
NCBI GI
BLAST score
                  316
                  4.0e-29
E value
                  97
Match length
                  62
% identity
NCBI Description
                  (Y14008) gibberellin 20-oxidase [Triticum aestivum]
                  293439
Seq. No.
                  LIB3066-007-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2702268
BLAST score
                  210
                  1.0e-16
E value
                  49
Match length
                  84
% identity.
                  (AC003033) putative cellulase [Arabidopsis thaliana]
NCBI Description
                  293440
Seq. No.
                  LIB3066-007-Q1-K1-C9
Seq. ID
Method
                  BLASTX
                  g4585708
NCBI GI
BLAST score
                  201
                  4.0e-17
E value
                  57
Match length
                  75
% identity
NCBI Description (AJ238117) putative phospholipase A2 [Oryza sativa]
Seq. No.
                  293441
Seq. ID
                  LIB3066-007-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  q1171161
BLAST score
                  537
E value
                  5.0e-55
                  130
Match length
% identity
                  73
NCBI Description (U41472) pectate lyase homolog [Medicago sativa]
                  293442
Seq. No.
                  LIB3066-007-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3426062
BLAST score
                  149
```

Method BLASTX
NCBI GI g3426062
BLAST score 149
E value 1.0e-09
Match length 75
% identity 43

NCBI Description (AJ007587) monooxygenase [Arabidopsis thaliana]

Seq. No. 293443

Seq. ID LIB3066-007-Q1-K1-E8

% identity

36



```
Method
                    BLASTX
  NCBI GI
                    g3687391
  BLAST score
                    418
E value
                    4.0e-41
 Match length
                    134
                    61
  % identity
 NCBI Description
                    (Y16125) putative phosphate transporter [Lycopersicon
                    esculentum]
  Seq. No.
                    293444
                    LIB3066-007-Q1-K1-F11
  Seq. ID
  Method
                    BLASTN
  NCBI GI
                    g3821780
  BLAST score
                    36
                    9.0e-11
  E value
  Match length
                    36
                    100
  % identity
  NCBI Description Xenopus laevis cDNA clone 27A6-1
  Seq. No.
                    293445
                    LIB3066-007-Q1-K1-F5
  Seq. ID
  Method
                    BLASTX
 NCBI GI
                    g2708741
 BLAST score
                    145
 E value
                    3.0e-09
 Match length
                    92
  % identity
                    40
  NCBI Description (AC003952) hypothetical protein [Arabidopsis thaliana]
  Seq. No.
                    293446
                    LIB3066-007-Q1-K1-H12
  Seq. ID
  Method
                    BLASTX
                    g639722
  NCBI GI
  BLAST score
                    417
                    4.0e-41
  E value
  Match length
                    105
  % identity
                    74
  NCBI Description (L27484) calcium-dependent protein kinase [Zea mays]
  Seq. No.
                    293447
  Seq. ID
                    LIB3066-008-Q1-K1-A2
  Method
                    BLASTX
  NCBI GI
                    g2911148
  BLAST score
                    146
  E value
                    2.0e-09
  Match length
                    32
  % identity
  NCBI Description (AB005808) NADP-malic enzyme [Aloe arborescens]
  Seq. No.
                    293448
                    LIB3066-008-Q1-K1-B12
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q4415915
  BLAST score
                    149
  E value
                    8.0e-10
  Match length
                    94
```

```
(AC006282) putative pectin methylesterase [Arabidopsis
NCBI Description
                  thalianal
                  293449
Seq. No.
Seq. ID
                  LIB3066-008-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  g2618689
BLAST score
                  396
E value
                  2.0e-38
Match length
                  138
% identity
                  65
                  (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
                  293450
Seq. No.
                  LIB3066-008-Q1-K1-C5
Seq. ID
Method
                  BLASTX
                  g4510348
NCBI GI
BLAST score
                  229
E value
                  6.0e-19
Match length
                  107
% identity
                  46
NCBI Description
                  (AC006921) unknown protein [Arabidopsis thaliana]
                  293451
Seq. No.
Seq. ID
                  LIB3066-008-Q1-K1-D7
Method
                  BLASTN
                  g3821780
NCBI GI
BLAST score
                  36
                  8.0e-11
E value
Match length
                  48
% identity
                  67
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  293452
                  LIB3066-008-Q1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4587513
BLAST score
                  358
E value
                  3.0e-34
Match length
                  97
                  69
% identity
NCBI Description
                  (AC007060) Contains eukaryotic protein kinase domain
                  PF 00069. [Arabidopsis thaliana]
```

Seq. No. 293453

Seq. ID LIB3066-008-Q1-K1-E7

Method BLASTX NCBI GI g1171866 BLAST score 247 E value 2.0e-21 Match length 73 % identity 64

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (COMPLEX I-20KD) (CI-20KD) >gi_629601_pir__S48826 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild cabbage >gi_562282_emb_CAA57725_ (X82274) PSST subunit of NADH: ubiquinone oxidoreductase [Brassica oleracea]

```
Seq. No.
                  293454
                  LIB3066-008-Q1-K1-E9
Seq. ID
Method
                  BLASTX
                  g3252805
NCBI GI
                  207
BLAST score
                  2.0e-16
E value
                  69
Match length
                  57
% identity
                  (AC004705) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3650027 (AC005396) hypothetical protein [Arabidopsis
                  thaliana]
                  293455
Seq. No.
Seq. ID
                  LIB3066-008-Q1-K1-F1
Method
                  BLASTX
                  g3367522
NCBI GI
BLAST score
                  175
                  1.0e-12
E value
Match length
                  55
% identity
                  64
                  (AC004392) EST gb_T04691 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  293456
Seq. No.
                  LIB3066-008-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2995384
BLAST score
                  203
                  3.0e-16
E value
Match length
                  67
% identity
                  61
                  (AJ004810) cytochrome P450 monooxygenase [Zea mays]
NCBI Description
                  293457
Seq. No.
                  LIB3066-008-Q1-K1-F5
Seq. ID
Method
                  BLASTN
                  g1498596
NCBI GI
BLAST score
                  56
                  8.0e-23
E value
                  96
Match length
                  90
% identity
NCBI Description Zea mays phospholipid transfer protein mRNA, complete cds
                   293458
Seq. No.
                  LIB3066-008-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                   g2829871
NCBI GI
BLAST score
                   193
                  1.0e-14
E value
Match length
                   84
% identity
                   52
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]
```

40946

293459

BLASTX

LIB3066-008-Q1-K1-F7

Seq. No. Seq. ID

Method

BLAST score

Match length

E value

148

60

2.0e-09



```
g1498597
NCBI GI
                  291
BLAST score
                  2.0e-26
E value
Match length
                  94
% identity
                  64
NCBI Description (U66105) phospholipid transfer protein [Zea mays]
Seq. No.
                  293460
                  LIB3066-008-Q1-K1-H2
Seq. ID
Method
                  BLASTX
                  g2832632
NCBI GI
                  174
BLAST score
                  1.0e-12
E value
Match length
                  77
% identity
                  49
NCBI Description (AL021711) hypothetical protein [Arabidopsis thaliana]
                  293461
Seq. No.
                  LIB3066-009-Q1-K1-A2
Seq. ID
Method
                  BLASTX
                  g2598589
NCBI GI
BLAST score
                  240
                  3.0e-20
E value
Match length
                  130
% identity
                  41
NCBI Description (Y15367) MtN19 [Medicago truncatula]
Seq. No.
                  293462
                  LIB3066-009-Q1-K1-B2
Seq. ID
Method
                  BLASTX
                  g2244785
NCBI GI
BLAST score
                  195
                  4.0e-15
E value
                  109
Match length
% identity
                  42
NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]
                  293463
Seq. No.
                  LIB3066-009-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2500980
BLAST score
                  206
                  3.0e-30
E value
Match length
                  95
% identity
                  79
                  GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE) (GLURS)
NCBI Description
                  >gi_1076718_pir__S51684 glutamate--tRNA ligase (EC
                  6.1.1.17) precursor - barley >gi_603849_emb_CAA58505_
                  (X83523) glutamate--tRNA ligase [Hordeum vulgare]
Seq. No.
                  293464
Seq. ID
                  LIB3066-009-01-K1-C4
Method
                  BLASTX
NCBI GI
                  g22422
```



```
% identity
NCBI Description
                  (X57743) polygalacturonase [Zea mays]
                  293465
Seq. No.
                  LIB3066-009-Q1-K1-E4
Seq. ID
Method
                  BLASTN
                  g1532072
NCBI GI
BLAST score
                  63
                  6.0e-27
E value
                  131
Match length
                  87
% identity
NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase
Seq. No.
                  293466
                  LIB3066-009-Q1-K1-F10
Seq. ID
                  BLASTX
Method
                  g2444176
NCBI GI
                  550
BLAST score
                  1.0e-56
E value
Match length
                  141
                  73
% identity
NCBI Description (U94782) unconventional myosin [Helianthus annuus]
                  293467
Seq. No.
Seq. ID
                  LIB3066-009-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g4586038
                  292
BLAST score
                  1.0e-26
E value
Match length
                  91
% identity
                  60
                  (AC007109) putative heat shock protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  293468
                  LIB3066-009-Q1-K1-G11
Seq. ID
Method
                  BLASTN
                  g600117
NCBI GI
BLAST score
                  78
E value
                  8.0e-36
Match length
                  181
% identity
NCBI Description Z.mays (B73) gene for extensin-like protein
Seq. No.
                  293469
                  LIB3066-009-Q1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2494151
BLAST score
                  171
                  4.0e-12
E value
Match length
                  50
                  64
% identity
```

NCBI Description DNAJ PROTEIN >gi_2119734_pir__JC4739 chaperonin dnaJ - Bacillus stearothermophilus >gi_1568475_emb_CAA62240_

(X90709) dnaJ [Bacillus stearothermophilus]

Seq. No. 293470



```
LIB3066-010-Q1-K1-B6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
                  5.0e-11
E value
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  293471
Seq. No.
                  LIB3066-010-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3608479
BLAST score
                  246
                  6.0e-21
E value
Match length
                  66
                  71
% identity
                  (AF088912) ribosomal protein L15 [Petunia x hybrida]
NCBI Description
Seq. No.
                  293472
                  LIB3066-010-Q1-K1-D2
Seq. ID
Method
                  BLASTN
                  g3821780
NCBI GI
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  293473
Seq. No.
Seq. ID
                  LIB3066-010-Q1-K1-E10
Method
                  BLASTX
                  g416731
NCBI GI
BLAST score
                  330
E value
                  9.0e-31
Match length
                  62
                  98
% identity
                  POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi 82655 pir JQ1107
NCBI Description
                  18.3K protein precursor, pollen - maize
                  >gi 255569 bbs 113677 (S44171) pollen specific protein [Zea
                  mays=corn, Peptide, 170 aa] [Zea mays]
                  >gi_1588669_prf__2209273A Zm13 [Zea mays]
Seq. No.
                  293474
                  LIB3066-010-Q1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1723328
BLAST score
                  386
E value
                  1.0e-37
                  94
Match length
% identity
                  74
NCBI Description
                  HYPOTHETICAL 54.4 KD PROTEIN YCF24 (ORF487)
                  >gi_2147530_pir__S73161 hypothetical protein 24 - Porphyra
```

purpurea chloroplast >gi 1276706 (U38804) hypothetical

chloroplast ORF 24. [Porphyra purpurea]

Seq. No. 293475



```
Seq. ID
                   LIB3066-010-Q1-K1-F8
Method
                   BLASTN
NCBI GI
                   a22421
BLAST score
                   52
                   1.0e-20
E value
Match length
                   140
% identity
                   84
NCBI Description Z.mays mRNA for polygalacturonase (clone PG3)
Seq. No.
                   293476
                   LIB3066-010-Q1-K1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1769897
BLAST score
                   152
E value
                   4.0e-10
Match length
                   109
% identity
                   32
NCBI Description (Y08010) lectin receptor kinase [Arabidopsis thaliana]
                   293477
Seq. No.
Seq. ID
                   LIB3066-010-Q1-K1-H6
Method
                   BLASTX
NCBI GI
                   g2231702
BLAST score
                   298
E value
                   4.0e-27
Match length
                   79
% identity
                   68
                   (U92086) clathrin assembly protein AP19 homolog [Arabidopsis thaliana] >gi_3080409_emb_CAA18728.1_
NCBI Description
                    (AL022604) clathrin assembly protein AP19 homolog
                   [Arabidopsis thaliana]
Seq. No.
                   293478
Seq. ID
                   LIB3066-011-Q1-K1-B7
Method
                   BLASTX
NCBI GI
                   g3869190
BLAST score
                   216
                   1.0e-17
E value
Match length
                   69
% identity
                   58
NCBI Description
                   (AB005746) inorganic phosphate transporter [Arabidopsis
                   thaliana]
Seq. No.
                   293479
Seq. ID
                   LIB3066-011-Q1-K1-D6
Method
                   BLASTX
NCBI GI
                   g2398679
BLAST score
                   528
E value
                   6.0e-54
Match length
                   130
% identity
                   80
NCBI Description
                   (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate
```

synthase [Morinda citrifolia]

Seq. No. 293480

Seq. ID LIB3066-011-Q1-K1-E6

Method BLASTX



```
NCBI GI
                  g112994
BLAST score
                  424
E value
                  9.0e-42
Match length
                  86
% identity
                  98
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >gi 82685 pir S04536 embryonic abundant protein,
                  glycine-rich - maize >gi 22313 emb CAA31077 (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi 226091 prf _1410284A abscisic acid inducible gene [Zea
                  mays]
                  293481
Seq. No.
Seq. ID
                  LIB3066-011-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g464470
BLAST score
                  231
E value
                  4.0e-40
                  91
Match length
% identity
                  93
                  PROFILIN 3 >gi 422033 pir S35798 profilin 3 - maize
NCBI Description
                  >gi 313142 emb CAA51720 (X73281) profilin 3 [Zea mays]
                  293482
Seq. No.
Seq. ID
                  LIB3066-011-Q1-K1-F2
Method
                  BLASTX
                  g3395938
NCBI GI
BLAST score
                  171
                  3.0e-12
E value
Match length
                  56
                  66
% identity
                  (AF076924) polypyrimidine tract-binding protein homolog
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  293483
                  LIB3066-011-Q1-K1-G4
Seq. ID
Method
                  BLASTN
                  g1185553
NCBI GI
BLAST score
                  38
                  2.0e-12
E value
Match length
                  43
% identity
                  53
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2)
NCBI Description
                  gene, complete cds
                  293484
Seq. No.
Seq. ID
                  LIB3066-011-Q1-K1-G7
Method
                  BLASTN
NCBI GI
                  q602605
BLAST score
                  48
E value
                  7.0e-18
Match length
                  92
% identity
                  88
NCBI Description Zea mays tandem genes for alphal-tubulin and alpha2-tubulin
```

Seq. No. 293485

Seq. ID LIB3066-012-Q1-K1-A8

NCBI GI

E value

BLAST score

g548493

6.0e-12

168

```
20 (Managarovota )
```

```
Method
                  BLASTX
NCBI GI
                  q4204258
BLAST score
                  162
E value
                  4.0e-11
Match length
                  55
                  56
% identity
NCBI Description
                  (AC005223) 14409 [Arabidopsis thaliana]
                  293486
Seq. No.
Seq. ID
                  LIB3066-012-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g1304270
BLAST score
                  145
                  4.0e-09
E value
                  102
Match length
% identity
                  34
NCBI Description (D45189) plasma membrane H+-ATPase [Zostera marina]
Seq. No.
                  293487
                  LIB3066-012-Q1-K1-C3
Seq. ID
Method
                  BLASTX
                  g4388726
NCBI GI
BLAST score
                  330
E value
                  8.0e-31
Match length
                  105
% identity
                  61
                  (AC006413) putative 12-oxophytodienoate-10,11-reductase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  293488
Seq. ID
                  LIB3066-012-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  q3108053
BLAST score
                  147
E value
                  2.0e-10
Match length
                  80
% identity
NCBI Description
                  (AF056326) myo-inositol 1-phosphate synthase; INO1 [Zea
                  mays]
Seq. No.
                  293489
Seq. ID
                  LIB3066-012-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  g4204313
BLAST score
                  234
E value
                  1.0e-19
Match length
                  103
% identity
                  51
                   (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  293490
Seq. No.
Seq. ID
                  LIB3066-012-Q1-K1-H4
Method
                  BLASTX
```



```
Match length
                  71
                  54
% identity
                  EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                  (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi_629854_pir__S30067 polygalacturonase - maize
                  >gi_288612_emb_CAA47052_ (X66422) polygalacturonase [Zea
                  mays]
                  293491
Seq. No.
                  LIB3066-012-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4581150
BLAST score
                  163
E value
                  3.0e-11
Match length
                  56
                  61
% identity
NCBI Description (AC006919) hypothetical protein [Arabidopsis thaliana]
                  293492
Seq. No.
                  LIB3066-013-Q1-K1-B1
Seq. ID
Method
                  BLASTX
                  g3831443
NCBI GI
BLAST score
                  149
E value
                  1.0e-09
Match length
                  64
                  45
% identity
                  (AC005819) putative auxin-regulated protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  293493
                  LIB3066-013-Q1-K1-B12
Seq. ID
Method
                  BLASTX
                  g4218991
NCBI GI
BLAST score
                  390
E value
                  1.0e-39
Match length
                  137
% identity
                  61
                  (AF098632) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  293494
                  LIB3066-013-Q1-K1-C4
Seq. ID
Method
                  BLASTX
                  g3355487
NCBI GI
BLAST score
                  154
E value
                  3.0e-10
                  89
Match length
% identity
                  37
NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]
Seq. No.
                  293495
Seq. ID
                  LIB3066-013-Q1-K1-E7
```

Method BLASTN NCBI GI q22458 BLAST score 126 E value 1.0e-64 Match length 233 % identity 88

```
Z.mays pollen specific mRNA C-terminal (clone 4H7)
NCBI Description
                  293496
Seq. No.
                  LIB3066-013-Q1-K1-F2
Seq. ID
                  BLASTN
Method
                  q22458
NCBI GI
BLAST score
                  168
                  1.0e-89
E value
Match length
                  248
                  93
% identity
                  Z.mays pollen specific mRNA C-terminal (clone 4H7)
NCBI Description
Seq. No.
                  293497
                  LIB3066-013-Q1-K1-F7
Seq. ID
Method
                  BLASTX
                  q2262105
NCBI GI
                  172
BLAST score
                   2.0e-12
E value
Match length
                  84
                  36
% identity
                  (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
                  293498
Seq. No.
Seq. ID
                  LIB3066-013-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                   q3341697
                   276
BLAST score
E value
                   2.0e-24
Match length
                  110
% identity
                   54
                  (AC003672) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   293499
Seq. No.
Seq. ID
                  LIB3066-014-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                   q2245066
BLAST score
                   302
E value
                   2.0e-27
Match length
                   145
% identity
                   46
NCBI Description
                  (Z97342) Beta-Amylase [Arabidopsis thaliana]
                   293500
Seq. No.
Seq. ID
                   LIB3066-014-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   q729944
BLAST score
                   343
E value
                   2.0e-32
Match length
                   74
% identity
                   86
                  POLLEN ALLERGEN ZEA M 1 (ZEA M I) >qi 478272 pir JC1524
NCBI Description
                  major allergen mI protein - maize >gi_293902 (L14271) Zea
```

Seq. No. 293501 Seq. ID LIB3066-014-Q1-K1-C7

mI [Zea mays]

Method BLASTX

E value

Match length

8.0e-49

130



```
- NCBI GI
                    g2230955
 BLAST score
                    143
                    3.0e-09
 E value
                    45
 Match length
                    58
 % identity
                   (Y11268) endo-1,4-beta-D-glucanase [Lycopersicon
 NCBI Description
                    esculentum]
                    293502
 Seq. No.
                    LIB3066-014-Q1-K1-D5
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g3821780
 BLAST score
                    36
 E value
                    1.0e-10
 Match length
                    36
                    100
 % identity
 NCBI Description Xenopus laevis cDNA clone 27A6-1
 Seq. No.
                    293503
                    LIB3066-014-Q1-K1-E11
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g134598
 BLAST score
                    452
 E value
                    5.0e-45
 Match length
                    101
 % identity
                    86
 NCBI Description SUPEROXIDE DISMUTASE-4AP (CU-ZN)
                    293504
 Seq. No.
                    LIB3066-014-Q1-K1-E3
 Seq. ID
                    BLASTN
 Method
                    g1061305
 NCBI GI
 BLAST score
                    68
 E value
                    8.0e-30
 Match length
                    177
                    84
 % identity
 NCBI Description Z.mays Dof2 mRNA
                    293505
 Seq. No.
 Seq. ID
                    LIB3066-014-Q1-K1-E9
 Method
                    BLASTX
 NCBI GI
                    q3548802
 BLAST score
                    527
                    7.0e-54
 E value
 Match length
                    136
 % identity
                    (AC005313) axi 1-like protein [Arabidopsis thaliana]
 NCBI Description
                    >gi 4335769 gb AAD17446 (AC006284) putative axil protein
                    [Nicotiana tabacum] [Arabidopsis thaliana]
 Seq. No.
                    293506
 Seq. ID
                    LIB3066-014-Q1-K1-F10
 Method
                    BLASTX
 NCBI GI
                    g1899188
 BLAST score
                    484
```

NCBI Description

```
% identity
NCBI Description
                  (U90212) DNA binding protein ACBF [Nicotiana tabacum]
Seq. No.
                  293507
Seq. ID
                  LIB3066-014-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  q226683
                  754
BLAST score
                  2.0e-80
E value
Match length
                  149
% identity
                  94
NCBI Description photosystem II 43kD protein [Oryza sativa]
                  293508
Seq. No.
Seq. ID
                  LIB3066-014-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  q3746431
BLAST score
                  333
                  3.0e-31
E value
Match length
                  63
% identity
                  98
NCBI Description
                  (AF038585) pyruvate dehydrogenase kinase isoform 1; PDK1
                  [Zea mays]
Seq. No.
                  293509
Seq. ID
                  LIB3066-015-Q1-K1-A6
Method
                  BLASTN
NCBI GI
                  g4140643
BLAST score
                  44
                  2.0e-15
E value
Match length
                  82
                  88
% identity
NCBI Description
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
                  complete sequence
Seq. No.
                  293510
Seq. ID
                  LIB3066-015-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  q1345587
BLAST score
                  458
E value
                  9.0e - 46
Match length
                  96
% identity
                  97
NCBI Description
                  14-3-3-LIKE PROTEIN GF14-6 >gi 998430 bbs 164522 (S77133)
                  GF14-6=14-3-3 protein homolog [Zea mays, XL80, Peptide, 261
                  aa] [Zea mays]
Seq. No.
                  293511
Seq. ID
                  LIB3066-015-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g322794
BLAST score
                  169
                  5.0e-12
E value
Match length
                  52
% identity
                  65
```

40956

potato >gi_21599_emb CAA79357 (Z18924)

UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -



UTP--glucose-1-phosphate uridylyltransferase [Solanum tuberosum]

Seq. No. 293512 Seq. ID LIB3066-

Seq. ID LIB3066-015-Q1-K1-H10

Method BLASTX
NCBI GI g1947137
BLAST score 203
E value 7.0e-16
Match length 127
% identity 31

NCBI Description (AF000264) similar to the ATP-binding transport protein

family (ABC transporters). [Caenorhabditis elegans]

Seq. No. 293513

Seq. ID LIB3066-016-Q1-K1-A12

Method BLASTX
NCBI GI g3256066
BLAST score 250
E value 1.0e-21
Match length 90
% identity 62

NCBI Description (Y13987) chloroplast NAD-MDH [Arabidopsis thaliana]

Seq. No. 293514

Seq. ID LIB3066-016-Q1-K1-A3

Method BLASTN
NCBI GI g433041
BLAST score 148
E value 1.0e-77
Match length 321
% identity 88

NCBI Description Zea mays W-22 clone PREM-1B retroelement PREM-1, partial

sequence

Seq. No. 293515

Seq. ID LIB3066-016-Q1-K1-A4

Method BLASTX
NCBI GI g4101703
BLAST score 267
E value 2.0e-23
Match length 107
% identity 45

NCBI Description (AF006078) glucose acyltransferase [Solanum berthaultii]

Seq. No. 293516

Seq. ID LIB3066-016-Q1-K1-B12

Method BLASTX
NCBI GI g133724
BLAST score 296
E value 9.0e-27
Match length 97
% identity 51

NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S11

>gi_1363597_pir__S58584 ribosomal protein S11 - maize
chloroplast >gi_552742 (M35831) ribosomal protein S11
(rpS11) [Zea mays] >gi_902254_emb_CAA60318_ (X86563)

Match length

39



ribosomal protein S11 [Zea mays]

```
Seq. No.
                   293517
                  LIB3066-016-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2494174
BLAST score
                   330
E value
                   9.0e-43
Match length
                   104
                   88
% identity
                  GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi 497979 (U10034)
NCBI Description
                   glutamate decarboxylase [Arabidopsis thaliana]
Seq. No.
                   293518
Seq. ID
                  LIB3066-016-Q1-K1-C8
Method
                  BLASTX
                   g3548802
NCBI GI
BLAST score
                   399
E value
                   6.0e-39
Match length
                   119
% identity
                   63
NCBI Description
                   (AC005313) axi 1-like protein [Arabidopsis thaliana]
                   >gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein
                   [Nicotiana tabacum] [Arabidopsis thaliana]
Seq. No.
                   293519
Seq. ID
                  LIB3066-016-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                   g416731
BLAST score
                   311
                   2.0e-28
E value
Match length
                  79
% identity
                   80
NCBI Description
                  POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi_82655_pir__JQ1107
                   18.3K protein precursor, pollen - maize
                   >gi_255569_bbs_113677 (S44171) pollen specific protein [Zea
                  mays=corn, Peptide, 170 aa] [Zea mays]
                   >gi 1588669 prf 2209273A Zm13 [Zea mays]
Seq. No.
                   293520
Seq. ID
                  LIB3066-016-01-K1-D2
Method
                  BLASTN
NCBI GI
                   g2340107
BLAST score
                   92
E value
                   3.0e-44
Match length
                   116
% identity
                   95
NCBI Description
                  Zea mays starch branching enzyme IIa (Sbe2a) mRNA, partial
Seq. No.
                   293521
Seq. ID
                  LIB3066-016-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  g2982459
BLAST score
                  157
E value
                  2.0e-10
```



```
% identity
NCBI Description
                  (AL022223) putative protein [Arabidopsis thaliana]
                  293522
Seq. No.
                  LIB3066-016-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4558557
BLAST score
                  166
                   6.0e-20
E value
                  109
Match length
                  43
% identity
                   (AC007138) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                  293523
Seq. No.
Seq. ID
                  LIB3066-016-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  g3928758
BLAST score
                  152
                  8.0e-10
E value
                   65
Match length
                   51
% identity
                   (AB007987) Lipoic acid synthase [Arabidopsis thaliana]
NCBI Description
                  >gi_4454462_gb_AAD20909_ (AC006234) putative lipoic acid
                   synthase [Arabidopsis thaliana]
                   293524
Seq. No.
                  LIB3066-016-Q1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3059131
                   173
BLAST score
                   2.0e-12
E value
                   63
Match length
% identity
                   52
                  (AJ000478) cytochrome P450 [Helianthus tuberosus]
NCBI Description
Seq. No.
                   293525
                   LIB3066-016-Q1-K1-H2
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1808687
BLAST score
                   82
                   3.0e-38
E value
Match length
                   283
                   79
% identity
NCBI Description S.stapfianus pSD.13 mRNA
Seq. No.
                   293526
Seq. ID
                   LIB3066-016-Q1-K1-H9
Method
                   BLASTX
```

NCBI GI q1360141 BLAST score 181 3.0e-13 E value 92 Match length 43 % identity

(X97980) protein kinase [Solanum berthaultii] NCBI Description

293527 Seq. No.

BLAST score

E value

449

5.0e-46



```
Seq. ID
                  LIB3066-017-01-K1-A5
Method
                  BLASTX
NCBI GI
                  q4585142
                   369
BLAST score
                  1.0e-35
E value
                  99
Match length
% identity
                   67
                  (AF088276) NADPH oxidase; gp91; phox homolog [Lycopersicon
NCBI Description
                  esculentum]
Seq. No.
                  293528
Seq. ID
                  LIB3066-017-Q1-K1-A6
Method
                  BLASTX
                  g3252807
NCBI GI
BLAST score
                  219
                  1.0e-17
E value
Match length
                  111
% identity
                   46
                  (AC004705) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   293529
Seq. No.
                  LIB3066-017-Q1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1903347
BLAST score
                   376
                  3.0e-36
E value
Match length
                  120
% identity
                   57
NCBI Description
                   (AC000104) EST qb ATTS5672 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   293530
Seq. ID
                  LIB3066-017-Q1-K1-C6
Method
                  BLASTN
NCBI GI
                   q3821780
BLAST score
                   36
E value
                   1.0e-10
Match length
                   36
% identity
                   100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   293531
Seq. No.
Seq. ID
                  LIB3066-017-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                   g4006913
                   292
BLAST score
E value
                   2.0e-26
Match length
                  111
% identity
                   50
                  (Z99708) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  293532
Seq. No.
Seq. ID
                  LIB3066-017-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g4006913
```

```
Match length
                  127
% identity
                  71
                  (Z99708) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  293533
Seq. No.
                  LIB3066-017-Q1-K1-D2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4417291
BLAST score
                  169
                  3.0e-18
E value
                  75
Match length
                  52
% identity
                  (AC007019) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  293534
                  LIB3066-017-Q1-K1-D8
Seq. ID
                  BLASTN
Method
                  g288378
NCBI GI
                  79
BLAST score
                                                      , "
                  1.0e-36
E value
                  155
Match length
                  88
% identity
NCBI Description Z.mays gene PG for polygalacturonase
                  293535
Seq. No.
                  LIB3066-017-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2147484
BLAST score
                  446
                  7.0e-45
E value
                  112
Match length
                  86
% identity
                  homeotic protein - Phalaenopsis sp >gi_1173622 (U34743)
NCBI Description
                  homeobox protein [Phalaenopsis sp. 'hybrid SM9108']
                  293536
Seq. No.
                  LIB3066-017-Q1-K1-F10
Seq. ID
Method
                  BLASTX
                  q3063449
NCBI GI
BLAST score
                   358
E value
                   4.0e-34
Match length
                  102
                   68
% identity
                  (AC003981) F22013.11 [Arabidopsis thaliana]
NCBI Description
                  293537
Seq. No.
                  LIB3066-017-Q1-K1-G2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g21856
BLAST score
                   55
```

E value 4.0e-22 Match length 163 % identity

NCBI Description Wheat rDNA 25S-18S intergenic region EcoRI-BamHI fragment

Seq. No. 293538

LIB3066-017-Q1-K1-G3 Seq. ID



```
Method
                  BLASTX
                  g4539295
NCBI GI
                  146
BLAST score
                  4.0e-09
E value
                  36
Match length
                  75
% identity
                  (AL049480) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  293539
                  LIB3066-017-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3281853
BLAST score
                  335
                  3.0e-31
E value
Match length
                  89
% identity
                  71
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                  293540
Seq. No.
                  LIB3066-017-Q1-K1-H5
Seq. ID
Method
                  BLASTX
                  g548493
NCBI GI
BLAST score
                  616
                  3.0e-64
E value
Match length
                  131
% identity
                  90
NCBI Description
                  EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
                  (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi_629854_pir__S30067 polygalacturonase - maize
                  >gi_288612_emb_CAA47052_ (X66422) polygalacturonase [Zea
                  mays]
                  293541
Seq. No.
                  LIB3066-017-Q1-K1-H9
Seq. ID
Method
                  BLASTX
                  g3461845
NCBI GI
BLAST score
                  318
                  2.0e-29
E value
                  99
Match length
% identity
                  68
NCBI Description (AC005315) hypothetical protein [Arabidopsis thaliana]
                  293542
Seq. No.
                  LIB3066-018-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548493
BLAST score
                  296
E value
                  6.0e-27
Match length
                  101
                  53
% identity
NCBI Description
                  EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
                   (GALACTURAN 1, 4-ALPHA-GALACTURONIDASE)
                  >gi_629854_pir__S30067 polygalacturonase - maize
                  >gi 288612 emb CAA47052 (X66422) polygalacturonase [Zea
                  mays]
```

Seq. No. 293543

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The second secon
```

```
LIB3066-018-Q1-K1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2832632
BLAST score
                   241
                   1.0e-20
E value
Match length
                   91
                   52
% identity
NCBI Description (AL021711) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   293544
                   LIB3066-018-Q1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3420057
BLAST score
                   170
                   5.0e-12
E value
Match length
                   63
% identity
                   52
                  (AC004680) putative ABC transporter [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   293545
                   LIB3066-018-Q1-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1362008
BLAST score
                   382
E value
                   5.0e-37
Match length
                   104
% identity
                   18
NCBI Description ubiquitin-like protein 12 - Arabidopsis thaliana
Seq. No.
                   293546
                   LIB3066-018-Q1-K1-D4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g293901
BLAST score
                   41
                   8.0e-14
E value
Match length
                   49
% identity
                   96
NCBI Description Zea mays Zea mI gene, complete cds
Seq. No.
                   293547
                   LIB3066-018-Q1-K1-D5
Seq. ID
Method
                   BLASTX
                   g283049
NCBI GI
BLAST score
                   271
E value
                   2.0e-24
Match length
                   64
% identity
NCBI Description
                   polygalacturonase (EC 3.2.1.15) precursor (clone W2247) -
                   maize (fragment) >gi_481079_pir__S37718 polygalacturonase -
                   maize >gi_22426_emb_CAA44248_ (X62384) polygalacturonase
                   [Zea mays] >gi_\(\bar{2}878\)\(\bar{3}0\)\(\ext{emb}_CA\(\bar{A}47234\)\(\text{\(X66692\)\)}
                   polygalacturonase [Zea mays]
```

Seq. No. 293548

Seq. ID LIB3066-018-Q1-K1-D8

Method BLASTN NCBI GI g293901

```
BLAST score
                  2.0e-57
E value
                  129
Match length
% identity
                  98
NCBI Description Zea mays Zea mI gene, complete cds
                  293549
```

Seq. No. Seq. ID LIB3066-018-Q1-K1-E2

Method BLASTN NCBI GI g313139 BLAST score 179 E value 4.0e-96 Match length 237 93 % identity

Z.mays ZmPRO2 mRNA for profilin NCBI Description

293550 Seq. No. Seq. ID

LIB3066-018-Q1-K1-F1 Method BLASTN

NCBI GI g3821780 BLAST score 36 1.0e-10 E value Match length 48 % identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

293551 Seq. No.

Seq. ID LIB3066-018-Q1-K1-H2

Method BLASTX NCBI GI q509810 BLAST score 358 E value 3.0e-34 Match length 104 % identity 65

NCBI Description (L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No. 293552

Seq. ID LIB3066-019-Q1-K1-A5

Method BLASTX NCBI GI g3738297 BLAST score 319 1.0e-29 E value Match length 94 % identity 32

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. Seq. ID 293553

LIB3066-019-Q1-K1-B7

Method BLASTX NCBI GI g3702351 BLAST score 263 6.0e-23 E value Match length 89 53 % identity

(AC005397) putative desiccation protectant protein NCBI Description

[Arabidopsis thaliana]



```
293554
Seq. No.
                  LIB3066-019-Q1-K1-E6
Seq. ID
                  {\tt BLASTN}
Method
NCBI GI
                  g3821780
BLAST score
                  36
                  5.0e-11
E value
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  293555
Seq. No.
                  LIB3066-019-Q1-K1-G10
Seq. ID
                  BLASTN
Method
NCBI GI
                   g3821780
BLAST score
                   36
                   4.0e-11
E value
                   36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   293556
Seq. No.
                  LIB3066-019-Q1-K1-H6
Seq. ID
                   BLASTX
Method
                   g4099919
NCBI GI
BLAST score
                   169
                   4.0e-12
E value
                   32
Match length
% identity
                   88
                  (U91981) pollen allergen homolog [Triticum aestivum]
NCBI Description
                   293557
Seq. No.
                   LIB3066-020-Q1-K1-A11
Seq. ID
                   BLASTN
Method
                   g3821780
NCBI GI
BLAST score
                   36
                   6.0e-11
E value
                   48
Match length
                   67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   293558
                   LIB3066-020-Q1-K1-B10
Seq. ID
Method
                   BLASTX
                   g1706260
NCBI GI
BLAST score
                   335
E value
                   2.0e-31
Match length
                   111
% identity
                   60
NCBI Description
                   CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir S59597
                   cysteine proteinase 1 precursor - maize
                   >gi 643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
                   mays]
```

Seq. No. 293559

Seq. ID LIB3066-020-Q1-K1-B11

Method BLASTX NCBI GI g2444180



```
BLAST score
E value
                  1.0e-45
                  149
Match length
                  58
% identity
                  (U94785) unconventional myosin [Helianthus annuus]
NCBI Description
                  293560
Seq. No.
                  LIB3066-020-Q1-K1-C2
Seq. ID
Method
                  BLASTX
                  g3256035
NCBI GI
BLAST score
                  302
E value
                  8.0e-28
Match length
                  91
% identity
                  60
                  (Y14274) putative serine/threonine protein kinase [Sorghum
NCBI Description
                  bicolor]
Seq. No.
                  293561
                  LIB3066-020-Q1-K1-C3
Seq. ID
Method
                  BLASTX
                  g3256035
NCBI GI
                  199
BLAST score
E value
                  9.0e-16
Match length
                  84
% identity
                  49
                  (Y14274) putative serine/threonine protein kinase [Sorghum
NCBI Description
                  bicolor]
                  293562
Seq. No.
                  LIB3066-020-Q1-K1-C4
Seq. ID
                  BLASTN
Method
                  g2062705
NCBI GI
BLAST score
                  36
E value
                  4.0e-11
                  36
Match length
% identity
                  100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  293563
                  LIB3066-020-Q1-K1-D10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g342616
BLAST score
                  39
E value
                  1.0e-12
Match length
                  155
                  82
% identity
                  Maize chloroplast ribosomal protein S12 gene, exons 2 and
NCBI Description
                  3, and ribosomal protein S7 gene, complete cds
Seq. No.
                  293564
                  LIB3066-020-Q1-K1-D8
Seq. ID
                  BLASTX
Method
                  g2244866
NCBI GI
BLAST score
                  254
                  5.0e-22
E value
Match length
                  87
```

40966

61

% identity

BLAST score

Match length

% identity

E value

64

131

44

2.0e-27



```
(Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  293565
                  LIB3066-020-Q1-K1-E12
Seq. ID
Method
                  BLASTX
                  g531829
NCBI GI
BLAST score
                  145
E value
                  2.0e-09
                  68
Match length
                  50
% identity
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
Seq. No.
                  293566
                  LIB3066-020-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g548493
BLAST score
                  229
                  5.0e-19
E value
Match length
                  107
% identity
                  49
                  EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                  (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi_629854_pir__S30067 polygalacturonase - maize
                  >gi_288612_emb_CAA47052_ (X66422) polygalacturonase [Zea
                  mays]
                  293567
Seq. No.
                  LIB3066-020-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462925
BLAST score
                  264
E value
                  3.0e-23
Match length
                  83
% identity
                  66
NCBI Description
                  (AJ000053) GTP cyclohydrolase II /
                  3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis
                  thaliana]
Seq. No.
                  293568
                  LIB3066-021-Q1-K1-B2
Seq. ID
Method
                  BLASTX
                  g2688830
NCBI GI
                  204
BLAST score
E value
                  3.0e-16
Match length
                  87
% identity
                  54
NCBI Description (AF000952) putative sugar transporter [Prunus armeniaca]
                  293569
Seq. No.
Seq. ID
                  LIB3066-021-Q1-K1-B3
Method
                  BLASTN
NCBI GI
                  q1185553
```

```
NCBI Description
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2)
                  gene, complete cds
                  293570
Seq. No.
                  LIB3066-021-Q1-K1-C4
Seq. ID
Method
                  BLASTX
                  g629852
NCBI GI
BLAST score
                  258
                  5.0e-29
E value
Match length
                  86
                  85
% identity
NCBI Description
                  polygalacturonase - maize >gi_288367_emb_CAA46680_ (X65845)
                  polygalacturonase [Zea mays]
                  293571
Seq. No.
                  LIB3066-021-Q1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4138914
BLAST score
                  145
                  3.0e-09
E value
Match length
                  94
                  36
% identity
NCBI Description
                  (AF059488) expansin precursor [Lycopersicon esculentum]
Seq. No.
                  293572
Seq. ID
                  LIB3066-021-Q1-K1-F5
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  36
E value
                  6.0e-11
Match length
                  36
                  100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  293573
Seq. ID
                  LIB3066-021-Q1-K1-F9
Method
                  BLASTN
NCBI GI
                  q313139
BLAST score
                  119
E value
                  3.0e-60
Match length
                  243
% identity
                  88
NCBI Description Z.mays ZmPRO2 mRNA for profilin
```

Seq. No. 293574

Seq. ID LIB3066-021-Q1-K1-G7

Method BLASTX NCBI GI q1502430 BLAST score 347 E value 8.0e-33 Match length 103

% identity NCBI Description

(U62331) phosphate transporter [Arabidopsis thaliana] >gi 2564661 (AF022872) phosphate transporter [Arabidopsis thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770)

phosphate transporter, AtPT2 [Arabidopsis thaliana]

Method

NCBI GI

BLASTX

g4455334

```
293575
Seq. No.
                  LIB3066-021-Q1-K1-H2
Seq. ID
Method
                  BLASTX
                  g3152590
NCBI GI
                  172
BLAST score
                  2.0e-12
E value
Match length
                  64
% identity
                  58
                   (AC002986) Similar to protein serine/threonine kinase NPK15
NCBI Description
                  gb D31737 from Nicotiana tabacum. [Arabidopsis thaliana]
                  293576
Seq. No.
Seq. ID
                  LIB3066-021-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  q3047098
BLAST score
                  253
                  5.0e-22
E value
                  93
Match length
% identity
                  53
NCBI Description
                  (AF058826) similar to eukaryotic protein kinase domains
                   (Pfam: pkinase.hmm, score: 171.43) [Arabidopsis thaliana]
                  293577
Seq. No.
Seq. ID
                  LIB3066-022-Q1-K1-A12
                  BLASTX
Method
NCBI GI
                  g1617274
BLAST score
                  262
                  2.0e-28
E value
                  141
Match length
% identity
                   46
                  (Z72152) AMP-binding protein [Brassica napus]
NCBI Description
                  293578
Seq. No.
                  LIB3066-022-Q1-K1-A9
Seq. ID
Method
                  BLASTX
                   g2088649
NCBI GI
BLAST score
                   205
E value
                   4.0e-16
Match length
                   68
% identity
                   56
                  (AF002109) unknown protein [Arabidopsis thaliana]
NCBI Description
                   293579
Seq. No.
                  LIB3066-023-Q1-K1-A12
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
E value
                   1.0e-10
Match length
                   36
% identity
                   100
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   293580
Seq. No.
Seq. ID
                  LIB3066-023-Q1-K1-A3
```

```
BLAST score
                  189
                  4.0e-14
E value
Match length
                  105
% identity
                  40
NCBI Description
                  (AL035525) myosin-like protein [Arabidopsis thaliana]
Seq. No.
                  293581
Seq. ID
                  LIB3066-023-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  g3510540
BLAST score
                  289
E value
                  7.0e-26
Match length
                  136
% identity
                  51
NCBI Description
                  (AF038815) expansin [Prunus armeniaca]
Seq. No.
                  293582
Seq. ID
                  LIB3066-023-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  g112994
BLAST score
                  335
E value
                  2.0e-31
Match length
                  77
% identity
                  90
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi 226091 prf 1410284A abscisic acid inducible gene [Zea
                  mays]
Seq. No.
                  293583
Seq. ID
                  LIB3066-023-Q1-K1-D1
Method
                  BLASTN
NCBI GI
                  g4185305
BLAST score
                  36
E value
                  1.0e-10
Match length
                  40
% identity
                  97
NCBI Description
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
                   (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes
                  293584
Seq. No.
Seq. ID
                  LIB3066-023-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  q4220527
BLAST score
                  146
                  3.0e-09
E value
                  127
Match length
% identity
                  31
```

NCBI Description

(AL035356) putative protein [Arabidopsis thaliana]

293585 Seq. No.

Seq. ID LIB3066-023-Q1-K1-F6

Method BLASTX

BLAST score

Match length

E value

363

108

1.0e-34

```
NCBI GI
                  g2911073
BLAST score
                  482
                  1.0e-48
E value
                  128
Match length
% identity
                  68
NCBI Description
                  (AL021960) putative protein [Arabidopsis thaliana]
                  293586
Seq. No.
Seq. ID
                  LIB3066-023-Q1-K1-G12
Method
                  BLASTN
NCBI GI
                  g2832242
BLAST score
                  43
E value
                  7.0e-15
Match length
                  95
% identity
                  86
NCBI Description
                  Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.
                  293587
Seq. ID
                  LIB3066-023-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  g231509
BLAST score
                  484
E value
                  8.0e-49
Match length
                  115
% identity
NCBI Description
                  ACTIN DEPOLYMERIZING FACTOR (ADF) >gi_419809_pir__$30935
                  actin-depolymerizing factor - trumpet lily
                  >gi_22748_emb_CAA78483_ (Z14110) actin depolymerizing
                  factor [Lilium longiflorum]
Seq. No.
                  293588
Seq. ID
                  LIB3066-023-Q1-K1-H11
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
                  7.0e-11
E value
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  293589
Seq. ID
                  LIB3066-024-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  g3402751
BLAST score
                  211
E value
                  7.0e-17
Match length
                  86
% identity
                  48
NCBI Description (AL031187) putative protein [Arabidopsis thaliana]
Seq. No.
                  293590
Seq. ID
                  LIB3066-024-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  g3901094
```

```
% identity
NCBI Description
                  (Z27090) pollen allergen Phl pI [Phleum pratense]
Seq. No.
                  293591
Seq. ID
                  LIB3066-024-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  g1931647
BLAST score
                  165
E value
                  2.0e-11
Match length
                  68
                  85
% identity
                  (U95973) endomembrane protein EMP70 precusor isolog
NCBI Description
                  [Arabidopsis thaliana]
                  293592
Seq. No.
Seq. ID
                  LIB3066-024-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  q3287270
BLAST score
                  677
E value
                  2.0e-71
Match length
                  147
                  86
% identity
NCBI Description (Y09533) involved in starch metabalism [Solanum tuberosum]
                  293593
Seq. No.
Seq. ID
                  LIB3066-024-Q1-K1-E11
Method
                  BLASTX
                  g129940
NCBI GI
BLAST score
                  507
E value
                  1.0e-51
Match length
                  127
                  83
% identity
                  EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                  (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi_100911_pir__S18570 polygalacturonase (EC 3.2.1.15)
                  precursor - maize >gi_22417_emb_CAA40850_ (X57627)
                  polygalacturonase [Zea mays] >gi_22419_emb_CAA44249_
                  (X62385) polygalacturonase [Zea mays]
                  >gi_288374 emb CAA46679 (X65844) polygalacturonase [Zea
                  mays]
Seq. No.
                  293594
Seq. ID
                  LIB3066-024-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g4038042
BLAST score
                  533
E value
                  1.0e-54
Match length
                  142
% identity
NCBI Description
                  (AC005936) putative DNA-binding protein [Arabidopsis
                  thaliana]
```

40972

293595

BLASTX

223

g4538896

LIB3066-024-Q1-K1-H2

Seq. No. Seq. ID

Method

NCBI GI

BLAST score

```
E value
                   3.0e-18
Match length
                   108
% identity
                   41
NCBI Description
                   (AL049482) putative protein [Arabidopsis thaliana]
Seq. No.
                   293596
Seq. ID
                  LIB3066-024-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                   q2980770
BLAST score
                   144
E value
                   2.0e-09
Match length
                   63
% identity
                   49
NCBI Description
                  (AL022198) putative protein kinase [Arabidopsis thaliana]
                  293597
Seq. No.
Seq. ID
                  LIB3066-024-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  q3513739
BLAST score
                  195
E value
                   5.0e-15
Match length
                  83
% identity
                   49
NCBI Description
                  (AF080118) Similar to uridine diphosphate glucose
                  epimerase; F8M12.10 [Arabidopsis thaliana]
Seq. No.
                  293598
Seq. ID
                  LIB3066-025-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  q4587550
BLAST score
                  188
E value
                   4.0e-14
Match length
                  79
% identity
                   44
NCBI Description
                  (ACO06577) EST gb R64848 comes from this gene. [Arabidopsis
                  thaliana]
                   293599
Seq. No.
Seq. ID
                  LIB3066-025-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  q4220484
BLAST score
                  239
E value
                  3.0e-20
Match length
                  95
% identity
                  58
NCBI Description
                  (AC006069) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  293600
Seq. ID
                  LIB3066-025-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  q3355471
BLAST score
                  366
E value
                  3.0e-35
Match length
                  102
% identity
                  60
NCBI Description
                  (AC004218) putative lysophospholipase [Arabidopsis
                  thaliana]
```

```
Seq. No.
                      293601
    Seq. ID
                      LIB3066-026-Q1-K1-A11
    Method
                      BLASTX
    NCBI GI
                      q2499708
    BLAST score
                       620
    E value
                       9.0e-65
Match length
                       145
    % identity
                      81
    NCBI Description
                      PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
                       (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                      >gi 1020409 dbj BAA11135 (D73410) phospholipase D [Zea
                      mays]
    Seq. No.
                       293602
    Seq. ID
                      LIB3066-026-Q1-K1-A12
    Method
                      BLASTX
    NCBI GI
                      g2454302
    BLAST score
                       242
    E value
                      2.0e-20
    Match length
                      111
    % identity
                       44
    NCBI Description
                      (AF000152) OS-4 protein [Homo sapiens]
    Seq. No.
                      293603
    Seq. ID
                      LIB3066-026-Q1-K1-B6
    Method
                      BLASTX
    NCBI GI
                      q2642215
    BLAST score
                       162
    E value
                       5.0e-11
    Match length
                       40
                      72
    % identity
    NCBI Description
                      (AF030386) NOI protein [Arabidopsis thaliana]
    Seq. No.
                       293604
    Seq. ID
                      LIB3066-026-Q1-K1-C2
    Method
                      BLASTX
    NCBI GI
                       g3056581
    BLAST score
                       307
                       5.0e-28
    E value
    Match length
                       86
    % identity
                       69
                      (AC004255) T1F9.2 [Arabidopsis thaliana]
    NCBI Description
                       293605
    Seq. No.
    Seq. ID
                      LIB3066-026-Q1-K1-F1
    Method
                      BLASTX
    NCBI GI
                      g1362086
    BLAST score
                      208
                      1.0e-16
    E value
                      54
    Match length
                      76
    % identity
    NCBI Description
                      5-methyltetrahydropteroyltriglutamate--homocysteine
                      S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                      >gi 2129919 pir S65957
                       5-methyltetrahydropteroyltriglutamate--homocysteine
```

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus] 293606 Seq. No. Seq. ID LIB3066-026-Q1-K1-F10 Method BLASTN g442525 NCBI GI BLAST score 191 1.0e-103 E value Match length 243 % identity 95 NCBI Description ZmERabp4=auxin-binding protein [Zea mays=corn, seedling, mRNA, 917 nt] Seq. No. 293607 LIB3066-026-Q1-K1-F5 Seq. ID Method BLASTX NCBI GI q4646218 BLAST score 148 E value 2.0e-09 Match length 57 51 % identity NCBI Description (AC007290) putative GTP-binding protein [Arabidopsis thaliana] Seq. No. 293608 Seq. ID LIB3066-026-Q1-K1-F6 Method BLASTX NCBI GI g3582340 BLAST score 146 4.0e-09 E value Match length 56 57 % identity NCBI Description (AC005496) unknown protein [Arabidopsis thaliana] Seq. No. 293609 Seq. ID LIB3066-026-Q1-K1-H2 Method BLASTX NCBI GI q729944 BLAST score 268 E value 2.0e-23 Match length 49 % identity 96 NCBI Description POLLEN ALLERGEN ZEA M 1 (ZEA M I) >gi_478272_pir__JC1524 major allergen mI protein - maize >gi_293902 (L14271) Zea mI [Zea mays] 293610 Seq. No. Seq. ID LIB3066-027-Q1-K1-B10 Method BLASTX NCBI GI g1076746

Method BLASTX
NCBI GI g1076746
BLAST score 439
E value 1.0e-43
Match length 100
% identity 86

NCBI Description heat shock protein 70 - rice (fragment)

>gi_763160_emb_CAA47948_ (X67711) heat shock protein 70



[Oryza sativa]

```
293611
Seq. No.
                  LIB3066-027-Q1-K1-E2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3819183
BLAST score
                  43
                  7.0e-15
E value
                  55
Match length
                  95
% identity
NCBI Description Hordeum vulgare partial mRNA; clone cMWG0645
Seq. No.
                  293612
                  LIB3066-027-Q1-K1-F6
Seq. ID
Method
                  BLASTX
                  q548493
NCBI GI
BLAST score
                  193
E value
                  7.0e-15
                  84
Match length
% identity
                  54
                  EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                   (GALACTURAN 1, 4-ALPHA-GALACTURONIDASE)
                  >gi_629854_pir__S30067 polygalacturonase - maize
                  >gi_288612_emb_CAA47052_ (X66422) polygalacturonase [Zea
                  mays]
                  293613
Seq. No.
                  LIB3066-027-Q1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1174600
BLAST score
                  157
E value
                  1.0e-10
Match length
                   66
% identity
                  52
                  TUBULIN BETA CHAIN >gi 493710 dbj BAA06382 (D30717)
NCBI Description
                  beta-tubulin [Oryza sativa]
Seq. No.
                   293614
Seq. ID
                  LIB3066-027-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  q629852
                  191
BLAST score
                  8.0e-15
E value
Match length
                  78
% identity
                   54
                  polygalacturonase - maize >gi 288367 emb CAA46680 (X65845)
NCBI Description
                  polygalacturonase [Zea mays]
                  293615
Seq. No.
Seq. ID
                  LIB3066-028-Q1-K1-A9
Method
                  BLASTX
                  q2239262
NCBI GI
BLAST score
                   165
E value
                  2.0e-11
Match length
                   66
                   45
% identity
NCBI Description (Y13285) pectin methylesterase-like protein [Zea mays]
```

Method

BLASTX

```
293616
Seq. No.
                  LIB3066-028-Q1-K1-B2
Seq. ID
                  BLASTX
Method
                  g4531442
NCBI GI
                  171
BLAST score
                  1.0e-13
E value
                  97
Match length
% identity
                  51
                  (AC006224) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  293617
Seq. No.
                  LIB3066-028-Q1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130137
BLAST score
                  617
                  2.0e-64
E value
Match length
                  134
                  46
% identity
                  homeotic protein Hox2b - maize >gi 1143707 emb CAA61910_
NCBI Description
                   (X89761) Hox2b [Zea mays]
                  293618
Seq. No.
                  LIB3066-028-Q1-K1-F9
Seq. ID
                  BLASTX
Method
                  g3885328
NCBI GI
BLAST score
                  281
                  5.0e-25
E value
                  139
Match length
                   44
% identity
                   (AC005623) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   293619
Seq. No.
                  LIB3066-028-Q1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4337196
BLAST score
                   244
                   9.0e-21
E value
Match length
                   69
% identity
                   67
                   (AC006403) putative serine/threonine receptor kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   293620
                   LIB3066-028-Q1-K1-G7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g602605
BLAST score
                   74
E value
                   1.0e-33
Match length
                   122
% identity
                   91
NCBI Description Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin
Seq. No.
                   293621
Seq. ID
                   LIB3066-029-Q1-K1-A8
```



```
NCBI GI
                  q1480670
BLAST score
                  201
E value
                  9.0e-16
Match length
                  76
                  55
% identity
NCBI Description
                   (U60267) delta 1-pyrroline-5-carboxylate synthetase
                   [Lycopersicon esculentum]
Seq. No.
                  293622
Seq. ID
                  LIB3066-029-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  q4586260
BLAST score
                  182
                  2.0e-13
E value
                  104
Match length
                  40
% identity
                  (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
                  293623
Seq. No.
Seq. ID
                  LIB3066-029-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  q548493
BLAST score
                  203
E value
                  1.0e-19
Match length
                  140
% identity
                   45
                  EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                   (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi_629854_pir__S30067 polygalacturonase - maize
                  >gi_288612_emb_CAA47052 (X66422) polygalacturonase [Zea
                  mays]
Seq. No.
                   293624
Seq. ID
                  LIB3066-029-Q1-K1-G3
Method
                  BLASTX
                   q548493
NCBI GI
BLAST score
                   143
                   6.0e-09
E value
Match length
                   91
% identity
                   43
                  EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                   (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                   >gi 629854 pir S30067 polygalacturonase - maize
                   >gi 288612 emb CAA47052 (X66422) polygalacturonase [Zea
                  mays]
                   293625
Seq. No.
Seq. ID
                  LIB3066-029-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                   g4206210
BLAST score
                   165
                   2.0e-11
E value
Match length
                   75
                   39
% identity
                  (AF071527) putative calcium channel [Arabidopsis thaliana]
NCBI Description
```

40978

channel [Arabidopsis thaliana]

>gi_4263043_gb_AAD15312_ (AC005142) putative calcium

```
293626
Seq. No.
                  LIB3066-030-Q1-E1-F2
Seq. ID
                  BLASTX
Method
                  g2668742
NCBI GI
                  390
BLAST score
                  6.0e-38
E value
Match length
                  86
                  87
% identity
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                  293627
Seq. No.
                  LIB3066-030-Q1-E1-G10
Seq. ID
Method
                  BLASTN
                  g2062705
NCBI GI
BLAST score
                  34
                  1.0e-09
E value
                  34
Match length
                  100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  293628
Seq. No.
                  LIB3066-030-Q1-E1-G6
Seq. ID
                  BLASTN
Method
                  g22480
NCBI GI
BLAST score
                  44
                  2.0e-15
E value
Match length
                  51
                  96
% identity
                  Maize mRNA for superoxide dismutase-3 isoenzyme (EC
NCBI Description
                  1.15.1.1)
                  293629
Seq. No.
                  LIB3066-030-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1654387
BLAST score
                   183
                   2.0e-13
E value
                   97
Match length
                   44
% identity
NCBI Description (U73172) manganese superoxide dismutase [Triticum aestivum]
                   293630
Seq. No.
                   LIB3066-030-Q1-K1-C11
Seq. ID
Method
                   BLASTN
                   q22292
NCBI GI
BLAST score
                   70
                   3.0e-31
E value
Match length
                   222
% identity
NCBI Description Z.mays mRNA for glycine-rich protein
```

Seq. No. 293631

Seq. ID LIB3066-030-Q1-K1-H8

Method BLASTX NCBI GI g4490311 BLAST score 309



```
3.0e-28
E value
Match length
                  113
% identity
                  54
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
                  293632
Seq. No.
                  LIB3066-031-Q1-K1-B10
Seq. ID
Method
                  BLASTN
                  g3821780
NCBI GI
                  36
BLAST score
                  6.0e-11
E value
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  293633
Seq. No.
                  LIB3066-031-Q1-K1-B2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2062705
BLAST score
                  36
                  8.0e-11
E value
Match length
                  36
                  100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  293634
Seq. No.
                  LIB3066-031-Q1-K1-B9
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
BLAST score
                  36
                  9.0e-11
E value
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  293635
Seq. No.
                  LIB3066-031-Q1-K1-C9
Seq. ID
Method
                  BLASTX
                  q1197461
NCBI GI
BLAST score
                  208
                  7.0e-17
E value
                  80
Match length
% identity
                  55
NCBI Description (X78819) casein kinase I [Arabidopsis thaliana]
                  293636
Seq. No.
Seq. ID
                  LIB3066-031-Q1-K1-D5
Method
                  BLASTN
NCBI GI
                  q313139
BLAST score
                  77
                  1.0e-35
E value
Match length
                  157
% identity
                  88
```

NCBI Description Z.mays ZmPRO2 mRNA for profilin

Seq. No. LIB3066-031-Q1-K1-F10 Seq. ID

293637

Seq. No.

Seq. ID

293642

LIB3066-032-Q1-E1-H1



```
BLASTX
Method
                  g4415922
NCBI GI
BLAST score
                  156
E value
                  2.0e-10
Match length
                  103
% identity
                  38
                  (AC006282) putative glucosyl transferase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  293638
                  LIB3066-031-Q1-K1-F2
Seq. ID
Method
                  BLASTX
                  g3757520
NCBI GI
BLAST score
                  194
                  9.0e-15
E value
Match length
                  99
% identity
                   40
                  (AC005167) unknown protein [Arabidopsis thaliana]
NCBI Description
                  293639
Sea. No.
Seq. ID
                  LIB3066-031-Q1-K1-G8
Method
                  BLASTX
                   g629849
NCBI GI
BLAST score
                  182
E value
                   1.0e-13
Match length
                   90
% identity
                   42
                  pectate lyase (EC 4.2.2.2) - maize >gi_405535 (L20140)
NCBI Description
                  homology with pectate lyase [Zea mays]
                   293640
Seq. No.
                   LIB3066-032-Q1-E1-D5
Seq. ID
                   BLASTX
Method
                   g71638
NCBI GI
                   170
BLAST score
                   6.0e-12
E value
                   117
Match length
                   41
% identity
                  actin - soybean >gi_18532_emb_CAA23728_ (V00450) actin
NCBI Description
                   [Glycine max] >gi 223413 prf 0804316A actin [Glycine max]
                   293641
Seq. No.
                   LIB3066-032-Q1-E1-F9
Seq. ID
                   BLASTX
Method
                   g548492
NCBI GI
BLAST score
                   165
                   2.0e-11
E value
                   104
Match length
                   41
% identity
                   EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                   (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                   >gi_629853_pir__S30066 polygalacturonase - maize
                   >gi 288379 emb CAA45751 (X64408) polygalacturonase [Zea
                   mays]
```



```
BLASTX
Method
NCBI GI
                  g2130073
                  182
BLAST score
                  2.0e-13
E value
Match length
                  141
                  40
% identity
NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
                  cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
                  C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301)
                  aldolase C-1 [Oryza sativa]
                  293643
Seq. No.
                  LIB3066-032-Q1-K1-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22457
                  169
BLAST score
                  4.0e-90
E yalue
Match length
                  367
% identity
                  88
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H3)
                  293644
Seq. No.
                  LIB3066-032-Q1-K1-A11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22457
BLAST score
                  89
                  2.0e-42
E value
                  240
Match length
% identity
                  85
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H3)
                  293645
Seq. No.
                  LIB3066-032-Q1-K1-A4
Seq. ID
Method
                  BLASTN
                  g3821780
NCBI GI
BLAST score
                  36
                  8.0e-11
E value
                  48
Match length
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  293646
Seq. No.
Seq. ID
                  LIB3066-032-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  q3063444
BLAST score
                   391
E value
                   5.0e-38
Match length
                   110
% identity
NCBI Description
                  (AC003981) F22013.5 [Arabidopsis thaliana]
                   293647
Seq. No.
                  LIB3066-032-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3386614
BLAST score
                  245
```

4.0e-21

E value



```
Match length
% identity
                   29
NCBI Description
                  (AC004665) putative transcription factor SF3 [Arabidopsis
                   thalianal
Seq. No.
                   293648
Seq. ID
                  LIB3066-032-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  g2459445
BLAST score
                  254
E value
                   5.0e-22
Match length
                   96
% identity
                   28
NCBI Description
                  (AC002332) putative ribonucleoprotein [Arabidopsis
                  thaliana]
                  293649
Seq. No.
Seq. ID;
                  LIB366-032-Q1-K1-C11
Method
                  BLASTN
                  g459267
NCBI GI
BLAST score
                  178
E value
                   2.0e-95
Match length
                   359
% identity
                  88
NCBI Description Z.mays gene for HMG protein
                  293650
Seq. No.
Seq. ID
                  LIB3066-032-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  q4586042
BLAST score
                   352
E value
                  2.0e-33
Match length
                  135
% identity
                   51
NCBI Description
                  (AC007020) putative APG protein isolog [Arabidopsis
                  thaliana]
Seq. No.
                   293651
Seq. ID
                  LIB3066-032-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  q135099
```

BLAST score 143 E value 5.0e-09 Match length 114 % identity

ASPARTYL-TRNA SYNTHETASE (ASPARTATE--TRNA LIGASE) (ASPRS) NCBI Description

> >gi_68531_pir__SYRTDT aspartate--tRNA ligase (EC 6.1.1.12) - rat >gi_203066 (J04487) aspartyl-tRNA synthetase [Rattus norvegicus] >gi_1773257 (U30812) aspartyl-tRNA synthetase

[Rattus norvegicus]

Seq. No. 293652

Seq. ID LIB3066-032-Q1-K1-D10

Method BLASTX NCBI GI g3608412 BLAST score 146 E value 4.0e-10

```
Match length
% identity
                  (AF079355) protein phosphatase-2c [Mesembryanthemum
NCBI Description
                  crystallinum]
                  293653
Seq. No.
Seq. ID
                  LIB3066-032-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  q4582488
                  220
BLAST score
E value
                  7.0e-18
Match length
                  53
% identity
                 (AL021768) putative protein [Arabidopsis thaliana]
NCBI Description
                  293654
Seq. No.
                  LIB3066-032-Q1-K1-D8
Seq. ID
Method
                  BLASTX
                  g2392772
NCBI GI
                  253
BLAST score
                  9.0e-22
E value
                  82
Match length
% identity
                  62
                  (AC002534) putative chloroplast prephenate dehydratase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  293655
                  LIB3066-032-Q1-K1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2062705
BLAST score
                  37
E value
                  2.0e-11
Match length
                  37
% identity
                  100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  293656
                  LIB3066-032-Q1-K1-G9
Seq. ID
Method
                  BLASTX
                  g4580394
NCBI GI
BLAST score
                  286
E value
                  1.0e-25
                  84
Match length
% identity
                  58
                  (AC007171) putative fatty acid elongase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  293657
Seq. ID
                  LIB3066-033-Q1-E1-D1
```

Method BLASTX NCBI GI q22422 BLAST score 161 E value 5.0e-11 Match length 105 40 % identity

NCBI Description (X57743) polygalacturonase [Zea mays]



```
293658
Seq. No.
                  LIB3066-033-Q1-E1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q626041
BLAST score
                  174
                  2.0e-12
E value
                  100
Match length
                  44
% identity
NCBI Description translation initiation factor eIF-1A - wheat (fragment)
                  293659
Seq. No.
                  LIB3066-033-Q1-K1-A1
Seq. ID
                  BLASTN
Method
                   g3821780
NCBI GI
BLAST score
                   36
E value
                   7.0e-11
Match length
                   36
% identity
                   100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   293660
Seq. No.
                   LIB3066-033-Q1-K1-A6
Seq. ID
Method
                   BLASTN
                   g3821780
NCBI GI
BLAST score
                   36
E value
                   8.0e-11
Match length
                   36
% identity
                   100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   293661
Seq. No.
                   LIB3066-033-Q1-K1-B4
Seq. ID
                   BLASTN
Method
                   g2062705
NCBI GI
                   37
BLAST score
                   2.0e-11
E value
                   49
Match length
                   67
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                   293662
Seq. No.
                   LIB3066-033-Q1-K1-D2
Seq. ID
                   BLASTX
Method
                   g4582459
NCBI GI
                   221
BLAST score
                   4.0e-18
E value
Match length
                   62
                   73
% identity
                   (AC007071) putative RanBP7/importin protein [Arabidopsis
NCBI Description
                   thaliana]
                   293663
Seq. No.
                   LIB3066-033-Q1-K1-G7
Seq. ID
                   BLASTX
Method
```

q283049

382 3.0e-37

NCBI GI BLAST score

E value



```
Match length
% identity
                   86
                   polygalacturonase (EC 3.2.1.15) precursor (clone W2247) -
NCBI Description
                   maize (fragment) >gi 481079_pir__S37718 polygalacturonase -
                   maize >gi_22426_emb_CAA44248_ (X62384) polygalacturonase [Zea mays] >gi_287830_emb_CAA47234_ (X66692)
                   polygalacturonase [Zea mays]
                   293664
Seq. No.
Seq. ID
                   LIB3066-033-Q1-K1-H10
Method
                   BLASTN
NCBI GI
                   q2062705
BLAST score
                   36
                   1.0e-10
E value
                   36
Match length
                   100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                   293665
Seq. No.
Seq. ID
                   LIB3066-034-Q1-K1-A2
Method
                   BLASTN
NCBI GI
                   q433042
BLAST score
                   85
E value
                   5.0e-40
                   176
Match length
% identity
                   Zea mays W-22 clone PREM-1C retroelement PREM-1, partial
NCBI Description
                   sequence
Seq. No.
                   293666
Seq. ID
                   LIB3066-034-Q1-K1-A3
Method
                   BLASTX
NCBI GI
                   g1778095
                   192
BLAST score
E value
                   1.0e-14
Match length
                   91
% identity
                   (U64903) putative sugar transporter; member of major
NCBI Description
                   facilitative superfamily; integral membrane protein [Beta
                   vulgaris]
                   293667
Seq. No.
Seq. ID
                   LIB3066-034-Q1-K1-B10
Method
                   BLASTX
                   g3738302
NCBI GI
                   170
BLAST score
                   4.0e-12
E value
Match length
                   107
% identity
                   40
                   (AC005309) tubby-like protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4249398 (AC006072) putative tubby protein [Arabidopsis
                   thaliana]
```

Seq. No. 293668

Seq. ID LIB3066-034-Q1-K1-D1

Method BLASTX NCBI GI q2583129



```
BLAST score
E value
                   2.0e-33
Match length
                   91
                   73
% identity
                   (AC002387) putative methionine aminopeptidase [Arabidopsis
NCBI Description
                  thaliana]
                   293669
Seq. No.
Seq. ID
                  LIB3066-034-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  g1168749
BLAST score
                   408
E value
                  5.0e-40
Match length
                  113
% identity
                   44
                  CALMODULIN-6 >gi_1076298_pir__S35187 calmodulin 6 -
NCBI Description
                  Arabidopsis thaliana >gi 16227 emb CAA78059 (Z12024)
                   calmodulin [Arabidopsis thaliana]
Seq. No.
                   293670
                  LIB3066-034-Q1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4581150
BLAST score
                  153
                   3.0e-10
E value
Match length
                   88
% identity
                   38
NCBI Description
                  (AC006919) hypothetical protein [Arabidopsis thaliana]
                  293671
Seq. No.
                  LIB3066-034-Q1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3152619
BLAST score
                   261
                   9.0e-23
E value
Match length
                   96
% identity
                   56
NCBI Description
                   (AC004482) putative (s)-acetone-cyanohydrin lyase
                   ((s)-hydroxymitrilase), 3'partial [Arabidopsis thaliana]
Seq. No.
                   293672
Seq. ID
                  LIB3066-035-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                   g2605887
BLAST score
                   190
E value
                   1.0e-23
Match length
                   78
% identity
NCBI Description (AF029242) dormancy-associated protein [Pisum sativum]
Seq. No.
                   293673
Seq. ID
                  LIB3066-035-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g444790
BLAST score
                  141
                  5.0e-09
E value
```

40987

52

Match length

```
% identity
NCBI Description nucleotide translocator [Arabidopsis thaliana]
                  293674
Seq. No.
                  LIB3066-035-Q1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2914706
BLAST score
                  216
                  2.0e-17
E value
Match length
                  70
% identity
                   63
NCBI Description
                  (AC003974) putative homeobox protein [Arabidopsis thaliana]
                  293675
Seq. No.
                  LIB3066-035-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1777376
BLAST score
                  511
E value
                  4.0e-52
Match length
                  114
                  76
```

% identity 76 NCBI Description (D78506) w-3 fatty acid desaturase [Oryza sativa]

 Seq. No.
 293676

 Seq. ID
 LIB3066-035-Q1-K1-B7

 Method
 BLASTX

 NCBI GI
 g2980770

BLAST score 415 E value 9.0e-41 Match length 102 % identity 72

NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 293677

Seq. ID LIB3066-035-Q1-K1-D10

Method BLASTX
NCBI GI g2444174
BLAST score 167
E value 1.0e-22
Match length 110
% identity 61

NCBI Description (U94781) unconventional myosin [Helianthus annuus]

Seq. No. 293678

Seq. ID LIB3066-035-Q1-K1-D11

Method BLASTX
NCBI GI g4582488
BLAST score 158
E value 1.0e-10
Match length 36
% identity 81

NCBI Description (AL021768) putative protein [Arabidopsis thaliana]

Seq. No. 293679

Seq. ID LIB3066-035-Q1-K1-F7

Method BLASTX NCBI GI g3063710

```
BLAST score
E value
                  8.0e-25
Match length
                  100
% identity
                  56
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]
Seq. No.
                  293680
Seq. ID
                  LIB3066-035-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  q2853072
BLAST score
                  225
E value
                  2.0e-18
Match length
                  143
% identity
                  42
NCBI Description (AL021768) putative protein [Arabidopsis thaliana]
                  293681
Seq. No.
Şeq. ID
                  LIB3066-035-Q1-K1-H4
                 BLASTX
Method -
NCBI GI
                  q4185139
BLAST score
                  440
E value
                  1.0e-43
Match length
                  133
% identity
                  59
NCBI Description
                  (AC005724) putative diacylglycerol kinase [Arabidopsis
                  thaliana]
Seq. No.
                  293682
Seq. ID
                  LIB3066-036-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  q3355486
BLAST score
                  263
E value
                  5.0e-23
Match length
                  84
% identity
                  67
NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]
Seq. No.
                  293683
Seq. ID
                  LIB3066-036-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g137460
BLAST score
                  178
E value
                  4.0e-13
Match length
                  72
% identity
                  53
                  VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
NCBI Description
                  SUBUNIT) >gi 67952 pir PXPZV9 H+-transporting ATPase (EC
                  3.6.1.35), vacuolar, 69K chain - carrot >gi_167560 (J03769)
                  vacular H+-ATPase [Daucus carota]
```

Seq. No. 293684

Seq. ID LIB3066-036-Q1-K1-C5

Method BLASTX
NCBI GI 971582
BLAST score 143
E value 2.0e-09
Match length 54

Match length

% identity

147

51



```
% identity
NCBI Description
                   tubulin alpha-1 chain - slime mold (Physarum polycephalum)
                    (fragment) >gi 3249 emb CAA26477 (X02625) alpha tubulin
                    (aa 1-446) [Physarum polycephalum]
Seq. No.
                   293685
Seq. ID
                   LIB3066-036-Q1-K1-F1
Method
                   BLASTX
NCBI GI
                   q3608412
BLAST score
                   264
E value
                   2.0e-33
Match length
                   122
% identity
                   (AF079355) protein phosphatase-2c [Mesembryanthemum
NCBI Description
                   crystallinum]
Seq. No.
                   293686
Seq. ID
                   LIB3066-036-Q1-K1-F5
Method
                   BLASTN
NCBI GI
                   q255568
BLAST score
                   59
E value
                   1.0e-24
Match length
                   75
% identity
                   96
NCBI Description pollen specific protein [Zea mays=corn, mRNA, 943 nt]
Seq. No.
                   293687
Seq. ID
                   LIB3066-036-01-K1-F8
Method
                   BLASTX
NCBI GI
                   g3913518
BLAST score
                   163
E value
                   1.0e-11
Match length
                   64
% identity
                   48
                   3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE
NCBI Description
                   (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE) (DPNPASE) >gi_1103921 (U40433) 3'(2'),5'-bisphosphate
                   nucleotidase [Arabidopsis thaliana]
                   293688
Seq. No.
Seq. ID
                   LIB3066-037-Q1-K1-F4
Method
                   BLASTN
NCBI GI
                   g2239261
BLAST score
                   54
E value
                   5.0e-22
                   106
Match length
                   89
% identity
NCBI Description Zea Mays mRNA for pectin methylesterase-like protein
Seq. No.
                   293689
Seq. ID
                   LIB3066-037-Q1-K1-F7
Method
                   BLASTX
NCBI GI
                   g1076809
BLAST score
                   331
E value
                   7.0e-31
```



```
NCBI Description
                   H+-transporting ATPase (EC 3.6.1.35) - maize
                   >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase
                   [Zea mays]
                   293690
Seq. No.
Seq. ID
                   LIB3066-038-Q1-K1-D6
Method
                   BLASTX
NCBI GI
                   q99809
BLAST score
                   259
E value
                   1.0e-22
Match length
                   97
% identity
                   54
NCBI Description
                   gene Bp10 protein - rape >gi_17795_emb_CAA47177_ (X66608)
                   Bplo [Brassica napus]
Seq. No.
                   293691
Seq. ID
                   LIB3066-038-Q1-K1-F11
Method
                   BLASTX
NCBI GI
                   g4510342
BLAST score
                   177
E value
                   8.0e-13
Match length
                   51
% identity
                   65
NCBI Description
                   (AC006921) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   293692
Seq. ID
                   LIB3066-038-Q1-K1-G2
Method
                   BLASTX
NCBI GI
                   g1843440
BLAST score
                   145
E value
                   2.0e-09
Match length
                   78
% identity
                   44
NCBI Description
                  (Z70521) unknown [Cucumis melo]
Seq. No.
                   293693
Seq. ID
                   LIB3066-038-Q1-K1-G3
Method
                   BLASTX
NCBI GI
                   g1805654
BLAST score
                   497
E value
                   2.0e-50
Match length
                   128
% identity
                   75
                   (X99972) calmodulin-stimulated calcium-ATPase [Brassica
NCBI Description
                   oleracea]
Seq. No.
                   293694
Seq. ID
                   LIB3066-038-Q1-K1-H5
Method
                   BLASTX
NCBI GI
                   g82708
                   308
BLAST score
                   3.0e-28
E value
Match length
                   86
                   70
% identity
```

NCBI Description Ocs-element binding factor 1 - maize



```
Seq. No.
                  293695
Seq. ID
                  LIB3066-038-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  g3702317
BLAST score
                  195
                  6.0e-15
E value
Match length
                  59
                   68
% identity
                  (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4559376_gb_AAD23036.1_AC006526_1 (AC006526) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  293696
                  LIB3066-040-Q1-K1-A5
Seq. ID
Method
                  BLASTN
                  g4218534
NCBI GI
BLAST score
                   33
E value
                  5.0e-09
Match length
                  41
                   95
% identity
                  Triticum sp. mRNA for GRAB1 protein
NCBI Description
                  293697
Seq. No.
Seq. ID
                  LIB3066-040-Q1-K1-C5
Method
                  BLASTX
                  q2829867
NCBI GI
                   154
BLAST score
                   3.0e-10
E value
Match length
                   128
% identity
                  (AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   293698
Seq. No.
Seq. ID
                   LIB3066-040-Q1-K1-E6
Method
                   BLASTX
NCBI GI
                   q729882
BLAST score
                   471
E value
                   2.0e-47
Match length
                   122
% identity
                   71
                  CASEIN KINASE II BETA' CHAIN (CK II)
NCBI Description
                   >gi 1076300 pir S47968 casein kinase II (EC 2.7.1.-) beta
                   chain CKB2 - Arabidopsis thaliana >gi_467975 (U03984)
                   casein kinase II beta subunit CKB2 [Arabidopsis thaliana]
                   >gi 2245122 emb CAB10544 (Z97343) unnamed protein product
                   [Arabidopsis thaliana]
Seq. No.
                   293699
                   LIB3066-040-Q1-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4539333
BLAST score
                   216
                   2.0e-17
E value
Match length
                   77
```

(AL035539) putative amino acid transport protein

55

[Arabidopsis thaliana]

% identity

NCBI Description

NCBI GI

E value

BLAST score

g3135274

342 3.0e-32

```
293700
Seq. No.
                  LIB3066-040-Q1-K1-F2
Seq. ID
                  BLASTX
Method
                  g3108075
NCBI GI
                  209
BLAST score
                  1.0e-16
E value
                  59
Match length
                  69
% identity
NCBI Description (AF060797) putative beta-ureidopropionase [Manduca sexta]
                  293701
Seq. No.
                  LIB3066-040-Q1-K1-F6
Seq. ID
Method
                  BLASTX
                  q3420055
NCBI GI
                  258
BLAST score
                  2.0e-22
E value
                  86
Match length
                  65
% identity
NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana]
                  293702
Seq. No.
                  LIB3066-042-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4239889
BLAST score
                   363
                  1.0e-34
E value
                  135
Match length
                   65
% identity
NCBI Description (AB016802) MAP kinase 5 [Zea mays]
                   293703
Seq. No.
                  LIB3066-042-Q1-K1-E3
Seq. ID
Method
                  BLASTX
                   g1773014
NCBI GI
BLAST score
                   320
                   9.0e-30
E value
Match length
                   82
% identity
NCBI Description (Y10338) chloride channel Stclc1 [Solanum tuberosum]
                   293704
Seq. No.
                   LIB3066-042-Q1-K1-E9
Seq. ID
Method
                   BLASTN
NCBI GI
                   q22542
                   97
BLAST score
                   4.0e-47
E value
                   145
Match length
% identity
                   92
NCBI Description Maize gene for Mr 19000 alpha zein and 5'-flanking region
                   293705
Seq. No.
                   LIB3066-042-Q1-K1-H4
Seq. ID
Method
                   BLASTX
```

BLAST score

Match length

% identity

E value

194

83

48

3.0e-15



```
Match length
                  116
% identity
                  54
                  (AC003058) putative beta-1,3-endoglucanase [Arabidopsis
NCBI Description
                  thaliana]
                  293706
Seq. No.
                  LIB3066-043-Q1-K1-A1
Seq. ID
Method
                  BLASTN
                  g3821780
NCBI GI
BLAST score
                  36
                  1.0e-10
E value
Match length
                  48
% identity
                  67
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  293707
Seq. No.
                  LIB3066-043-Q1-K1-A3
Seq. ID
Method
                  BLASTX
                  g629533
NCBI GI
BLAST score
                   371
E value
                  1.0e-35
Match length
                  142
                  52
% identity
NCBI Description myosin heavy chain MYA3 - Arabidopsis thaliana (fragment)
                  293708
Seq. No.
                  LIB3066-043-Q1-K1-B1
Seq. ID
                  BLASTX
Method
                  g1076800
NCBI GI
BLAST score
                  206
                  3.0e-16
E value
Match length
                  95
                  51
% identity
NCBI Description
                  L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
                  maize >gi_600116_emb_CAA84406_ (Z34934) cytosolic ascorbate
                  peroxidase [Zea mays] >gi_1096503_prf__2111423A ascorbate
                  peroxidase [Zea mays]
                   293709
Seq. No.
Seq. ID
                  LIB3066-043-Q1-K1-B3
Method
                  BLASTX
                   g2062155
NCBI GI
BLAST score
                   233
E value
                   2.0e-19
Match length
                   75
                   65
% identity
                  (AC001645) mitochondrial processing peptidase alpha subunit
NCBI Description
                  precusor isolog [Arabidopsis thaliana]
Seq. No.
                   293710
Seq. ID
                   LIB3066-043-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                   q4138647
```

NCBI Description



```
NCBI Description (AJ011939) peroxidase [Trifolium repens]
Seq. No.
                  293711
                  LIB3066-043-Q1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82512
                  576
BLAST score
E value
                  1.0e-59
                  127
Match length
                  40
% identity
                  ubiquitin precursor - rice (fragment)
NCBI Description
                  >gi 218189 dbj BAA02241 (D12776) poly-ubiquitin [Oryza
                  sativa]
Seq. No.
                  293712
                  LIB3066-043-Q1-K1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4239888
BLAST score
                  114
E value
                  2.0e-57
                  154
Match length
% identity
                  94
NCBI Description Zea mays mRNA for MAP kinase 5, complete cds
Seq. No.
                  293713
                  LIB3066-043-Q1-K1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  8.0e-11
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  293714
                  LIB3066-043-Q1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q464980
BLAST score
                  177
E value
                  7.0e-13
                  40
Match length
% identity
                   82
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 166422 (L06967)
                  ubiquitin carrier protein [Medicago sativa]
                  293715
Seq. No.
Seq. ID
                  LIB3066-043-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  q4263717
BLAST score
                  271
                  5.0e-24
E value
Match length
                  83
% identity
                   60
```

40995

[Arabidopsis thaliana]

(AC006223) putative inositol polyphosphate 5-phosphatase

BLAST score

E value

36

1.0e-10



```
293716
Seq. No.
Seq. ID
                  LIB3066-043-Q1-K1-G8
Method
                  BLASTN
                  g255568
NCBI GI
BLAST score
                  72
E value
                  1.0e-32
Match length
                  200
% identity
NCBI Description pollen specific protein [Zea mays=corn, mRNA, 943 nt]
                  293717
Seq. No.
Seq. ID
                  LIB3066-044-Q1-K1-B3
Method
                  BLASTN
                  g3821780
NCBI GI
BLAST score
                  36
                  8.0e-11
E value
Match length
                  48
% identity
                  67
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  293718
Seq. No.
Seq. ID
                  LIB3066-044-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g3540182
BLAST score
                  296
E value
                  8.0e-27
Match length
                  131
% identity
                  50
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]
                  293719
Seq. No.
                  LIB3066-044-Q1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539292
                  337
BLAST score
E value
                  8.0e-32
Match length
                  85
                  72
% identity
NCBI Description
                  (AL049480) putative ribosomal protein S10 [Arabidopsis
                  thaliana]
Seq. No.
                  293720
Seq. ID
                  LIB3066-044-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g2832245
BLAST score
                  738
E value
                  1.0e-78
Match length
                  144
% identity
NCBI Description
                  (AF031569) hypothetical protein [Zea mays]
                  293721
Seq. No.
Seq. ID
                  LIB3066-044-Q1-K1-E11
Method
                  BLASTN
NCBI GI
                  g2062705
```



```
Match length
                  100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  293722
Seq. No.
Seq. ID
                  LIB3066-044-Q1-K1-G12
Method
                  BLASTN
                  g2062705
NCBI GI
                  36
BLAST score
                  8.0e-11
E value
Match length
                  36
% identity
                  100
```

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. LIB3066-044-Q1-K1-H9 Seq. ID Method BLASTX g1777312 NCBI GI 202 BLAST score 9.0e-16 E value

293723

Match length 72 % identity 53

(D30622) novel serine/threonine protein kinase [Arabidopsis NCBI Description

thaliana]

Seq. No. 293724

Seq. ID LIB3066-045-Q1-K1-A6

Method BLASTX NCBI GI q1346756 173 BLAST score E value 1.0e-12 Match length 69 % identity

SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 3 NCBI Description

>gi_421852_pir__S31087 phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain (clone TOPP3) - Arabidopsis thaliana >gi_166799 (M93410) phosphoprotein phosphatase 1

[Arabidopsis thaliana]

Seq. No. 293725

LIB3066-045-Q1-K1-B2 Seq. ID

Method BLASTX NCBI GI g3046695 BLAST score 178 7.0e-22 E value Match length 84 % identity

NCBI Description (AL022224) putative protein [Arabidopsis thaliana]

Seq. No. 293726

LIB3066-045-Q1-K1-C3 Seq. ID

Method BLASTX NCBI GI g1632768 BLAST score 166 2.0e-11 E value 37 Match length 84 % identity

NCBI Description



```
NCBI Description (D84408) calcium dependent protein kinase [Zea mays]
                  293727
Seq. No.
                  LIB3066-045-Q1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1171005
BLAST score
                  159
                  8.0e-11
E value
                  100
Match length
                  41
% identity
                  MAJOR POLLEN ALLERGEN HOL L 1 PRECURSOR (HOL L I)
NCBI Description
                  >gi_1085628_pir__S38581 allergen Hol-II - Holcus lanatus
                  >gi 414703 emb CAA81610 (Z27084) allergen Hol-II [Holcus
                  lanatus]
                  293728
Seq. No.
                  LIB3066-045-Q1-K1-E2
Seq. ID
Method
                  BLASTX
                  g4185139
NCBI GI
                  271
BLAST score
                  5.0e-24
E value
                  96
Match length
                  54
% identity
                  (AC005724) putative diacylglycerol kinase [Arabidopsis
NCBI Description
                  thaliana]
                  293729
Seq. No.
                  LIB3066-045-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4558666
BLAST score
                  165
                  2.0e-11
E value
Match length
                  142
% identity
                   35
                  (AC007063) putative Na/H antiporter isolog [Arabidopsis
NCBI Description
                  thaliana]
                   293730
Seq. No.
                  LIB3066-045-Q1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2252840
                   381
BLAST score
                   1.0e-36
E value
                   141
Match length
% identity
                   (AF013293) contains regions of similarity to Haemophilus
NCBI Description
                   influenzae permease (SP:P38767) [Arabidopsis thaliana]
Seq. No.
                   293731
Seq. ID
                   LIB3066-045-Q1-K1-G7
Method
                   BLASTX
NCBI GI
                   g1197461
BLAST score
                   310
                   8.0e-34
E value
Match length
                   113
                   65
% identity
```

40998

(X78819) casein kinase I [Arabidopsis thaliana]

NCBI GI

```
293732
Seq. No.
                  LIB3066-046-Q1-K1-D5
Seq. ID
Method
                  BLASTN
                  g2062705
NCBI GI
                  36
BLAST score
                  9.0e-11
E value
Match length
                  36
                  100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  293733
Seq. No.
                  LIB3066-046-Q1-K1-F2
Seq. ID
Method
                  BLASTX
                  g3024122
NCBI GI
                  449
BLAST score
                  7.0e-45
E value
                  108
Match length
                  82
% identity
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
                  ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821
                  (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]
                  293734
Seq. No.
Seq. ID
                  LIB3066-046-Q1-K1-F7
                  BLASTN
Method
                  g3821780
NCBI GI
                  36
BLAST score
                  9.0e-11
E value
                  48
Match length
                  67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  293735
Seq. No.
                  LIB3066-047-Q1-K1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4160401
BLAST score
                  49
                  9.0e-19
E value
Match length
                  89
                  89
% identity
NCBI Description Zea mays eIF-5 gene, exons 1-2
                  293736
Seq. No.
                  LIB3066-047-Q1-K1-B1
Seq. ID
Method
                  BLASTX
                  g1197461
NCBI GI
                  265
BLAST score
E value
                  4.0e-23
Match length
                  59
% identity
                  80
NCBI Description (X78819) casein kinase I [Arabidopsis thaliana]
                   293737
Seq. No.
                  LIB3066-047-Q1-K1-D10
Seq. ID
Method
                   BLASTX
```

40999

g1076315



```
BLAST score
                  5.0e-27
E value
Match length
                  124
                  45
% identity
NCBI Description
                  cytochrome P450 - Arabidopsis thaliana
                  >gi 853719 emb CAA60793 (X87367) CYP90 protein
                  [Arabidopsis thaliana] >gi 871988 emb CAA60794 (X87368)
                  CYP90 protein [Arabidopsis thaliana]
Seq. No.
                  293738
                  LIB3066-047-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2624498
BLAST score
                  358
                  4.0e-34
E value
Match length
                  90
                  73
% identity
NCBI Description Crystal Structure Of Barley Grain Peroxidase
                  293739
Seq. No.
                  LIB3066-047-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4585142
BLAST score
                  464
E value
                  2.0e-46
                  135
Match length
% identity
                  67
NCBI Description
                  (AF088276) NADPH oxidase; gp91; phox homolog [Lycopersicon
                  esculentum]
                  293740
Seq. No.
Seq. ID
                  LIB3066-047-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g1710841
BLAST score
                  337
E value
                  1.0e-31
Match length
                  91
                  74
% identity
NCBI Description
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
                  HYDROLASE) (ADOHCYASE) >gi_758247_emb CAA56278 (X79905)
                  S-adenosylhomocysteine hydrolase [Phalaenopsis sp.]
Seq. No.
                  293741
Seq. ID
                  LIB3066-047-Q1-K1-G6
```

Method BLASTX NCBI GI q4006888 BLAST score 168 7.0e-12E value Match length 77

44 % identity

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

293742 Seq. No.

Seq. ID LIB3066-048-Q1-K1-A9

Method BLASTX NCBI GI q4138920 BLAST score 144

```
E value
                  74
Match length
% identity
NCBI Description (AF059491) expansin [Lycopersicon esculentum]
                  293743
Seq. No.
                  LIB3066-048-Q1-K1-B3
Seq. ID
                  BLASTX
Method
                  a22380
NCBI GI
                  459
BLAST score
                  7.0e-46
E value
                  117
Match length
% identity
                 (X59714) CAAT-box DNA binding protein subunit B (NF-YB)
NCBI Description
                   [Zea mays]
                   293744
Seq. No.
                  LIB3066-048-Q1-K1-B4
Seq. ID
                  BLASTX
Method
                   q3236250
NCBI GI
                   145
BLAST score
                   2.0e-09
E value
                   38
Match length
                   66
% identity
NCBI Description (AC004684) hypothetical protein [Arabidopsis thaliana]
                   293745
Seq. No.
                   LIB3066-048-Q1-K1-D7
Seq. ID
                   BLASTX
Method
                   q1657619
NCBI GI
                   182
BLAST score
                   2.0e-13
E value
                   110
Match length
                   37
% identity
                  (U72504) G5p [Arabidopsis thaliana] >gi_3068710 (AF049236)
NCBI Description
                   putative transmembrane protein G5p [Arabidopsis thaliana]
                   293746
Seq. No.
                   LIB3066-048-Q1-K1-F1
 Seq. ID
                   BLASTX
Method
                   q2984709
 NCBI GI
 BLAST score
                   339
 E value
                   5.0e-32
Match length
                   66
                   97
 % identity
 NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                   293747
 Seq. No.
```

Seq. ID LIB3066-048-Q1-K1-H4

Method BLASTX
NCBI GI g1332579
BLAST score 350
E value 2.0e-33
Match length 88
% identity 9

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]



```
Seq. No.
Seq. ID
                  LIB3066-049-Q1-K1-A7
                  BLASTN
Method
                  g4416300
NCBI GI
                  105
BLAST score
                  6.0e-52
E value
Match length
                  312
% identity
                  88
                  Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                  region, complete sequence
                  293749
Seq. No.
                  LIB3066-049-Q1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076813
BLAST score
                  323
                  3.0e-30
E value
                  88
Match length
                  73
% identity
NCBI Description initiator-binding protein - maize
Seq. No.
                  293750
                  LIB3066-050-Q1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1169754
BLAST score
                  160
                   5.0e-11
E value
Match length
                  65
                   54
% identity
                  CELL DIVISION PROTEIN FTSH HOMOLOG >gi 2126621 pir S28533
NCBI Description
                   tma protein - Lactococcus lactis >gi_44027_emb CAA48877
                   (X69123) Tma protein [Lactococcus lactis]
                   293751
Seq. No.
                  LIB3066-050-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2213871
BLAST score
                   315
E value
                   4.0e-29
Match length
                   119
% identity
                   61
                  (AF003126) poly(A)-binding protein [Mesembryanthemum
NCBI Description
                   crystallinum]
```

Seq. No. 293752

LIB3066-050-Q1-K1-C9 Seq. ID

BLASTX Method NCBI GI g4263717 BLAST score 216 E value 2.0e-17 Match length 75 53 % identity

(AC006223) putative inositol polyphosphate 5-phosphatase NCBI Description

[Arabidopsis thaliana]

293753 Seq. No.

LIB3066-050-Q1-K1-E11 Seq. ID



```
Method
                   q2425066
NCBI GI
                   312
BLAST score
E value
                   7.0e-29
Match length
                   66
                   89
% identity
NCBI Description (AF019147) cysteine proteinase Mir3 [Zea mays]
                   293754
Seq. No.
                   LIB3066-050-Q1-K1-E6
Seq. ID
Method
                   BLASTN
                   q639721
NCBI GI
                   103
BLAST score
                   1.0e-50
E value
Match length
                   312
% identity
                   86
                   Zea mays calcium-dependent protein kinase (CDPK) gene,
NCBI Description
                   exons 1-7 and partial cds
                   293755
Seq. No.
                   LIB3066-050-Q1-K1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2149127
                   213
BLAST score
                   5.0e-17
E value
                   113
Match length
                   39
% identity
                   (U81293) UDP-glucose:indole-3-acetate
NCBI Description
                   beta-D-glucosyltransferase [Arabidopsis thaliana]
Seq. No.
                   293756
                   LIB3066-051-Q1-K1-B11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
                   6.0e-11
E value
Match length
                   36
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   293757
                   LIB3066-051-Q1-K1-C11
Seq. ID
Method
                   BLASTX
                   q3785983
NCBI GI
                   172
BLAST score
E value
                   3.0e-12
                   70
Match length
% identity
                   46
                   (AC005560) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   293758
Seq. No.
                   LIB3066-051-Q1-K1-D7
Seq. ID
                   BLASTN
Method
                   g3821780
NCBI GI
                   36
BLAST score
E value
                   1.0e-10
```

48

Match length



```
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  293759
Seq. No.
                  LIB3066-051-Q1-K1-H12
Seq. ID
                  BLASTX
Method
                  g4510373
NCBI GI
BLAST score
                  162
                  4.0e-11
E value
                  72
Match length
% identity
                  (AC007017) putative harpin-induced protein [Arabidopsis
NCBI Description
                  thaliana]
                  293760
Seq. No.
                  LIB3066-052-Q1-K1-A1
Seq. ID
                  BLASTX
Method
                   q1703200
NCBI GI
                   229
BLAST score
                   6.0e-19
E value
                   70
Match length
                   64
% identity
                   PROTEIN KINASE AFC2 >gi 601789 (U16177) protein kinase
NCBI Description
                   [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353)
                   protein kinase [Arabidopsis thaliana]
                   >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2)
                   [Arabidopsis thaliana]
                   293761
Seq. No.
                   LIB3066-052-Q1-K1-C1
Seq. ID
                   BLASTN
Method
                   g558364
NCBI GI
                   89
BLAST score
                   2.0e-42
E value
                   113
Match length
                   95
% identity
NCBI Description Z.mays mRNA for ADP-glucose pyrophosphorylase
                   293762
 Seq. No.
                   LIB3066-052-Q1-K1-D2
 Seq. ID
                   BLASTX
Method
                   g1314711
NCBI GI
                   314
 BLAST score
                   7.0e-29
 E value
Match length
                   70
 % identity
                   (U54615) calcium-dependent protein kinase [Arabidopsis
 NCBI Description
                   thaliana] >gi 3068712 (AF049236) calcium dependent protein
                   kinase [Arabidopsis thaliana]
                   293763
 Seq. No.
 Seq. ID
                   LIB3066-052-Q1-K1-D9
```

BLASTX

326 3.0e-30

129

q3236238

Method NCBI GI

E value

BLAST score

Match length



% identity 55

NCBI Description (AC004684) putative ARF1 GTPase activating protein

[Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_

(AB017876) Aspl [Arabidopsis thaliana]

Seq. No.

Seq. ID

LIB3066-052-Q1-K1-E10

Method BLASTN
NCBI GI g313141
BLAST score 229
E value 1.0e-126

Match length 319 % identity 96

NCBI Description Z.mays ZmPRO3 mRNA for profilin

Seq. No.

293765

Seq. ID LIB3066-052-Q1-K1-E2

Method BLASTX
NCBI GI g2293566
BLAST score 518
E value 8.0e-53
Match length 105
% identity 97

NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]

Seq. No.

293766

Seq. ID LIB3066-052-Q1-K1-G6

Method BLASTX
NCBI GI g3047098
BLAST score 345
E value 2.0e-44
Match length 142
% identity 73

NCBI Description (AF058826) similar to eukaryotic protein kinase domains (Pfam: pkinase.hmm, score: 171.43) [Arabidopsis thaliana]

Seq. No.

293767

Seq. ID LIB3066-052-Q1-K1-H7

Method BLASTX
NCBI GI g286124
BLAST score 506
E value 2.0e-51
Match length 143
% identity 75

NCBI Description (D14577) glutamine synthetase [Zea mays]

Seq. No.

293768

Seq. ID LIB3066-053-Q1-K1-A12

Method BLASTX
NCBI GI g4586031
BLAST score 274
E value 3.0e-24
Match length 63
% identity 83

NCBI Description (AC007109) unknown protein [Arabidopsis thaliana]

Seq. No.

```
LIB3066-053-Q1-K1-D2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3367582
                  152
BLAST score
                  7.0e-10
E value
                  69
Match length
                  45
% identity
NCBI Description (AL031135) putative protein [Arabidopsis thaliana]
                  293770
Seq. No.
                  LIB3066-053-Q1-K1-D4
Seq. ID
                  BLASTX
Method
                  q531389
NCBI GI
BLAST score
                  347
                  1.0e-32
E value
                  127
Match length
                  54
% identity
                  (U12626) copia-like retrotransposon Hopscotch polyprotein
NCBI Description
                  [Zea mays]
                  293771
Seq. No.
                  LIB3066-053-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4138914
BLAST score
                  152
                  4.0e-10
E value
                  58
Match length
                  50
% identity
NCBI Description (AF059488) expansin precursor [Lycopersicon esculentum]
                  293772
Seq. No.
                  LIB3066-053-Q1-K1-F9
Seq. ID
                  BLASTX
Method
                  g2529707
NCBI GI
BLAST score
                  419
                  3.0e-41
E value
                  113
Match length
                   68
% identity
NCBI Description (AF001434) Hpast [Homo sapiens]
```

Seq. No. 293773

Seq. ID LIB3066-053-Q1-K1-H11

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 9.0e-11
Match length 48
% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 293774

Seq. ID LIB3066-054-Q1-K1-B8

Method BLASTX
NCBI GI g4581150
BLAST score 464
E value 1.0e-46
Match length 128

```
% identity
                  (AC006919) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  293775
Seq. No.
                  LIB3066-054-Q1-K1-D12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  9.0e-11
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  293776
Seq. No.
                  LIB3066-054-Q1-K1-D7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3452301
BLAST score
                  107
                   4.0e-53
E value
Match length
                   119
                   97
% identity
                  Zea mays retrotransposon Kake-1 5' LTR, partial sequence
NCBI Description
```

Seq. No. 293777
Seq. ID LIB3066-054-Q1-K1-D8

Seq. ID LIB3066-0
Method BLASTX
NCBI GI g4586107
BLAST score 473
E value 2.0e-47
Match length 143
% identity 12

NCBI Description (ALO49638) putative disease resistance protein [Arabidopsis

ن..

thaliana]

Seq. No. 293778 Seq. ID LIB3066-054-Q1-K1-E10

Method BLASTX
NCBI GI g902586
BLAST score 490
E value 1.0e-49
Match length 124
% identity 18

NCBI Description (U29162) ubiquitin [Zea mays]

Seq. No. 293779

Seq. ID LIB3066-054-Q1-K1-E9

Method BLASTN
NCBI GI g1628481
BLAST score 74

E value 2.0e-33 Match length 78 % identity 99

NCBI Description Z.mays dek34 gene

Seq. No. 293780

Seq. ID LIB3066-054-Q1-K1-F10

Method BLASTX

```
q4539377
NCBI GI
                  150
BLAST score
                  6.0e-10
E value
                  73
Match length
% identity
                  (ALO49525) acyl-CoA synthetase-like protein (fragment)
NCBI Description
                   [Arabidopsis thaliana]
                  293781
Seq. No.
                  LIB3066-054-Q1-K1-G6
Seq. ID
                  BLASTX
Method
                  g1946329
NCBI GI
                  276
BLAST score
                  2.0e-24
E value
                  82
Match length
                  67
% identity
NCBI Description (U69154) prohibitin [Nicotiana tabacum]
Seq. No.
                   293782
                  LIB3066-055-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4587573
                   252
BLAST score
                   1.0e-21
E value
Match length
                   127
                   42
% identity
                   (AC006550) Similar to clathrin assembly protein gb_AF041374
NCBI Description
                   (CALM) from Rattus norvegicus. [Arabidopsis thaliana]
Seq. No.
                   293783
                   LIB3066-055-Q1-K1-C8
Seq. ID
                   BLASTX
Method
                   g4544438
NCBI GI
                   200
BLAST score
E value
                   2.0e-15
Match length
                   94
                   47
% identity
NCBI Description (AC006592) hypothetical protein [Arabidopsis thaliana]
                   293784
Seq. No.
                   LIB3066-055-Q1-K1-E5
Seq. ID
                   {\tt BLASTX}
Method
                   g129940
NCBI GI
BLAST score
                   603
E value
                   8.0e-63
                   126
Match length
                   90
```

% identity

EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE) NCBI Description

(GALACTURAN 1, 4-ALPHA-GALACTURONIDASE)

>gi_100911_pir__S18570 polygalacturonase (EC 3.2.1.15) precursor - maize >gi_22417_emb_CAA40850_ (X57627) polygalacturonase [Zea mays] >gi_22419_emb_CAA44249_

(X62385) polygalacturonase [Zea mays]

>gi 288374 emb CAA46679 (X65844) polygalacturonase [Zea

mays]

293785 Seq. No.

Method

NCBI GI

BLASTX

g3643607



```
LIB3066-055-Q1-K1-H9
Seq. ID
                  BLASTX
Method
                   q2183223
NCBI GI
BLAST score
                   164
                   2.0e-11
E value
                   63
Match length
% identity
NCBI Description (AF002017) arginine decarboxylase [Dianthus caryophyllus]
                   293786
Seq. No.
                   LIB3066-056-Q1-K1-A4
Seq. ID
                   BLASTX
Method
                   q2827520
NCBI GI
BLAST score
                   237
E value
                   7.0e-20
                   131
Match length
                   40
% identity
                   (AL021633) receptor kinase - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   293787
Seq. No.
                   LIB3066-056-Q1-K1-A6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2244788
BLAST score
                   46
                   1.0e-16
E value
Match length
                   74
% identity
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                   293788
Seq. No.
                   LIB3066-056-Q1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2288981
BLAST score
                   452
                   5.0e-45
E value
                   135
Match length
                   64
% identity
                    (AC002335) calcium binding protein isolog [Arabidopsis
NCBI Description
                   thaliana] >gi_3763938 (AC004450) putative calcium binding
                   protein [Arabidopsis thaliana]
                   293789
Seq. No.
                   LIB3066-056-Q1-K1-D11
Seq. ID
Method
                   BLASTN
                   g22458
NCBI GI
                   185
BLAST score
                    1.0e-99
E value
                   281
Match length
                    91
 % identity
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)
                    293790
 Seq. No.
 Seq. ID
                   LIB3066-056-Q1-K1-E12
```

NCBI Description

```
479
BLAST score
                  3.0e-48
E value
                  114
Match length
                  74
% identity
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
                  293791
Seq. No.
                  LIB3066-056-Q1-K1-E7
Seq. ID
                  BLASTX
Method
                  g3482932
NCBI GI
                   434
BLAST score
                   5.0e-43
E value
                   121
Match length
% identity
                   64
NCBI Description (AC003970) Hypothetical protein [Arabidopsis thaliana]
                   293792
Seq. No.
                   LIB3066-056-Q1-K1-G12
Seq. ID
Method
                   BLASTX
                   g3292833
NCBI GI
                   152
BLAST score
E value
                   6.0e-10
                   73
Match length
                   42
% identity
NCBI Description (AL031018) putative membrane protein [Arabidopsis thaliana]
                   293793
Seq. No.
                   LIB3066-056-Q1-K1-G2
Seq. ID
                   BLASTX
Method
                   g4376203
NCBI GI
                   380
BLAST score
                   1.0e-36
E value
                   153
Match length
% identity
                   51
                   (U35226) putative cytochrome P-450 [Nicotiana
NCBI Description
                   plumbaginifolia]
                   293794
 Seq. No.
Seq. ID
                   LIB3066-056-Q1-K1-G4
                   BLASTX
Method
                   g3128176
 NCBI GI
                   175
 BLAST score
                   2.0e-12
 E value
 Match length
                   66
 % identity
                   45
                   (AC004521) unknown protein [Arabidopsis thaliana]
 NCBI Description
                   293795
 Seq. No.
                   LIB3066-056-Q1-K1-G8
 Seq. ID
                   BLASTX
 Method
                   q639722
 NCBI GI
                   813
 BLAST score
                    2.0e-87
 E value
 Match length
                   159
 % identity
```

(L27484) calcium-dependent protein kinase [Zea mays]

```
293796
Seq. No.
                  LIB3066-056-Q1-K1-H2
Seq. ID
                  BLASTN
Method
                  g639721
NCBI GI
                  75
BLAST score
                  5.0e-34
E value
                  110
Match length
% identity
                  93
                  Zea mays calcium-dependent protein kinase (CDPK) gene,
NCBI Description
                  exons 1-7 and partial cds
                   293797
Seq. No.
                  LIB3066-056-Q1-K1-H8
Seq. ID
Method
                  BLASTX
                   g123078
NCBI GI
BLAST score
                   180
                   4.0e-13
E value
                   143
Match length
% identity
                   30
                   BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSOR
NCBI Description
                   (N-ACETYL-BETA-GLUCOSAMINIDASE)
                   (BETA-N-ACETYLHEXOSAMINIDASE) >gi_84092_pir_ A30766
                   beta-N-acetylhexosaminidase (EC 3.2.1.52) A precursor -
                   slime mold (Dictyostelium discoideum) >gi_167841 (J04065)
                   beta-N-acetylhexosaminidase precursor (EC 3.2.1.52)
                   [Dictyostelium discoideum]
                   293798
Seq. No.
                   LIB3067-001-Q1-K1-A4
Seq. ID
Method
                   BLASTX
                   g1053059
NCBI GI
                   255
BLAST score
                   2.0e-22
E value
                   66
Match length
                   79
% identity
NCBI Description (U38423) histone H3 [Triticum aestivum]
                   293799
Seq. No.
                   LIB3067-001-Q1-K1-B4
Seq. ID
                   BLASTX
Method
                   g4038030
NCBI GI
                   160
BLAST score
                   5.0e-11
E value
                   76
Match length
% identity
                   (AC005936) putative protein kinase, 5' partial [Arabidopsis
NCBI Description
                   thaliana]
                   293800
Seq. No.
Seq. ID
                   LIB3067-001-Q1-K1-B6
                   BLASTX
Method
                   q485459
NCBI GI
BLAST score
                   162
                   4.0e-11
E value
Match length
                   82
 % identity
NCBI Description hypothetical protein 2 (phaCl 5' region) - Pseudomonas
```





```
aeruginosa >gi_45390_emb_CAA47150_ (X66592) ORF2 [Pseudomonas aeruginosa]
```

```
293801
Seq. No.
                  LIB3067-001-Q1-K1-B7
Seq. ID
                  BLASTX
Method
                  g1419370
NCBI GI
                  207
BLAST score
                  1.0e-16
E value
                  64
Match length
                  67
% identity
NCBI Description (X97726) actin depolymerizing factor [Zea mays]
                  293802
Seq. No.
                  LIB3067-001-Q1-K1-C9
Seq. ID
                  BLASTX
Method
                  g4558672
NCBI GI
BLAST score
                  144
                  5.0e-09
E value
Match length
                  64
% identity
                  (AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis
NCBI Description
                  thaliana]
                   293803
Seq. No.
                  LIB3067-001-Q1-K1-D9
Seq. ID
                   BLASTX
Method
                   g2668742
NCBI GI
                   151
BLAST score
                   6.0e-10
E value
                   63
Match length
% identity
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]
                   293804
Seq. No.
                   LIB3067-001-Q1-K1-E11
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3821780
BLAST score
                   36
                   7.0e-11
E value
                   48
Match length
                   67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   293805
Seq. No.
                   LIB3067-001-Q1-K1-G10
Seq. ID
                   BLASTX
Method
                   g1001935
NCBI GI
BLAST score
                   347
                   1.0e-32
E value
                   137
Match length
 % identity
                   (X81199) ZMM1 [Zea mays] >gi_1167914 (U31522) MADS box
NCBI Description
                   protein [Zea mays]
```

293806

LIB3067-001-Q1-K1-H6

Seq. No.

Seq. ID

```
Method
NCBI GI
                  q82696
                   227
BLAST score
                   6.0e-19
E value
                   55
Match length
                   78
% identity
                  glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
                   293807
Seq. No.
                  LIB3067-002-Q1-K1-A12
Seq. ID
                  BLASTX
Method
                   g3342821
NCBI GI
                   477
BLAST score
                   5.0e-48
E value
                   114
Match length
                   77
% identity
                   (AF076954) eukaryotic translation initiation factor small
NCBI Description
                   subunit [Zea mays]
                                                             1
                   293808
Seq. No.
                   LIB3067-002-Q1-K1-B10 📡 🗇
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3851332
                   180
BLAST score
                   9.0e-97
E value
                   315
Match length
                   100
% identity
                   Z.mays mRNA for putative MADS-domain transcription factor,
NCBI Description
                   ZMM7
                   293809
Seq. No.
Seq. ID
                   LIB3067-002-Q1-K1-B3
                   BLASTN
Method
                   g287829
NCBI GI
                   73
BLAST score
                   5.0e-33
E value
                   97
Match length
                   94
% identity
                   Z.mays gene for polygalacturonase
NCBI Description
                   293810
Seq. No.
Seq. ID
                   LIB3067-002-Q1-K1-D1
Method
                   BLASTX
                   q1504008
NCBI GI
                   222
BLAST score
                   4.0e-18
E value
                   92
Match length
```

% identity 52

(D86967) Containing ATP/GTP-binding site motif A(P-loop): NCBI Description Similar to C.elegans protein(P1:CEC47E128); Similar to Mouse

alpha-mannosidase(P1:B54407) [Homo sapiens]

Seq. No. 293811

LIB3067-002-Q1-K1-D4 Seq. ID

BLASTX Method NCBI GI q4567310

NCBI Description



```
BLAST score
                   6.0e-28
E value
Match length
                  99
                  71
% identity
NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]
                  293812
Seq. No.
                  LIB3067-002-Q1-K1-D8
Seq. ID
                  BLASTX
Method
                  g1749576
NCBI GI
                  148
BLAST score
                   6.0e-10
E value
                   66
Match length
                   48
% identity
                   (D89184) similar to Saccharomyces cerevisiae acetyl-CoA
NCBI Description
                   acetyltransferase, SWISS-PROT Accession Number P41338
                   [Schizosaccharomyces pombe]
                   293813
Seq. No.
                   LIB3067-002-Q1-K1-F11
Seq. ID
                   BLASTN
Method
                   g2832242
NCBI GI
                   301
BLAST score
                   1.0e-169
E value
                   414
Match length
                   95
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                   293814
Seq. No.
                   LIB3067-002-Q1-K1-F4
Seq. ID
                   {\tt BLASTX}
Method
                   g1370603
NCBI GI
                   248
BLAST score
E value
                   9.0e-22
                   67
Match length
                   75
% identity
NCBI Description (X98245) annexin p35 [Zea mays]
Seq. No.
                   293815
                   LIB3067-002-Q1-K1-F5
Seq. ID
Method
                   BLASTX
                   g1370603
NCBI GI
BLAST score
                   217
E value
                   5.0e-18
                   69
Match length
% identity
                   (X98245) annexin p35 [Zea mays]
NCBI Description
Seq. No.
                   293816
                   LIB3067-002-Q1-K1-G7
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1778146
BLAST score
                   172
E value
                   6.0e-92
Match length
                   292
                   90
% identity
```

Zea mays plastid phosphate/phosphoenolpyruvate translocator



precursor (MZPPT1) mRNA, complete cds

```
293817
Seq. No.
                  LIB3067-003-Q1-K1-A10
Seq. ID
                  BLASTX
Method
                  g1084457
NCBI GI
                  329
BLAST score
                  1.0e-30
E value
Match length
                  142
                  54
% identity
                  elongation factor 1-beta - Rice >gi_432368_dbj_BAA04903_
NCBI Description
                   (D23674) elongation factor 1 beta [Oryza sativa]
                  293818
Seq. No.
                  LIB3067-003-Q1-K1-H11
Seq. ID
                  BLASTN
Method
                  q168500
NCBI GI
                  86
BLAST score
                  2.0e-40
E value
Match length
                  122
                   93
% identity
NCBI Description Maize (Zea mays) histone H4 gene (H4C14), complete cds
                   293819
Seq. No.
                  LIB3067-004-Q1-K1-A4
Seq. ID
Method
                  BLASTX
                   q3935169
NCBI GI
                   173
BLAST score
                   2.0e-12
E value
                   66
Match length
% identity
                   56
                   (AC004557) F17L21.12 [Arabidopsis thaliana]
NCBI Description
                   293820
Seq. No.
                   LIB3067-004-Q1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2492519
BLAST score
                   159
E value
                   3.0e-11
Match length
                   42
                   76
% identity
                   26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
NCBI Description
                   7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase
                   subunit [Spinacia oleracea]
                   293821
Seq. No.
                   LIB3067-004-Q1-K1-C5
Seq. ID
                   BLASTX
Method
                   g1170182
NCBI GI
                   199
BLAST score
                   2.0e-15
E value
                   87
Match length
                   51
 % identity
                   TRANSCRIPTION FACTOR HBP-1B >gi 479793 pir S35439
NCBI Description
                   transcription factor HBP-1b homolog - Arabidopsis thaliana
                   >gi_217827_dbj_BAA00933_ (D10042) AHBP-1b [Arabidopsis
```

thaliana]



```
293822
Seq. No.
                  LIB3067-004-Q1-K1-E11
Seq. ID
                  BLASTN
Method
                  g22292
NCBI GI
                  56
BLAST score
                  4.0e-23
E value
Match length
                  80
% identity
                  93
NCBI Description Z.mays mRNA for glycine-rich protein
                  293823
Seq. No.
                  LIB3067-004-Q1-K1-E4
Seq. ID
Method
                  BLASTN
                  g22338
NCBI GI
                  78
BLAST score
                  9.0e-36
E value
                  158
Match length
                  88
% identity
NCBI Description Maize mRNA for an 18kDa heat shock protein
                  293824
Seq. No.
                  LIB3067-004-Q1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3559935
BLAST score
                  186
                   5.0e-14
E value
                   57
Match length
                   63
% identity
                   (AJ005253) ClpP protease [Mus musculus]
NCBI Description
                   >qi 4454289 emb CAA09966 (AJ012249) ClpP protease [Mus
                  musculus]
                   293825
Seq. No.
                  LIB3067-004-Q1-K1-H5
Seq. ID
                   BLASTX
Method
                   q4102600
NCBI GI
                   285
BLAST score
E value
                   1.0e-25
                   119
Match length
                   51
% identity
NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]
                   293826
Seq. No.
                   LIB3067-005-Q1-K1-A12
Seq. ID
                   BLASTX
Method
                   g1524370
NCBI GI
                   248
BLAST score
                   4.0e-21
E value
                   82
Match length
                   55
% identity
NCBI Description
                  (X92491) TOM20 [Solanum tuberosum]
                   293827
Seq. No.
Seq. ID
                   LIB3067-005-Q1-K1-B1
```

BLASTX

q2984709

Method NCBI GI

BLAST score

Match length

E value

228

71

8.0e-19



```
BLAST score
                  3.0e-14
E value
Match length
                  61
                  61
% identity
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                  293828
Seq. ID
                  LIB3067-005-Q1-K1-B4
                  BLASTX
Method
NCBI GI
                  q3152613
                  153
BLAST score
                  1.0e-10
E value
                  39
Match length
                   67
% identity
NCBI Description (AC004482) hypothetical protein [Arabidopsis thaliana]
                  293829
Seq. No.
Seq. ID
                  LIB3067-005-Q1-K1-B5
                  BLASTN
Method
NCBI GI
                   g2668739
BLAST score
                  267
                   1.0e-148
E value
                   294
Match length
                   98
% identity
                   Zea mays translation initiation factor GOS2 (TIF) mRNA,
NCBI Description
                   complete cds
                   293830
Seq. No.
                   LIB3067-005-Q1-K1-E5
Seq. ID
                   BLASTX
Method
                   g3831453
NCBI GI
                   149
BLAST score
                   1.0e-09
E value
Match length
                   54
% identity
                   43
NCBI Description (AC005700) unknown protein [Arabidopsis thaliana]
                   293831
Seq. No.
Seq. ID
                   LIB3067-006-Q1-K1-C11
                   BLASTX
Method
                   g1076800
NCBI GI
BLAST score
                   285
E value
                   7.0e-26
Match length
                   69
% identity
                   80
                   L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
NCBI Description
                   maize >gi_600116_emb_CAA84406_ (Z34934) cytosolic ascorbate
                   peroxidase [Zea mays] >gi_1096503_prf__2111423A ascorbate
                   peroxidase [Zea mays]
                   293832
Seq. No.
                   LIB3067-006-Q1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3202030
```



```
% identity
                  (AF069318) geranylgeranyl hydrogenase [Mesembryanthemum
NCBI Description
                  crystallinum]
                  293833
Seq. No.
                  LIB3067-006-Q1-K1-F2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3844597
                  209
BLAST score
                  1.0e-16
E value
                  110
Match length
                  41
% identity
                  (U28941) contains similarity to human copine I (GB:U83246)
NCBI Description
                   [Caenorhabditis elegans]
                  293834
Seq. No.
                  LIB3067-006-Q1-K1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4263791
BLAST score
                  227
                   3.0e-32
E value
Match length
                  100
                   79
% identity
                   (AC006068) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                  293835
Seq. No.
                  LIB3067-007-Q1-K1-B5
Seq. ID
                  BLASTN
Method
NCBI GI
                   g3821780
BLAST score
                   36
E value
                   7.0e-11
                   36
Match length
% identity
                   100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   293836
Seq. No.
Seq. ID
                   LIB3067-007-Q1-K1-C7
Method
                   BLASTN
NCBI GI
                   g311238
BLAST score
                   49
E value
                   5.0e-19
                   77
Match length
% identity
                   92
NCBI Description Z.mays cat1 gene for catalase
                   293837
Seq. No.
                   LIB3067-007-Q1-K1-D7
Seq. ID
Method
                   BLASTX
```

NCBI GI g2443329
BLAST score 224
E value 2.0e-18
Match length 43
% identity 91

NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No. 293838



```
Seq. ID LIB3067-007-Q1-K1-E3
```

Method BLASTX
NCBI GI g585661
BLAST score 330
E value 5.0e-31
Match length 97

Match length 97 % identity 69

NCBI Description PEROXIDASE PRECURSOR >gi_287401_dbj_BAA03644_ (D14997)

peroxidase [Oryza sativa]

Seq. No. 293839

Seq. ID LIB3067-007-Q1-K1-E5

Method BLASTX
NCBI GI g122085
BLAST score 388
E value 1.0e-37
Match length 83
% identity 96

NCBI Description HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >qi 82482 pir S04099 histone H3 (variant H3R-21)

- rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays]

>gi_168497 (M13379) histone H3 [Zea mays] >gi_168506

(M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738 emb_CAA59111 (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754 emb_CAA57811 (X82414)

Histone H3 [Asparagus officinalis] >gi 1667592 (U77296) histone 3 [Oryza sativa] >gi 3249101 (AC003114) Match to histone H3 gene gb M17131 and gb M35387 from A. thaliana. ESTs gb H76511 gb H76255, gb AA712452, gb N65260 and gb T42306 come from this gene. [Arabidopsis thaliana] >gi 225459 prf 1303352A histone H3 [Helicoverpa zea]

>gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 293840

Seq. ID LIB3067-007-Q1-K1-F2

Method BLASTN
NCBI GI g342625
BLAST score 207
E value 1.0e-113
Match length 293
% identity 96

NCBI Description Maize chloroplast 50S ribosomal protein (secX) gene,

complete cds

Seq. No. 293841

Seq. ID LIB3067-007-Q1-K1-F4

Method BLASTX

```
q2129826
NCBI GI
                  154
BLAST score
                  2.0e-10
E value
                  64
Match length
% identity
                  dynamin-like protein phragmoplastin 5 - soybean >gi 1218004
NCBI Description
                  (U36430) SDL5A [Glycine max]
                  293842
Seq. No.
                  LIB3067-007-Q1-K1-F6
Seq. ID
```

BLASTX Method g2827709 NCBI GI 193 BLAST score 7.0e-19 E value 91 Match length % identity

NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]

LIB3067-008-Q1-K1-C7 Seq. ID Method BLASTN NCBI GI q485952 39 BLAST score 7.0e-13 E value 59 Match length 92 % identity

Seq. No.

NCBI Description O.sativa mRNA for glutaredoxin

293843

293844 Seq. No. Seq. ID LIB3067-008-Q1-K1-D1 BLASTX Method q3236249 NCBI GI BLAST score 194 5.0e-15 E value 73 Match length

% identity

(AC004684) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 293845 LIB3067-008-Q1-K1-F3 Seq. ID Method BLASTX

NCBI GI g121950 BLAST score 161 E value 4.0e-11 Match length 47 % identity

HISTONE H1 >gi_22321_emb_CAA40362_ (X57077) H1 histone [Zea NCBI Description

mays]

293846 Seq. No.

LIB3067-008-Q1-K1-F5 Seq. ID

BLASTX Method NCBI GI g585783 BLAST score 310 1.0e-28 E value 64 Match length 92 % identity

% identity

NCBI Description



```
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN/TC4 >gi_1076544_pir__S46498
                  GTP-binding protein ran homolog - fava bean
                  >gi 395072_emb_CAA80845 (Z24678) guanine nucleotide
                  regulatory protein [Vicia faba]
                  293847
Seq. No.
                  LIB3067-009-Q1-K1-A1
Seq. ID
Method
                  BLASTN
                  g3821780
NCBI GI
                  36
BLAST score
                  1.0e-10
E value
                  36
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  293848
Seq. No.
                  LIB3067-009-Q1-K1-B7
Seq. ID
                  BLASTX
Method
                  g2459442
NCBI GI
                  226
BLAST score
                   1.0e-18
E value
                   67
Match length
                   73
% identity
                   (AC002332) putative DNA-binding protein PD1 [Arabidopsis
NCBI Description
                   thaliana]
                   293849
Seq. No.
                   LIB3067-009-Q1-K1-C2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2160712
                   401
BLAST score
                   4.0e-39
E value
                   81
Match length
% identity
NCBI Description (U82966) Ca2+-ATPase [Oryza sativa]
                   293850
Seq. No.
Seq. ID
                   LIB3067-009-Q1-K1-C5
                   BLASTN
Method
                   g1419369
NCBI GI
BLAST score
                   60
                   4.0e-25
E value
                   104
Match length
% identity
                   89
NCBI Description Z.mays ZmABP3 mRNA for actin depolymerizing factor
                   293851
Seq. No.
                   LIB3067-009-Q1-K1-F10
Seq. ID
Method
                   BLASTX
                   g1946331
NCBI GI
                   439
BLAST score
                   1.0e-43
E value
                   114
Match length
                   79
```

41021

(U66593) prohibitin 3 [Arabidopsis thaliana]

(U69155) prohibitin [Arabidopsis thaliana] >gi 4097692



```
Seq. No.
                  LIB3067-009-Q1-K1-G6
Seq. ID
                  BLASTX
Method
                  q2501555
NCBI GI
BLAST score
                  335
E value
                  2.0e-31
                  77
Match length
                  81
% identity
                  POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi 549984 (U13148)
NCBI Description
                  possible apospory-associated protein [Pennisetum ciliare]
Seq. No.
                  293853
                  LIB3067-010-Q1-K1-A1
Seq. ID
                  BLASTN
Method
                  g22292
NCBI GI
BLAST score
                  53
                  4.0e-21
E value
                  169
Match length
                  83
% identity
NCBI Description Z.mays mRNA for glycine-rich protein
                   293854
Seq. No.
                  LIB3067-010-Q1-K1-A4
Seq. ID
                   BLASTX
Method
                   q2190007
NCBI GI
                   191
BLAST score
                   3.0e-18
E value
                   104
Match length
% identity
                   (AB004109) phosphatidylserine synthase II [Cricetulus
NCBI Description
                   griseus]
                   293855
Seq. No.
Seq. ID
                   LIB3067-010-Q1-K1-B2
                   BLASTX
Method
                   q2154609
NCBI GI
                   630
BLAST score
E value
                   7.0e-66
                   149
Match length
% identity
                   (D63509) endoxyloglucan transferase related protein
NCBI Description
                   [Arabidopsis thaliana] >gi 4522010 gb AAD21783.1
                   (AC007069) endoxyloglucan transferase [Arabidopsis
                   thaliana]
                   293856
Seq. No.
                   LIB3067-010-Q1-K1-B8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3834307
BLAST score
                   380
E value
                   2.0e-36
```

Match length

108

% identity

67

NCBI Description

(AC005679) Strong similarity to gene T10I14.120 gi 2832679 putative protein from Arabidopsis thaliana BAC gb_AL021712.

ESTs qb N65887 and qb N65627 come from this gene.

[Arabidopsis thaliana]

Seq. ID Method



```
293857
Seq. No.
Seq. ID
                  LIB3067-010-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  q4417271
BLAST score
                  547
                  3.0e-56
E value
                  105
Match length
                  89
% identity
                   (AC007019) putative cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                  293858
Seq. No.
Seq. ID
                  LIB3067-010-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                   q4539660
BLAST score
                  215
E value
                   3.0e-17
                   113
Match length
% identity
                   41
NCBI Description (AF061282) polyprotein [Sorghum bicolor]
                   293859
Seq. No.
                   LIB3067-010-Q1-K1-E1
Seq. ID
Method
                   BLASTN
                   g2062705
NCBI GI
BLAST score
                   37
                   2.0e-11
E value
                   37
Match length
% identity
                   100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                   293860
Seq. ID
                   LIB3067-010-Q1-K1-F12
Method
                   BLASTX
NCBI GI
                   g4406766
BLAST score
                   149
                   9.0e-10
E value
Match length
                   75
                   39
% identity
                   (AC006836) putative flavonol sulfotransferase [Arabidopsis
NCBI Description
                   thaliana]
                   293861
Seq. No.
                   LIB3067-010-Q1-K1-H7
Seq. ID
                   BLASTN
Method
                   g218088
NCBI GI
                   48
BLAST score
                   7.0e-18
E value
                   96
Match length
                   89
% identity
NCBI Description 'Rice mRNA for ribosomal protein 117 (249 gene), partial
                   sequence
                   293862
Seq. No.
```

41023

LIB3067-011-Q1-K1-A5

BLASTX

E value

Match length

7.0e-35

85



```
g1709000
NCBI GI
BLAST score
                  244
E value
                  7.0e-21
Match length
                   63
% identity
                  78
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >qi 960357 dbj BAA09895 (D63835) S-adenosylmethionine
                  synthetase [Hordeum vulgare]
Seq. No.
                  293863
Seq. ID
                  LIB3067-011-Q1-K1-G1
Method
                  BLASTN
NCBI GI
                   g558366
BLAST score
                   34
E value
                   1.0e-09
Match length
                   102
% identity
                   83
NCBI Description Z.mays CYP71C3 mRNA for cytochrome P-450
                   293864
Seq. No.
Seq. ID
                  LIB3067-011-Q1-K1-H12
Method
                   BLASTN
NCBI GI
                   g3859567
BLAST score
                   38
                   3.0e-12
E value
Match length
                   66
% identity
                   89
NCBI Description Oryza sativa clone FIL1 unknown mRNA
                   293865
Seq. No.
Seq. ID
                   LIB3067-011-Q1-K1-H7
Method
                   BLASTX
NCBI GI
                   g2443329
BLAST score
                   279
E value
                   3.0e-25
Match length
                   77
% identity
                   64
NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana]
Seq. No.
                   293866
Seq. ID
                   LIB3067-012-Q1-K1-A12
Method
                   BLASTX
NCBI GI
                   g3269288
BLAST score
                   205
                   1.0e-16
E value
Match length
                   43
% identity
                   88
                   (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                   293867
Seq. No.
                   LIB3067-012-Q1-K1-A9
Seq. ID
Method
                   BLASTX
                   q625509
NCBI GI
BLAST score
                   362
```



```
% identity
                  ubiquitin precursor - Arabidopsis thaliana (fragment)
NCBI Description
                  293868
Seq. No.
Seq. ID
                  LIB3067-012-Q1-K1-B9
Method
                  BLASTX
                  g2760086
NCBI GI
                  203
BLAST score
                  8.0e-16
E value
Match length
                  45
% identity
NCBI Description (Y16046) leucine-rich repeat protein [Arabidopsis thaliana]
                  293869
Seq. No.
                  LIB3067-012-Q1-K1-C10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g439653
BLAST score
                  256
E value
                  1.0e-142
                  268
Match length
                  99
% identity
NCBI Description G.hirsutum mRNA for ribosomal protein 16, small subunit
                  293870
Seq. No.
                  LIB3067-012-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2541876
BLAST score
                  345
                  1.0e-32
E value
Match length
                  135
% identity
                   54
                  (D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                   [Nicotiana tabacum]
                   293871
Seq. No.
Seq. ID
                  LIB3067-012-Q1-K1-C9
Method
                   BLASTX
NCBI GI
                   g231660
BLAST score
                   223
E value
                   4.0e-26
Match length
                   139
% identity
                   50
NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)
                   293872
Seq. No.
                   LIB3067-012-Q1-K1-D9
Seq. ID
Method
                   BLASTN
                   g1143223
```

NCBI GI BLAST score 104 E value 1.0e-51 Match length 192 % identity 26

NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

Seq. No.

293873

Seq. ID

LIB3067-012-Q1-K1-E11

Method

BLASTX

BLAST score

E value

427 4.0e-42

```
g2065531
 NCBI GI
                   260
BLAST score
                   3.0e-23
 E value
                   73
 Match length
 % identity
                   (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
 NCBI Description
                   293874
 Seq. No.
                   LIB3067-012-Q1-K1-E12
 Seq. ID
                   BLASTX
 Method
                   g4587526
 NCBI GI
                   143
 BLAST score
                   5.0e-09
 E value
                   105
 Match length
 % identity
                    (AC007060) Strong similarity to F19I3.2 gi 3033375 putative
 NCBI Description
                   berberine bridge enzyme from Arabidopsis thaliana BAC
                    gb AC004238. ESTs gb_F19886, gb_Z30784 and gb_Z30785 come
                    from this gene
                    293875
 Seq. No.
                   LIB3067-012-Q1-K1-F9
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g4455207
                    386
 BLAST score
                    1.0e-37
 E value
                    88
 Match length
                    88
 % identity
 NCBI Description (AL035440) ubiquitin-like protein [Arabidopsis thaliana]
                    293876
 Seq. No.
                    LIB3067-012-Q1-K1-G9
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g1084358
                    167
 BLAST score
                    3.0e-12
 E value
                    67
 Match length
                    55
 % identity
 NCBI Description ATP synthase - soybean
                    293877
 Seq. No.
                    LIB3067-012-Q1-K1-H10
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1732511
                    141
 BLAST score
                    3.0e-09
 E value
                    44
· Match length
 % identity
                    (U62742) Ran binding protein 1 homolog [Arabidopsis
 NCBI Description
                    thaliana]
                    293878
 Seq. No.
 Seq. ID
                    LIB3067-012-Q1-K1-H12
 Method
                    BLASTX
                    g3334405
 NCBI GI
```

```
Match length 100
% identity 85
VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
>gi 2267583 (AF009338) vacuolar H+-ATPase subunit E
[Gossypium hirsutum]

Seq. No. 293879
```

Seq. ID LIB3067-013-Q1-K1-A2 Method BLASTX NCBI GI g4063770 BLAST score 281 E value 8.0e-29 Match length 132 % identity 54

NCBI Description (AB004906) transposase [Ipomoea purpurea]

Seq. ID LIB3067-013-Q1-K1-C6
Method BLASTX
NCBI GI g4262250
BLAST score 296
E value 4.0e-27
Match length 62
% identity 87

Seq. No.

293880

NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]

 Seq. No.
 293881

 Seq. ID
 LIB3067-013-Q1-K1-D6

 Method
 BLASTX

 NCBI GI
 g542175

 BLAST score
 169

 E value
 4.0e-12

E value 4.0e-12
Match length 84
% identity 56

NCBI Description endoxyloglucan transferase - wheat >gi_469511_dbj_BAA03924_ (D16457) endo-xyloglucan transferase [Triticum aestivum]

Seq. No. 293882
Seq. ID LIB3067-013-Q1-K1-E5

Method BLASTX
NCBI GI g3851331
BLAST score 590
E value 3.0e-61
Match length 123
% identity 96

NCBI Description (Y09301) putative MADS-domain transcription factor [Zea

mays]

 Seq. No.
 293883

 Seq. ID
 LIB3067-013-Q1-K1-F4

 Method
 BLASTX

Method BLASTX
NCBI GI g1655932
BLAST score 228
E value 8.0e-19
Match length 129
% identity 35

NCBI Description (U66565) RUSH-1beta [Oryctolagus cuniculus]

Seq. ID

Method

NCBI GI

BLASTN

g2062705



```
293884
Seq. No.
Seq. ID
                  LIB3067-013-Q1-K1-G12
                  BLASTN
Method
                  g3821780
NCBI GI
BLAST score
                  36
                  8.0e-11
E value
                  48
Match length
                  67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  293885
Seq. No.
                  LIB3067-014-Q1-K1-C11
Seq. ID
                  BLASTX
Method
                  g3342821
NCBI GI
                  250
BLAST score
                  1.0e-21
E value
                   68
Match length
                   71
% identity
                   (AF076954) eukaryotic translation initiation factor small
NCBI Description
                   subunit [Zea mays]
                   293886
Seq. No.
                   LIB3067-014-Q1-K1-D10
Seq. ID
                   BLASTX
Method
                   q488571
NCBI GI
BLAST score
                   322
                   7.0e-30
E value
                   79
Match length
                   87
% identity
                  (U09462) histone H3.2 [Medicago sativa]
NCBI Description
                   293887
Seq. No.
                   LIB3067-014-Q1-K1-E5
Seq. ID
                   BLASTX
Method
                   g4507943
NCBI GI
BLAST score
                   206
E value
                   3.0e-16
                   87
Match length
                   43
% identity
                   exportin 1 (CRM1, yeast, homolog) >gi_2626840_dbj_BAA23415_
NCBI Description
                   (D89729) CRM1 protein [Homo sapiens]
                   293888
Seq. No.
                   LIB3067-014-Q1-K1-E6
Seq. ID
                   BLASTN
Method
                   g2642323
NCBI GI
BLAST score
                   35
                   4.0e-10
E value
Match length
                   35
                   100
% identity
                   Zea mays profilin (PRO4) mRNA, complete cds
NCBI Description
                   293889
Seq. No.
                   LIB3067-014-Q1-K1-E9
```

Match length

176



```
ya buji si ni K
       BLAST score
                          2.0e-11
       E value
                          37
       Match length
                          100
        % identity
       NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
        Seq. No.
                          293890
                          LIB3067-014-Q1-K1-G10
       Seq. ID
       Method
                          BLASTX
       NCBI GI
                          g1488297
       BLAST score
                          155
       E value
                          2.0e-10
                          82
       Match length
                          46
        % identity
        NCBI Description (U63530) osRAD23 [Oryza sativa]
                          293891
        Seq. No.
        Seq. ID
                          LIB3067-014-Q1-K1-G12
       Method
                          BLASTX
       NCBI GI
                          g4567245
       BLAST score
                          264
                           5.0e-23
       E value
       Match length
                          66
                           77
        % identity
        NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]
                           293892
        Seq. No.
        Seq. ID
                          LIB3067-014-Q1-K1-G5
                          BLASTN
        Method
        NCBI GI
                           g4416300
        BLAST score
                           232
        E value
                           1.0e-128
        Match length
                           288
                           77
        % identity
                          Zea mays chromosome 4 22 kDa zein-associated intercluster
        NCBI Description
                           region, complete sequence
        Seq. No.
                           293893
                           LIB3067-014-Q1-K1-G6
        Seq. ID
                           BLASTX
        Method
                           g4586252
        NCBI GI
        BLAST score
                           164
        E value
                           1.0e-11
        Match length
                           77
        % identity
                          (AL049640) hypothetical protein [Arabidopsis thaliana]
        NCBI Description
                           293894
        Seq. No.
        Seq. ID
                           LIB3067-014-Q1-K1-G9
        Method
                           BLASTN
        NCBI GI
                           g1420923
        BLAST score
                           134
        E value
                           2.0e-69
```

% identity 64 Zea mays repressor-like protein (in1) gene, complete cds NCBI Description

```
293895
Seq. No.
Seq. ID
                  LIB3067-016-Q1-K1-B10
                  BLASTX
Method
                  g1778149
NCBI GI
                  252
BLAST score
                  4.0e-22
E value
Match length
                  60
% identity
                  90
NCBI Description (U66404) phosphate/phosphoenolpyruvate translocator
                  precursor [Zea mays]
                  293896
Seq. No.
                  LIB3067-016-Q1-K1-B3
Seq. ID
Method
                  BLASTX
                  g2501021
NCBI GI
                  354
BLAST score
                  6.0e-35
E value
                  125
Match length
% identity
                  63
                  LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS)
NCBI Description
                   >gi 1652562 dbj BAA17483 (D90906) lysyl-tRNA synthetase
                   [Synechocystis sp.]
Seq. No.
                   293897
                  LIB3067-016-Q1-K1-F4
Seq. ID
                  BLASTX
Method
                   g4406770
NCBI GI
                   172
BLAST score
E value
                   9.0e-13
                   52
Match length
                   67
% identity
NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]
                   293898
Seq. No.
                   LIB3067-017-Q1-K1-B4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q70774
BLAST score
                   201
E value
                   1.0e-15
                   41
Match length
                   95
% identity
                  histone H4 (TH091) - wheat >gi_170747 (M12277) histone H4
NCBI Description
                   [Triticum aestivum]
                   293899
Seq. No.
Seq. ID
                   LIB3067-017-Q1-K1-C9
                   BLASTX
Method
NCBI GI
                   g3600040
BLAST score
                   152
E value
                   7.0e-10
Match length
                   145
% identity
                   34
                   (AF080119) similar to Arabidopsis thaliana disease
```

NCBI Description

LIB3067-017-Q1-K1-D1 Seq. ID

resistance protein RPS2 (GB:U14158) [Arabidopsis thaliana]



```
Method
                  q2842490
NCBI GI
                  377
BLAST score
                  3.0e-36
E value
Match length
                  116
% identity
                  69
                  (AL021749) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                  293901
Seq. No.
                  LIB3067-017-Q1-K1-F7
Seq. ID
Method
                  BLASTX
                  g3287696
NCBI GI
                  401
BLAST score
                  4.0e-39
E value
                  129
Match length
% identity
                   (AC003979) Strong similarity to phosphoribosylanthranilate
NCBI Description
                  transferase gb D86180 from Pisum sativum. This ORF may be
                  part of a larger gene that lies in the overlapping region.
                   [Arabidopsis thaliana]
                   293902
Seq. No.
                  LIB3067-018-Q1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4126809
                   323
BLAST score
                   4.0e-30
E value
Match length
                   80
% identity
NCBI Description
                   (AB017042) glyoxalase I [Oryza sativa]
                   293903
Seq. No.
Seq. ID
                   LIB3067-018-Q1-K1-A5
Method
                   BLASTN
NCBI GI
                   g21794
BLAST score
                   36
                  9.0e-11
E value
Match length
                   36
% identity
NCBI Description
                   Wheat histone H4 gene
Seq. No.
                   293904
Seq. ID
                   LIB3067-018-Q1-K1-E11
Method
                   BLASTX
                   g2443388
NCBI GI
BLAST score
                   392
                   4.0e-38
E value
Match length
                   105
% identity
                   69
                   (D38452) calcium-dependent protein kinase-related kinase
NCBI Description
                   [Zea mays]
```

Seq. ID LIB3067-018-Q1-K1-F11

Method BLASTX NCBI GI g3786011 BLAST score 261

1.0e-22 E value 98 Match length % identity

(AC005499) putative elongation factor [Arabidopsis NCBI Description

thaliana]

Seq. No.

293906

Seq. ID

LIB3067-018-Q1-K1-F12

BLASTX Method g2668742 NCBI GI 405 BLAST score 1.0e-39 E value 81 Match length

96 % identity

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No.

293907

LIB3067-018-Q1-K1-F2 Seq. ID

BLASTN Method g22324 NCBI GI 135 BLAST score 6.0e-70 E value 263 Match length 88 % identity

NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)

Seq. No.

293908 LIB3067-018-Q1-K1-F8 Seq. ID

BLASTX Method g3915131 NCBI GI BLAST score 272 6.0e-24

E value 72 Match length 69 % identity

THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1) NCBI Description

>gi 426442 dbj BAA04864 (D21836) thioredoxin h [Oryza sat $\overline{\text{iva}}$] >g $\overline{\text{i}}$ _45 $\overline{\text{4}}$ 882_dbj_ $\overline{\text{B}}$ AA05546_ (D26547) rice thioredoxin h [Oryza sativa] $>\overline{gi}_1\overline{9}30072$ (U $\overline{9}2541$) thioredoxin h [Oryza

sativa]

293909 Seq. No.

LIB3067-018-Q1-K1-H11 Seq. ID

Method BLASTX NCBI GI q1854378 158 BLAST score 6.0e-11 E value Match length 65 49 % identity

(AB001338) Sucrose-Phosphate Synthase [Saccharum NCBI Description

officinarum]

293910 Seq. No.

LIB3067-019-Q1-K1-C10 Seq. ID

Method BLASTX g399854 NCBI GI 189 BLAST score 3.0e-16 E value



Match length 98 % identity 54

NCBI Description HISTONE H2B.2 >gi 283042 pir S28049 histone H2B - maize >gi 22325 emb CAA40565 (X57313) H2B histone [Zea mays]

Seq. No. 293911

Seq. ID LIB3067-019-Q1-K1-C12

Method BLASTX
NCBI GI g1708107
BLAST score 248
E value 5.0e-23
Match length 84
% identity 76

NCBI Description HISTONE H2B >gi_473605 (U08226) histone H2B [Zea mays]

Seq. No. 293912

Seq. ID LIB3067-019-Q1-K1-D12

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 8.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 293913

Seq. ID LIB3067-019-Q1-K1-D9

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 9.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 293914

Seq. ID LIB3067-019-Q1-K1-E7

Method BLASTX
NCBI GI g145203
BLAST score 423
E value 1.0e-41
Match length 125
% identity 59

NCBI Description (M74924) adenylosuccinate lyase [Escherichia coli]

Seq. No. 293915

Seq. ID LIB3067-019-Q1-K1-G1

Method BLASTX
NCBI GI g1922938
BLAST score 324
E value 4.0e-30
Match length 117
% identity 50

NCBI Description (AC000106) Similar to Caenorhabditis hypothetical protein

CO7A9.11 (gb Z29094). [Arabidopsis thaliana]

Seq. No. 293916



```
LIB3067-021-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g22422
                  209
BLAST score
                  1.0e-16
E value
Match length
                  94
% identity
                   (X57743) polygalacturonase [Zea mays]
NCBI Description
                  293917
Seq. No.
Seq. ID
                  LIB3067-021-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g3449282
BLAST score
                  163
                   3.0e-11
E value
                  39
Match length
% identity
                   (AB006139) phosphoribosylformimino-5-aminoimidazole
NCBI Description
                   carboxamide ribotide isomerase [Arabidopsis thaliana]
                  >gi 3449284 dbj BAA32457 (AB008929)
                  N'-5'-phosphoribosyl-formimino-5-aminoimidazole-
                   4-carboxamide ribonucleotide isomerase [Arabidopsis
                   thaliana] >gi 4510353 gb AAD21442.1 (AC006921)
 5.7
                  phosphoribosylformimino-5-aminoimidazole carboxamide
                  ribotide isomerase [Arabidopsis thaliana]
                   293918
Seq. No.
                   LIB3067-021-Q1-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1556380
                   202
BLAST score
                   8.0e-16
E value
Match length
                   45
% identity
                  (X84228) citrate (si)-synthase [Beta vulgaris]
NCBI Description
Seq. No.
                   293919
                   LIB3067-022-Q1-K1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g478740
BLAST score
                   211
E value
                   6.0e-17
Match length
                   70
% identity
                   63
                  phenylalanine ammonia-lyase (EC 4.1.3.5) - rice
NCBI Description
                   293920
Seq. No.
                   LIB3067-022-Q1-K1-C10
Seq. ID
                   BLASTX
Method
                   g3452091
NCBI GI
BLAST score
                  . 173
                   2.0e-12
E value
Match length
                   42
% identity
                   74
                  (AJ004899) rudimentary enhancer [Glycine max]
NCBI Description
```

41034

293921

Seq. No.

BLAST score

E value

149

7.0e-10



```
LIB3067-022-Q1-K1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2586142
BLAST score
                  46
                  9.0e-17
E value
Match length
                  54
% identity
                  96
                  Musa acuminata ripening-associated protein mRNA, partial
NCBI Description
                  293922
Seq. No.
Seq. ID
                  LIB3067-022-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g4249385
BLAST score
                  213
                  2.0e-17
E value
Match length
                  52
                  81
% identity
NCBI Description (AC005966) T2K10.11 [Arabidopsis thaliana]
                  293923
Seq. No.
Seq. ID
                  LIB3067-022-Q1-K1-D10
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
                  8.0e-11
E value
                  36
Match length
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  293924
Seq. No.
Seq. ID
                  LIB3067-022-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  q4263712
BLAST score
                  245
E value
                   7.0e-21
Match length
                   69
% identity
                   67
                   (AC006223) putative ribosomal protein S12 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   293925
Seq. ID
                  LIB3067-022-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                   q3719211
BLAST score
                  158
E value
                   1.0e-10
Match length
                   90
% identity
                   38
                  (U97021) UIP2 [Arabidopsis thaliana]
NCBI Description
                   293926
Seq. No.
                  LIB3067-022-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1703129
```



Match length 52 58 % identity

ACTIN 11 >gi 2129522 pir S68109 actin 11 - Arabidopsis NCBI Description thaliana >gi 1002533 (U27981) actin-11 [Arabidopsis

thaliana]

Seq. No.

293927

Seq. ID

LIB3067-022-Q1-K1-F8

Method BLASTX NCBI GI g129810 191 BLAST score 1.0e-14 E value 57 Match length

67 % identity

PEROXIDASE 2 >gi_81569_pir__S11870 peroxidase (EC 1.11.1.7) NCBI Description

- cucumber (fragment) >gi_167517 (M32742) peroxidase

(CuPer2) [Cucumis sativus]

Seq. No.

293928

Seq. ID

LIB3067-023-Q1-K1-A7

Method BLASTX g66009 NCBI GI BLAST score 170 E value 8.0e-19 87 Match length 66 % identity

glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C, NCBI Description

cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH

(AA 1-337) [Zea mays]

293929 Seq. No.

Seq. ID LIB3067-023-Q1-K1-E1

Method BLASTX NCBI GI g123549 236 BLAST score 1.0e-23 E value 77 Match length % identity 81

17.5 KD CLASS II HEAT SHOCK PROTEIN >gi 100885 pir S14998 NCBI Description

heat shock protein, 18K - maize >gi 22339 emb CAA38013

(X54076) 18kDa heat shock protein [Zea mays]

Seq. No. 293930

Seq. ID LIB3067-023-Q1-K1-E7

BLASTN Method g1244652 NCBI GI BLAST score 54 E value 1.0e-21 Match length 82 91 % identity

Zea mays copia-type retroelement PREM-2 gag gene, complete NCBI Description

Seq. No. 293931

LIB3067-023-Q1-K1-F4 Seq. ID

Method BLASTX NCBI GI q1895084

% identity

88



```
BLAST score
                   2.0e-21
E value
                                                   ٠<u>٠</u>
                  89
Match length
                   60
% identity
NCBI Description (U89897) golgi associated protein se-wap41 [Zea mays]
                  293932
Seq. No.
                  LIB3067-023-Q1-K1-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3746581
                   163
BLAST score
                   1.0e-19
E value
                   97
Match length
                   50
% identity
NCBI Description (AF062403) glutathione S-transferase II [Oryza sativa]
                   293933
Seq. No.
                   LIB3067-025-Q1-K1-A12
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2286152
                   59
BLAST score
                   1.0e-24
E value
                   202
Match length
                   89
% identity
                   Zea mays cytoplasmic malate dehydrogenase mRNA, complete
NCBI Description
                   cds
                   293934
Seq. No.
                   LIB3067-025-Q1-K1-B9
Seq. ID
                   BLASTN
Method
                   g3132824
NCBI GI
BLAST score
                   50
                   5.0e-19
E value
Match length
                   96
                   89
% identity
                   Zea mays putative cytosine-5 DNA methyltransferase (ZMET1)
NCBI Description
                   gene, complete cds
                   293935
Seq. No.
                   LIB3067-025-Q1-K1-D1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2702263
BLAST score
                   257
E value
                   3.0e-22
                   79
Match length
% identity
                   (AC003033) mitochondrial F1-ATPase, gamma subunit
NCBI Description
                   [Arabidopsis thaliana]
                   293936
Seq. No.
                   LIB3067-025-Q1-K1-G1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g668986
BLAST score
                   34
E value
                   1.0e-09
Match length
                   66
```





```
NCBI Description S.tuberosum TYKY2 mRNA for NADH:ubiquinone oxidoreductase
                  293937
Seq. No.
Seq. ID
                  LIB3067-025-Q1-K1-H1
                  BLASTX
Method
NCBI GI
                  g1780757
BLAST score
                  174
E value
                  1.0e-12
Match length
                  46
                  67
% identity
                  (Y10291) highly expressed in proliferating cells
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  293938
                  LIB3067-026-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1173456
BLAST score
                  156
E value
                  1.0e-13
Match length
                  84
                  48
% identity
                  SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN
NCBI Description
                  D3) (SM-D3) >gi 600750 (U15009) Sm D3 [Homo sapiens]
Seq. No.
                  293939
                  LIB3067-026-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3287695
BLAST score
                  196
E value
                  3.0e-15
Match length
                  60
                  60
% identity
                  (AC003979) Similar to hypothetical protein C34B7.2
NCBI Description
                  gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis
                  thaliana]
                  293940
Seq. No.
Seq. ID
                  LIB3067-026-Q1-K1-E8
                  BLASTX
Method
NCBI GI
                  g462195
                  388
BLAST score
                  1.0e-37
E value
                  80
Match length
                  91
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi_100682_pir__S21636 GOS2 protein - rice
                   >gi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]
                   >qi 3789950 (AF094774) translation initiation factor [Oryza
                   satīva]
Seq. No.
                   293941
Seq. ID
                  LIB3067-027-Q1-K1-A4
                  BLASTX
Method
NCBI GI
                   g22465
BLAST score
                   157
```

7.0e-11

63

E value

Match length

```
% identity
                   (Y00322) ribulose 1,5-bisphosphate carboxylase/oxygenase
NCBI Description
                   [Zea mays]
                  293942
Seq. No.
Seq. ID
                  LIB3067-027-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  g2865177
                   170
BLAST score
                   4.0e-12
E value
                   68
Match length
% identity
                   46
```

NCBI Description (AB010946) AtRer1B [Arabidopsis thaliana]

Seq. ID LIB3067-027-Q1-K1-B3 BLASTX Method NCBI GI g3273243 686 BLAST score 2.0e-72 E value 146 Match length

% identity 91

Seq. No.

(AB004660) NLS receptor [Oryza sativa] NCBI Description

>qi 3273245 dbj BAA31166 (AB004814) NLS receptor [Oryza

sativa]

293943

293944 Seq. No.

Seq. ID LIB3067-027-Q1-K1-D6

Method BLASTX NCBI GI g4510342 BLAST score 147 E value 1.0e-09 35 Match length 77 % identity

(AC006921) putative serine/threonine protein kinase NCBI Description

[Arabidopsis thaliana]

293945 Seq. No.

LIB3067-027-Q1-K1-G9 Seq. ID

BLASTX Method NCBI GI g3928843 BLAST score 167 E value 1.0e-11 Match length 62 % identity

(AF063248) homeobox protein [Picea abies] NCBI Description

293946 Seq. No.

LIB3067-028-Q1-K1-A4 Seq. ID

Method BLASTX NCBI GI g100598 BLAST score 434 E value 6.0e-43Match length 114 80 % identity

ubiquitin / ribosomal protein S27a-1 - barley >gi_167073 NCBI Description

(M60175) ubiquitin [Hordeum vulgare]



```
293947
Seq. No.
                  LIB3067-028-Q1-K1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4204858
BLAST score
                  94
E value
                  2.0e-45
                  122
Match length
                  94
% identity
NCBI Description Triticum aestivum heat shock protein 80 mRNA, complete cds
                  293948
Seq. No.
Seq. ID
                  LIB3067-028-Q1-K1-F11
                  BLASTX
Method
                  g2739044
NCBI GI
BLAST score
                  144
                   5.0e-09
E value
Match length
                   84
% identity
                   36
                   (AF024651) polyphosphoinositide binding protein Ssh1p
NCBI Description
                   [Glycine max]
                   293949
Seq. No.
Seq. ID
                  LIB3067-028-Q1-K1-F12
Method
                  BLASTX
                   g2739044
NCBI GI
                   347
BLAST score
E value
                   7.0e-33
                   104
Match length
                   65
% identity
                   (AF024651) polyphosphoinositide binding protein Ssh1p
NCBI Description
                   [Glycine max]
                   293950
Seq. No.
                   LIB3067-028-Q1-K1-H6
Seq. ID
                   BLASTX
Method
                   g1914838
NCBI GI
BLAST score
                   223
                   3.0e-18
E value
                   49
Match length
% identity
                  (U78890) MADS box protein [Oryza sativa]
NCBI Description
Seq. No.
                   293951
Seq. ID
                   LIB3067-028-Q1-K1-H8
Method
                   BLASTX
NCBI GI
                   q4587514
BLAST score
                   573
E value
                   3.0e-59
Match length
                   137
                   78
% identity
                   (AC007060) Similar to WO8E3.3 gi 3880615 putative
NCBI Description
                   GTP-binding protein from C. elegans cosmid gb_Z92773. EST
                   gb AA597331 comes from this gene. [Arabidopsis thaliana]
```

293952

LIB3067-029-Q1-K1-C11

Seq. No.

Seq. ID



```
Method
                  BLASTN
NCBI GI
                  g1276931
BLAST score
                  153
                  1.0e-80
E value
                  157
Match length
                  99
% identity
NCBI Description Zea luxurians Doebley M018 ITS1, 5.8S ribosomal RNA, ITS2
                  293953
Seq. No.
                  LIB3067-029-Q1-K1-C3
Seq. ID
Method
                  BLASTX
                  g585551
NCBI GI
BLAST score
                  168
                  1.0e-11
E value
                  34
Match length
                  94
% identity
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                  >gi_629798_pir__S43330 nucleoside-diphosphate kinase (EC
                  2.7.4.6) - rice >gi 303849 dbj_BAA03798_ (D16292)
                  nucleoside diphosphate kinase [Oryza sativa]
                  293954
Seq. No.
Seq. ID
                  LIB3067-029-Q1-K1-C7
Method
                  BLASTX
                  g1773014
NCBI GI
                  496
BLAST score
                  3.0e-50
E value
                  150
Match length
                  58
% identity
NCBI Description (Y10338) chloride channel Stclc1 [Solanum tuberosum]
                   293955
Seq. No.
Seq. ID
                  LIB3067-029-Q1-K1-F8
                  BLASTN
Method
                   q747914
NCBI GI
                   57
BLAST score
                   3.0e-23
E value
Match length
                   61
% identity
NCBI Description Z.mays CaM1 mRNA for calmodulin
                   293956
Seq. No.
Seq. ID
                   LIB3067-029-Q1-K1-G12
Method
                   BLASTX
                   q4510395
NCBI GI
BLAST score
                   298
E value
                   4.0e-27
Match length
                   66
% identity
                   80
                  (AC006587) putative beta-galactosidase precursor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   293957
Seq. ID
                   LIB3067-029-Q1-K1-H5
Method
                   BLASTX
```

41041

g3036795

217

NCBI GI BLAST score



```
2.0e-17
E value
                  140
Match length
                  41
% identity
                   (AL022373) putative protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3805857 emb_CAA21477_ (AL031986) putative protein
                  [Arabidopsis thaliana]
                  293958
Seq. No.
                  LIB3067-030-Q1-K1-A2
Seq. ID
                  BLASTX
Method
                  g2293360
NCBI GI
                  388
BLAST score
                  1.0e-37
E value
                  103
Match length
                   62
% identity
```

NCBI Description (D87670) polyphenol oxidase [Malus domestica]

```
293959
Seq. No.
                  LIB3067-030-Q1-K1-A7
Seq. ID
                   BLASTX
Method
                   g576773
NCBI GI
                   485
BLAST score
                   6.0e-49
E value
                   142
Match length
                   15
% identity
```

NCBI Description (U16956) polyubiquitin [Filobasidiella neoformans]

```
293960
Seq. No.
                  LIB3067-030-Q1-K1-B2
Seq. ID
                  BLASTX
Method
                   g3201969
NCBI GI
BLAST score
                   627
                   1.0e-65
E value
```

118 Match length 96 % identity

NCBI Description (AF068332) submergence induced protein 2A [Oryza sativa]

```
293961
Seq. No.
                   LIB3067-030-Q1-K1-C5
Seq. ID
                   BLASTX
Method
                   q1931647
NCBI GI
BLAST score
                   211
                   7.0e-17
E value
Match length
                   130
```

43

% identity (U95973) endomembrane protein EMP70 precusor isolog NCBI Description

[Arabidopsis thaliana]

```
Seq. No.
                   293962
                   LIB3067-030-Q1-K1-D11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4584355
```

BLAST score 445 E value 3.0e-44Match length 155 55 % identity

(AC006420) putative Ac-like transposase [Ipomea purpurea] NCBI Description

Seq. ID



[Arabidopsis thaliana]

```
293963
Seq. No.
                  LIB3067-030-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g283047
                  222
BLAST score
                  4.0e-18
E value
                  92
Match length
% identity
NCBI Description 130K protein - maize mitochondrial plasmid-like DNA S-2
                  293964
Seq. No.
                  LIB3067-030-Q1-K1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2129472
BLAST score
                   219
                   2.0e-18
E value
                   76
Match length
                   59
% identity
                   glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
NCBI Description
                   precursor - Scotch pine >gi_1100225 (L32561)
                   glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
                   293965
Seq. No.
                   LIB3067-030-Q1-K1-E4
Seq. ID
                   BLASTX
Method
                   g1362009
NCBI GI
                   181
BLAST score
E value
                   2.0e-13
                   45
Match length
                   82
% identity
                   ubiquitin-like protein 7 - Arabidopsis thaliana
NCBI Description
                   293966
Seq. No.
                   LIB3067-030-Q1-K1-F11
Seq. ID
Method
                   BLASTX
                   g3650029
NCBI GI
BLAST score
                   141
                   7.0e-09
E value
                   56
Match length
 % identity
                   48
                   (AC005396) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   293967
 Seq. No.
                   LIB3067-031-Q1-K1-B2
 Seq. ID
                   BLASTX
Method
                   g1732511
 NCBI GI
                   157
 BLAST score
                   4.0e-11
 E value
                   58
 Match length
                    50
 % identity
                   (U62742) Ran binding protein 1 homolog [Arabidopsis
 NCBI Description
                    thaliana]
                    293968
 Seq. No.
```

41043

LIB3067-031-Q1-K1-C5



```
Method
NCBI GI
                  g82696
                  240
BLAST score
                  2.0e-20
E value
                  58
Match length
                  81
% identity
NCBI Description glycine-rich protein - maize >gi_22293 emb_CAA43431_
                   (X61121) glycine-rich protein [Zea mays]
                  293969
Seq. No.
Seq. ID
                  LIB3067-031-Q1-K1-D8
                  BLASTN
Method
                  g507770
NCBI GI
                   91
BLAST score
                   2.0e-43
E value
                   203
Match length
                   86
% identity
                  Zea mays D3L H(+)-transporting ATPase (Mha1) gene, complete
NCBI Description
Seq. No.
                   293970
                  LIB3067-031-Q1-K1-F1
Seq. ID
                  BLASTN
Method
NCBI GI
                   g3821780
BLAST score
                   36
                   5.0e-11
E value
                  36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   293971
Seq. No.
                   LIB3067-031-Q1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3168840
                   179
BLAST score
                   3.0e-13
E value
                   53
Match length
                   68
% identity
NCBI Description (U88711) copper homeostasis factor [Arabidopsis thaliana]
                   293972
Seq. No.
                   LIB3067-031-Q1-K1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2924509
BLAST score
                   281
E value
                   6.0e-25
                   152
Match length
% identity
                   43
                   (AL022023) subtilisin proteinase - like [Arabidopsis
NCBI Description
                   thaliana]
```

293973

Seq. ID

LIB3067-031-Q1-K1-H12

Method BLASTX NCBI GI g1350742 BLAST score 161 E value 5.0e-11



```
Match length
                  61
% identity
                  PROBABLE 60S RIBOSOMAL PROTEIN L35A >gi_1086831 (U41264)
NCBI Description
                  coded for by C. elegans cDNA yk64g10.5; coded for by C.
                  elegans cDNA yk51f3.5; coded for by C. elegans cDNA
                  yk115e7.3; coded for by C. elegans cDNA yk99d1.3; coded for
                  by C. elegans cDNA yk99d1.5; coded for by C. elegans cDNA
                  yk64g1
                  293974
Seq. No.
                  LIB3067-031-Q1-K1-H5
Seq. ID
                  BLASTN
Method
                  g939784
NCBI GI
                  40
BLAST score
                  4.0e-13
E value
                  84
Match length
                  87
% identity
NCBI Description Zea mays MADS-box protein (ZAP1) mRNA, complete cds
                  293975
Seq. No.
                  LIB3067-032-Q1-K1-D12
Seq. ID
                  BLASTX
Method
                  q1421730
NCBI GI
                  379
BLAST score
                  1.0e-36
E value
                  108
Match length
                  71
% identity
NCBI Description (U43082) RF2 [Zea mays]
                  293976
Seq. No.
                  LIB3067-032-Q1-K1-D4
Seq. ID
                  BLASTN
Method
                  g22292
NCBI GI
BLAST score
                  102
                   3.0e-50
E value
                  181
Match length
                   94
% identity
NCBI Description Z.mays mRNA for glycine-rich protein
                   293977
Seq. No.
                   LIB3067-032-Q1-K1-D6
Seq. ID
Method
                   BLASTN
NCBI GI
                   q6598348
BLAST score
                   34
                   1.0e-09
E value
                   70
Match length
                   87
% identity
                  Arabidopsis thaliana chromosome II BAC T9D9 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
```

LIB3067-032-Q1-K1-E6 Seq. ID

Method BLASTN NCBI GI q487295 BLAST score 42 2.0e-14 E value 54 Match length



```
% identity
NCBI Description Rice mRNA EN242, partial sequence
                  293979
Seq. No.
                  LIB3067-032-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130076
BLAST score
                  211
E value
                  5.0e-17
Match length
                  56
% identity
                   68
NCBI Description homeobox protein - rice
                  293980
Seq. No.
                  LIB3067-032-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g416913
BLAST score
                   162
E value
                   3.0e-11
                   87
Match length
% identity
                   40
                   DNA POLYMERASE I (POL I) >gi_419652_pir__JX0256
NCBI Description
                   DNA-directed DNA polymerase (EC 2.7.7.7) - Bacillus
                   caldotenax >gi_912445_dbj_BAA02361_ (D12982) DNA polymerase
                   [Bacillus caldotenax]
Seq. No.
                   293981
                   LIB3067-033-Q1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3668089
                   515
BLAST score
                   2.0e-52
E value
                   134
Match length
                   71
% identity
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
                   293982
Seq. No.
                   LIB3067-033-Q1-K1-H7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2668742
BLAST score
                   403
                   2.0e-39
E value
                   94
Match length
% identity
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]
Seq. No.
                   293983
                   LIB3067-034-Q1-K1-A8
Seq. ID
Method
                   BLASTN
                   g3821780
NCBI GI
BLAST score
                   36
                   1.0e-10
E value
Match length
                   48
% identity
                   67
                   Xenopus laevis cDNA clone 27A6-1
NCBI Description
```



```
LIB3067-034-Q1-K1-C2
Seq. ID
                  BLASTN
Method
                  g3004949
NCBI GI
                  93
BLAST score
                  6.0e-45
E value
                  212
Match length
                  87
% identity
                  Zea mays tonoplast intrinsic protein (ZmTIP1) mRNA,
NCBI Description
                  complete cds
                  293985
Seq. No.
                  LIB3067-034-Q1-K1-C4
Seq. ID
                  BLASTN
Method
NCBI GI
                  q556685
                  118
BLAST score
                  1.0e-59
E value
                  129
Match length
                  98
% identity
NCBI Description Z.mays mRNA for ADP-ribosylation factor
                   293986
Seq. No.
                  LIB3067-034-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2706450
BLAST score
                   141
                   4.0e-09
E value
Match length
                   34
                   76
% identity
                  (AJ225172) magnesium dependent soluble inorganic
NCBI Description
                   pyrophosphatase [Solanum tuberosum]
                   293987
Seq. No.
                   LIB3067-034-Q1-K1-F8
Seq. ID
                   BLASTN
Method
                   q248338
NCBI GI
                   100
BLAST score
                   3.0e-49
E value
                   188
Match length
                   88
% identity
NCBI Description polyubiquitin [maize, Genomic, 3439 nt]
                   293988
Seq. No.
Seq. ID
                   LIB3067-035-Q1-K1-A10
                   BLASTN
Method
                   q507770
NCBI GI
                   42
BLAST score
                   3.0e-14
E value
                   86
Match length
                   87
% identity
                   Zea mays D3L H(+)-transporting ATPase (Mhal) gene, complete
NCBI Description
                   293989
Seq. No.
Seq. ID
                   LIB3067-035-Q1-K1-B6
Method
                   BLASTN
```

41047

q435542

205

NCBI GI

BLAST score

NCBI GI

E value

BLAST score

q4335750

1.0e-12

175



```
1.0e-111
E value
                  213
Match length
                   99
% identity
                  Z.mays mRNA for calmodulin
NCBI Description
                  293990
Seq. No.
Seq. ID
                  LIB3067-035-Q1-K1-C1
Method
                  BLASTN
NCBI GI
                   g2668739
BLAST score
                   66
                   4.0e-29
E value
                   139
Match length
                   96
% identity
                   Zea mays translation initiation factor GOS2 (TIF) mRNA,
NCBI Description
                   complete cds
                   293991
Seq. No.
                   LIB3067-035-Q1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2529663
BLAST score
                   339
                   8.0e-32
E value
                   135
Match length
                   49
% identity
                   (AC002535) putative lysophospholipase [Arabidopsis
NCBI Description
                   thaliana] >gi_3738277 (AC005309) putative lysophospholipase
                   [Arabidopsis thaliana]
                   293992
Seq. No.
                   LIB3067-035-Q1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4309728
                   253
BLAST score
                   9.0e-22
E value
                   51
Match length
                   90
% identity
                   (AC006439) putative ADP-ribosylation factor [Arabidopsis
NCBI Description
                   thaliana]
                   293993
Seq. No.
Seq. ID
                   LIB3067-035-Q1-K1-F1
                   BLASTX
Method
NCBI GI
                   g550542
BLAST score
                   236
                   9.0e-20
E value
Match length
                   49
% identity
                   96
                   (X81831) cytochrome P450 [Zea mays]
NCBI Description
                   >gi 1850903 emb CAA72196 (Y11368) cytochrome p450 [Zea
                   mays]
                   293994
Seq. No.
Seq. ID
                   LIB3067-035-Q1-K1-G2
Method
                   BLASTX
```



Match length 53 % identity 53

NCBI Description (AC006284) putative beta-1,3-endoglucanase {Arabidopsis

thaliana]

Seq. No. 293995

Seq. ID LIB3067-035-Q1-K1-H2

Method BLASTX
NCBI GI g4220514
BLAST score 419
E value 2.0e-41
Match length 117
% identity 68

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 293996

Seq. ID LIB3067-036-Q1-K1-G5

Method BLASTN
NCBI GI g393399
BLAST score 83
E value 1.0e-38
Match length 225
% identity 85

NCBI Description Z. mays Irma and En1 element DNA

Seq. No. 293997

Seq. ID LIB3067-037-Q1-K1-B12

Method BLASTX
NCBI GI g3935148
BLAST score 629
E value 8.0e-66
Match length 147
% identity 79

NCBI Description (AC005106) T25N20.12 [Arabidopsis thaliana]

Seq. No. 293998

Seq. ID LIB3067-037-Q1-K1-B9

Method BLASTN
NCBI GI g22243
BLAST score 91
E value 2.0e-43
Match length 223
% identity 86

NCBI Description Zea mays Cin1 repeat from Cin1 middle repetitive family

Seq. No. 293999

Seq. ID LIB3067-037-Q1-K1-C12

Method BLASTX
NCBI GI g2664210
BLAST score 227
E value 1.0e-18
Match length 49
% identity 86

NCBI Description (AJ222644) asparaginyl-tRNA synthetase [Arabidopsis

thaliana]

Seq. No. 294000

Seq. ID

Method NCBI GI



```
LIB3067-037-Q1-K1-C8
Seq. ID
                  BLASTN
Method
                  q2984708
NCBI GI
                  144
BLAST score
E value
                  2.0e-75
Match length
                  144
                   100
% identity
                  Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
NCBI Description
Seq. No.
                   294001
Seq. ID
                  LIB3067-037-Q1-K1-E10
                  BLASTX
Method
                   g4538896
NCBI GI
                   230
BLAST score
E value
                   4.0e-25
Match length
                   109
                   55
% identity
NCBI Description (ALO49482) putative protein [Arabidopsis thaliana]
                   294002
Seq. No.
Seq. ID
                   LIB3067-037-Q1-K1-F1
                   BLASTX
Method
                   g4204275
NCBI GI
                   277
BLAST score
                   2.0e-24
E value
Match length
                   149
% identity
                   44
NCBI Description (AC004146) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   294003
                   LIB3067-037-Q1-K1-F12
Seq. ID
Method
                   BLASTX
                   q4505387
NCBI GI
BLAST score
                   301
E value
                   2.0e-27
                   131
Match length
% identity
                   11
                   nuclear transcription factor, X-box binding 1
NCBI Description
                   >gi 2498629_sp_Q12986_NFX1_HUMAN TRANSCRIPTIONAL REPRESSOR
                   NF-X1 >gi_2135825_pir__138869 NFX1 - human >gi_563217
                   (U15306) NFX1 [Homo sapiens]
Seq. No.
                   294004
                   LIB3067-037-Q1-K1-F4
Seq. ID
Method
                   BLASTN
NCBI GI
                   q22324
BLAST score
                   99
                   1.0e-48
E value
Match length
                   123
% identity
                   95
NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)
Seq. No.
                   294005
```

g3242328

BLASTX

LIB3067-037-Q1-K1-H1

Method

NCBI GI

BLASTX

g2149640



```
BLAST score
E value
                  1.0e-37
Match length
                  77
% identity
                  97
NCBI Description
                  (X98083) cinnamoyl-CoA reductase [Zea mays]
Seq. No.
                  294006
                  LIB3067-038-Q1-K1-A8
Seq: ID
Method
                  BLASTX
NCBI GI
                  q4432863
BLAST score
                  265
E value
                  4.0e-23
                  78
Match length
% identity
                  (AC006300) putative phosphate/phosphoenolpyruvate
NCBI Description
                  translocator protein [Arabidopsis thaliana]
Seq. No.
                  294007
Seq. ID
                  LIB3067-038-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  g112994
BLAST score
                  207
                  2.0e-16
E value
Match length
                  44
% identity
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >gi 82685 pir S04536 embryonic abundant protein,
                  glycine-rich - maize >gi 22313 emb CAA31077 (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi 226091 prf 1410284A abscisic acid inducible gene [Zea
                  mays]
Seq. No.
                  294008
Seq. ID
                  LIB3067-038-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g2340953
BLAST score
                  453
E value
                  3.0e-45
Match length
                  87
% identity
                  95
NCBI Description
                  (X99969) ESR2g2 [Zea mays] >gi 2340959 emb CAA67124
                   (X98498) ESR2c1 [Zea mays]
                  294009
Seq. No.
                  LIB3067-038-Q1-K1-D6
Seq. ID
Method
                  BLASTX
                  g3600054
NCBI GI
BLAST score
                  293
                  9.0e-29
E value
Match length
                  121
% identity
                  49
NCBI Description
                  (AF080120) No definition line found [Arabidopsis thaliana]
Seq. No.
                  294010
Seq. ID
                  LIB3067-038-Q1-K1-E7
```



```
BLAST score
                  1.0e-25
E value
                  113
Match length
                  53
% identity
NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]
Seq. No.
                  294011
                  LIB3067-038-Q1-K1-G12
Seq. ID
                  BLASTX
Method
                  g1778147
NCBI GI
BLAST score
                  290
E value
                  2.0e-26
                  75
Match length
                  85
% identity
NCBI Description (U66403) phosphate/phosphoenolpyruvate translocator
                  precursor [Zea mays]
                   294012
Seq. No.
                  LIB3067-038-Q1-K1-G8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2244989
                  175
BLAST score
                   1.0e-12
E value
                   54
Match length
                   61
% identity
NCBI Description (Z97340) strong similarity to naringenin 3-dioxygenase
                   [Arabidopsis thaliana]
                   294013
Seq. No.
Seq. ID
                   LIB3067-039-Q1-K1-A3
                   BLASTX
Method
NCBI GI
                   q2459435
BLAST score
                   471
                   3.0e-47
E value
                   141
Match length
% identity
                   62
                   (AC002332) putative serine carboxypeptidase [Arabidopsis
NCBI Description
                   thaliana]
                   294014
Seq. No.
                   LIB3067-039-Q1-K1-B3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2773153
BLAST score
                   127
                   5.0e-65
E value
                   239
Match length
% identity
                   89
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                   (Asr1) mRNA, complete cds
                   294015
Seq. No.
                   LIB3067-039-Q1-K1-B4
Seq. ID
Method
                   BLASTX
                   g1480012
NCBI GI
                   150
BLAST score
                   3.0e-10
E value
```

41052

35

Match length



```
% identity
                  (D78492) putative ubiquitin extension protein [Brassica
NCBI Description
                  rapa]
                  294016
Seq. No.
Seq. ID
                  LIB3067-039-Q1-K1-D10
                  BLASTN
Method
                  g1743387
NCBI GI
                  50
BLAST score
                  4.0e-19
E value
Match length
                  150
% identity
NCBI Description S.bicolor mRNA for pSbaNS5 protein
                  294017
Seq. No.
Seq. ID
                  LIB3067-039-Q1-K1-E2
Method
                  BLASTN
NCBI GI
                  g3452304
BLAST score
                  63
                  5.0e-27
E value
                  79
Match length
                  95
% identity
                  Zea mays retrotransposon Opie-1 5' LTR, partial sequence
NCBI Description
                  294018
Seq. No.
                  LIB3067-039-Q1-K1-F4
Seq. ID
Method
                  BLASTX
                  g2995321
NCBI GI
                  506
BLAST score
E value
                  2.0e-51
                   151
Match length
% identity
                   66
                  (Z68759) amino acid carrier [Ricinus communis]
NCBI Description
                   294019
Seq. No.
Seq. ID
                   LIB3067-039-Q1-K1-G4
Method
                   BLASTX
NCBI GI
                   g4249382
BLAST score
                   390
E value
                   8.0e-38
Match length
                   113
% identity
                   (AC005966) Strong similarity to gi_3337350 F13P17.3
NCBI Description
                   putative permease from Arabidopsis thaliana BAC
                   qb AC004481. [Arabidopsis thaliana]
                   294020
Seq. No.
                   LIB3067-040-Q1-K1-A11
Seq. ID
                   BLASTX
Method
                   g4454010
NCBI GI
BLAST score
                   199
E value
                   1.0e-15
```

Match length 72 51 % identity

(AL035396) putative protein [Arabidopsis thaliana] NCBI Description

294021 Seq. No.



Seq. ID LIB3067-040-Q1-K1-A7

Method BLASTN
NCBI GI g257040
BLAST score 241
E value 1.0e-133
Match length 361
% identity 32

NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No. 294022

Seq. ID LIB3067-040-Q1-K1-B2

Method BLASTN
NCBI GI g3821780
BLAST score 37
E value 3.0e-11
Match length 49
% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 294023

Seq. ID LIB3067-040-Q1-K1-B6

Method BLASTX
NCBI GI g2924523
BLAST score 221
E value 5.0e-18
Match length 106
% identity 41

NCBI Description (AL022023) putative protein [Arabidopsis thaliana]

Seq. No. 294024

Seq. ID LIB3067-040-Q1-K1-C1

Method BLASTX
NCBI GI g1169238
BLAST score 501
E value 4.0e-51
Match length 129
% identity 78

NCBI Description GLUTAMATE DECARBOXYLASE (GAD) >gi 1076648_pir__A48767

glutamate decarboxylase (EC 4.1.1.15), calmodulin-binding - garden petunia >qi 294112 (L16797) glutamate decarboxylase

[Petunia hybrida] >gi_309680 (L16977) glutamate

decarboxylase [Petunia hybrida]

Seq. No. 294025

Seq. ID LIB3067-040-Q1-K1-C4

Method BLASTN
NCBI GI g3851330
BLAST score 248
E value 1.0e-137
Match length 264
% identity 98

NCBI Description Z.mays mRNA for putative MADS-domain transcription factor,

ZMM3

Seq. No. 294026

Seq. ID LIB3067-040-Q1-K1-D2

Method BLASTN



NCBI GI g393400
BLAST score 45
E value 3.0e-16
Match length 73
% identity 90

NCBI Description Z.mays mRNA for alpha-tubulin

Seq. No. 294027

Seq. ID LIB3067-040-Q1-K1-E11

Method BLASTN
NCBI GI g4185305
BLAST score 48
E value 7.0e-18
Match length 68
% identity 93

NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No. 294028

Seq. ID LIB3067-040-Q1-K1-F2

Method BLASTX
NCBI GI g2498706
BLAST score 194
E value 6.0e-15
Match length 110
% identity 37

NCBI Description ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi_1113103

(U40269) atOrc2p [Arabidopsis thaliana] >gi_3236239

(AC004684) origin recognition complex protein [Arabidopsis

thaliana]

Seq. No. 294029

Seq. ID LIB3067-040-Q1-K1-F3

Method BLASTX
NCBI GI g1532168
BLAST score 172
E value 3.0e-12
Match length 66
% identity 47

NCBI Description (U63815) localized according to blastn similarity to EST

sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop codon could not be precisely determined [Arabidopsis

thaliana]

Seq. No. 294030

Seq. ID LIB3067-040-Q1-K1-F6

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1



```
294031
Seq. No.
                  LIB3067-040-Q1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2623295
BLAST score
                  207
                  2.0e-16
E value
Match length
                  78
                  49
% identity
NCBI Description (AC002409) hypothetical protein [Arabidopsis thaliana]
                  294032
Seq. No.
                  LIB3067-042-Q1-K1-A5
Seq. ID
Method
                  BLASTX
                  q4038042
NCBI GI
BLAST score
                  160
                   2.0e-11
E value
Match length
                  72
% identity
                   46
                  (AC005936) putative DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                  294033
Seq. No.
                  LIB3067-042-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1708107
BLAST score
                  245
                   9.0e-21
E value
Match length
                  85
% identity
                   62
NCBI Description HISTONE H2B >gi 473605 (U08226) histone H2B [Zea mays]
                   294034
Seq. No.
                  LIB3067-042-Q1-K1-B5
Seq. ID
Method
                  BLASTX
                  g2281090
NCBI GI
BLAST score
                   257
                   2.0e-22
E value
Match length
                   91
% identity
                   57
NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   294035
                   LIB3067-042-Q1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1709358
BLAST score
                   238
E value
                   4.0e-20
Match length
                   106
% identity
                   44
NCBI Description
                  NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE
                   PHOSPHOHYDROLASE) (NTPASE) >gi 629638 pir S48859
                   nucleoside triphosphatase - garden pea
                   >gi 2129890 pir S65147 nucleoside triphosphatase
                   precursor, chromatin-associated - garden pea
```

41056

>gi_563612_emb_CAA83655_ (Z32743) nucleoside triphosphatase
[Pisum sativum] >gi_4519173_dbj_BAA75506.1_ (AB022319)
nucleoside triphosphatase (NTPase) [Pisum sativum]



```
294036
Seq. No.
Seq. ID
                  LIB3067-042-Q1-K1-G3
Method
                  BLASTN
NCBI GI
                  g22312
BLAST score
                  50
                  1.0e-19
E value
                  105
Match length
                   90
% identity
                  Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                   abscisic acid)
                   294037
Seq. No.
Seq. ID
                  LIB3067-042-Q1-K1-G8
                   BLASTX
Method
NCBI GI
                   g927575
BLAST score
                   141
E value
                   3.0e-09
                   59
Match length
                   42
% identity
                  (U12926) alpha galactosidase [Glycine max]
NCBI Description
                   294038
Seq. No.
                   LIB3067-043-Q1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g902525
BLAST score
                   380
                   9.0e-37
E value
                   106
Match length
% identity
                   76
                   (U29160) ubiquitin fusion protein [Zea mays]
NCBI Description
                   >gi_1589387_prf__2211240A ubiquitin fusion protein [Zea
                   mays]
                   294039
Seq. No.
                   LIB3067-043-Q1-K1-C5
Seq. ID
Method
                   BLASTX
                   g3360291
NCBI GI
BLAST score
                   137
                   9.0e-09
E value
Match length
                   37
                   73
% identity
                   (AF023165) leucine-rich repeat transmembrane protein kinase
NCBI Description
                   2 [Zea mays]
                   294040
Seq. No.
                   LIB3067-043-Q1-K1-D6
Seq. ID
Method
                   BLASTX
                   g606815
NCBI GI
                   297
BLAST score
                   5.0e-27
E value
                   87
Match length
% identity
                   24
                   (U08403) carbonic anhydrase [Zea mays]
NCBI Description
```

41057

294041

LIB3067-043-Q1-K1-D7

Seq. No.

Seq. ID



```
Method
                  BLASTN
NCBI GI
                  g22292
                  47
BLAST score
                  2.0e-17
E value
                  47
Match length
% identity
                  100
NCBI Description Z.mays mRNA for glycine-rich protein
                  294042
Seq. No.
                  LIB3067-043-Q1-K1-E1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q118104
BLAST score
                  474
                  9.0e-48
E value
                  107
Match length
                  85
% identity
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >qi 68408 pir CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi 168461 (M55021) cyclophilin [Zea mays]
                  >qi 82914\overline{8} emb CAA48638 (X68678) cyclophilin [Zea mays]
                  294043
Seq. No.
Seq. ID
                  LIB3067-043-Q1-K1-H3
                  BLASTX
Method
                  g1076386
NCBI GI
                  369
BLAST score
E value
                  1.0e-35
                  79
Match length
% identity
NCBI Description protein kinase ADK1 - Arabidopsis thaliana >gi 1216484
                   (U48779) dual specificity kinase 1 [Arabidopsis thaliana]
Seq. No.
                   294044
                  LIB3067-044-Q1-K1-A11
Seq. ID
Method
                  BLASTX
                   g1707998
NCBI GI
BLAST score
                   288
                   3.0e-26
E value
                   78
Match length
% identity
                   76
NCBI Description
                  SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >gi 481944 pir S40218 glycine
                   hydroxymethyltransferase (EC 2.1.2.1) - potato
                   >qi 438247 emb CAA81082 (Z25863) glycine
                   hydroxymethyltransferase [Solanum tuberosum]
Seq. No.
                   294045
Seq. ID
                   LIB3067-044-Q1-K1-A5
                   BLASTN
Method
NCBI GI
                   g22330
BLAST score
                   65
E value
                   2.0e-28
Match length
                   97
```

NCBI Description Z.mays Zmhoxla mRNA for homeobox protein

93

% identity

```
294046
Seq. No.
Seq. ID
                  LIB3067-044-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  q4587598
BLAST score
                  480
E value
                  2.0e-48
Match length
                  128
                  72
% identity
                  (AC006951) putative 3-oxoacyl carrier protein synthase II
NCBI Description
                  [Arabidopsis thaliana]
                  294047
Seq. No.
Seq. ID
                  LIB3067-044-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  q2290202
BLAST score
                  228
E value
                  8.0e-19
                  89
Match length
                  53
% identity
                  (U87148) nucellin [Hordeum vulgare] >gi 2290204 (U87149)
NCBI Description
                  nucellin [Hordeum vulgare]
Seq. No.
                  294048
                  LIB3067-044-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2500354
```

 Seq. No.
 294048

 Seq. ID
 LIB3067-044-Q1-K1-F2

 Method
 BLASTX

 NCBI GI
 g2500354

 BLAST score
 285

 E value
 8.0e-26

 Match length
 71

 % identity
 80

NCBI Description 60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_ (AB001891) QM family protein [Solanum melongena]

Seq. ID LIB3067-044-Q1-K1-F9
Method BLASTN
NCBI GI g22320
BLAST score 40
E value 4.0e-13
Match length 64
% identity 91

Seq. No.

NCBI Description Maize H1 mRNA for H1 histone

294049

Seq. No. 294050

Seq. ID LIB3067-045-Q1-K1-A1

Method BLASTX
NCBI GI g100598
BLAST score 489
E value 2.0e-49
Match length 124
% identity 81

NCBI Description ubiquitin / ribosomal protein S27a-1 - barley >gi_167073

(M60175) ubiquitin [Hordeum vulgare]

Seq. No. 294051

Seq. ID LIB3067-045-Q1-K1-A3

E value

Match length

1.0e-48

131



```
BLASTX
Method
                  g1044940
NCBI GI
BLAST score
                  152
E value
                  3.0e-10
Match length
                  50
% identity
                  64
NCBI Description (X92422) fusion gene [Zea mays]
Seq. No.
                  294052
Seq. ID
                  LIB3067-045-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  g3980397
BLAST score
                  246
E value
                  6.0e-21
Match length
                  118
% identity
                  47
                  (AC004561) putative protein phosphatase 2C [Arabidopsis
NCBI Description
                  thaliana]
                  294053
Seq. No.
Seq. ID
                  LIB3067-045-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  g1845197
BLAST score
                  238
E value
                  5.0e-20
Match length
                  93
% identity
NCBI Description (Y08298) HMGc2 [Zea mays]
Seq. No.
                  294054
                  LIB3067-045-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4204310
BLAST score
                   371
                   1.0e-35
E value
                   97
Match length
                  72
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  294055
Seq. No.
Seq. ID
                  LIB3067-045-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                   g4582436
BLAST score
                   358
                   3.0e-34
E value
                  83
Match length
                  83
% identity
NCBI Description (AC007196) unknown protein [Arabidopsis thaliana]
Seq. No.
                   294056
Seq. ID
                   LIB3067-045-Q1-K1-F12
Method
                   BLASTX
NCBI GI
                   g4455210
BLAST score
                   482
```



% identity 70
NCBI Description (AL035440) putative aspartate-tRNA ligase [Arabidopsis
thaliana]

Seq. No. 294057

Seq. ID LIB3067-045-Q1-K1-G8

Method BLASTX
NCBI GI 9464707
BLAST score 268
E value 4.0e-27
Match length 91
% identity 69

NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal

protein S18.A - Arabidopsis thaliana

>gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
[Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)

S18 ribosomal protein [Arabidopsis thaliana]

>gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1 (AL049482) S18.A ribosomal

protein [Arabidopsis thaliana]

Seq. No. 294058

Seq. ID LIB3067-045-Q1-K1-H2

Method BLASTN NCBI GI g3411265

BLAST score 34

E value 1.0e-09
Match length 46

% identity 93

NCBI Description Zea mays pullulanase-type starch debranching enzyme (zpul)

mRNA, complete cds

Seq. No. 294059

Seq. ID LIB3067-046-Q1-K1-C2

Method BLASTN
NCBI GI g1864000
BLAST score 46
E value 7.0e-17
Match length 106
% identity 86

NCBI Description Maize DNA for Fd III, complete cds

Seq. No. 294060

Seq. ID LIB3067-046-Q1-K1-C6

Method BLASTX
NCBI GI g3819164
BLAST score 306
E value 6.0e-28
Match length 101
% identity 62



(AJ012318) cytosolic chaperonin, delta-subunit [Glycine NCBI Description Seq. No. 294061 Seq. ID LIB3067-046-Q1-K1-D1 Method BLASTX NCBI GI g2129622 BLAST score 260 E value 1.0e-22 Match length 63 % identity 79

immunophilin FKBP15-1 - Arabidopsis thaliana >gi_1272406 NCBI Description (U52046) immunophilin [Arabidopsis thaliana]

294062 Seq. No. Seq. ID LIB3067-046-Q1-K1-F7 Method BLASTX NCBI GI q417154

BLAST score 299 2.0e-27 E value 64 Match length % identity 97

HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock NCBI Description

protein 82 - rice (strain Taichung Native One)

>gi 20256 emb CAA77978 (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 294063

Seq. ID LIB3067-046-Q1-K1-G4

Method BLASTX NCBI GI g4522004 BLAST score 245 E value 6.0e-21 Match length 88 % identity 59

(AC007069) putative histidine kinase, sensory transduction NCBI Description

[Arabidopsis thaliana]

294064 Seq. No.

LIB3067-046-Q1-K1-H5 Seq. ID

Method BLASTX NCBI GI g2262143 BLAST score 349 4.0e-33 E value Match length 96 68 % identity

(AC002330) putative serine/threonine protein kinase NCBI Description

[Arabidopsis thaliana]

294065 Seq. No.

LIB3067-046-Q1-K1-H9 Seq. ID

Method BLASTX NCBI GI g1154954 BLAST score 211 4.0e-17 E value Match length 52 % identity 87





```
(X94693) histone H2A [Triticum aestivum]
NCBI Description
                  294066
Seq. No.
                  LIB3067-047-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2541876
BLAST score
                  179
                   5.0e-13
E value
                  113
Match length
                   38
% identity
                   (D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                   [Nicotiana tabacum]
                   294067
Seq. No.
                  LIB3067-047-Q1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1085973
BLAST score
                   218
E value
                   9.0e-18
                   45
Match length
                   91
% identity
                   isopentyl pyrophosphate isomerase - Clarkia breweri
NCBI Description
                   (fragment) >gi 572635 emb CAA57947 (X82627) isopentenyl
                   pyrophosphate isomerase [Clarkia breweri]
                   294068
Seq. No.
                   LIB3067-047-Q1-K1-C10
Seq. ID
Method
                   BLASTX
                   g4510363
NCBI GI
BLAST score
                   375
                   5.0e-36
E value
                   85
Match length
% identity
                   (AC007017) putative DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   294069
Seq. ID
                   LIB3067-047-Q1-K1-C2
Method
                   BLASTX
NCBI GI
                   g2286111
BLAST score
                   307
                   4.0e-28
E value
Match length
                   94
% identity
                   (U78891) MADS box protein [Oryza sativa]
NCBI Description
                   294070
Seq. No.
                   LIB3067-047-Q1-K1-D1
Seq. ID
Method
                   BLASTN
```

NCBI GI g4416300
BLAST score 109
E value 3.0e-54
Match length 371
% identity 83

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster

region, complete sequence



```
Seq. No.
                  294071
                  LIB3067-047-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3660469
BLAST score
                  568
E value
                  1.0e-58
Match length
                  145
                  80
% identity
                  (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis
NCBI Description
                  thaliana] >gi 4512693 gb AAD21746.1_ (AC006569)
                  succinyl-CoA ligase beta subunit [Arabidopsis thaliana]
Seq. No.
                  294072
Seq. ID
                  LIB3067-047-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  q3426038
BLAST score
                  315
E value
                  8.0e-32
                  125
Match length
                  62
% identity
                  (AC005168) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  294073
Seq. ID
                  LIB3067-047-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  g1708107
BLAST score
                  196
E value
                  4.0e-15
Match length
                  39
% identity
                  100
NCBI Description HISTONE H2B >gi 473605 (U08226) histone H2B [Zea mays]
                  294074
Seq. No.
                  LIB3067-047-Q1-K1-E3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1170898
BLAST score
                  214
                  3.0e-17
E value
                  109
Match length
% identity
                  49
                  MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >qi 629659 pir S44167 malate dehydrogenase, mitochondrial
                  - cider tree >gi 473206 emb CAA55383 (X78800)
                  mitochondrial malate dehydrogenase [Eucalyptus gunnii]
                  294075
Seq. No.
                  LIB3067-048-Q1-K1-A12
Seq. ID
Method
                  BLASTN
                  g257040
NCBI GI
```

Method BLASTN
NCBI GI g257040
BLAST score 230
E value 1.0e-126
Match length 398
% identity 89

NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No. 294076

Seq. ID LIB3067-048-Q1-K1-A4



```
BLASTX
Method
                  q4588012
NCBI GI
BLAST score
                   405
E value
                  2.0e-39
Match length
                  142
                  55
% identity
                  (AF085717) putative callose synthase catalytic subunit
NCBI Description
                   [Gossypium hirsutum]
Seq. No.
                  294077
                  LIB3067-048-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1084427
BLAST score
                  221
E value
                   5.0e-18
Match length
                  53
% identity
                   66
                  gip1 protein - garden petunia >gi 825524 emb CAA60677
NCBI Description
                   (X87225) gip1 [Petunia x hybrida]
Seq. No.
                  294078
                  LIB3067-048-Q1-K1-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4416300
BLAST score
                  182
E value
                  7.0e-98
Match length
                   194
% identity
                   36
NCBI Description
                   region, complete sequence
Seq. No.
                   294079
```

Zea mays chromosome 4 22 kDa zein-associated intercluster

LIB3067-048-Q1-K1-F9 Seq. ID

Method BLASTN g296593 NCBI GI BLAST score 51 E value 1.0e-19 75 Match length % identity 92

NCBI Description H. vulgare pZE40 gene

294080 Seq. No.

LIB3067-048-Q1-K1-G3 Seq. ID

Method BLASTX NCBI GI q1709000 BLAST score 529 5.0e-54 E value 127 Match length 83 % identity

S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi 960357 dbj BAA09895 (D63835) S-adenosylmethionine

synthetase [Hordeum vulgare]

294081 Seq. No.

LIB3067-048-Q1-K1-H1 Seq. ID

Method BLASTX

```
NCBI GI
                  g1362162
BLAST score
                  157
                  1.0e-10
E value
Match length
                  87
% identity
                  39
                  beta-glucosidase BGQ60 precursor - barley >gi 804656
NCBI Description
                  (L41869) beta-glucosidase [Hordeum vulgare]
                  294082
Seq. No.
Seq. ID
                  LIB3067-049-Q1-K1-C4
Method
                  BLASTN
NCBI GI
                  g939784
BLAST score
                  79
                  4.0e-37
E value
Match length
                  99
% identity
                  96
NCBI Description Zea mays MADS-box protein (ZAP1) mRNA, complete cds
                  294083
Seq. No.
                  LIB3067-049-Q1-K1-D7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3851332
BLAST score
                  216
E value
                  1.0e-118
                  232
Match length
% identity
                  99
NCBI Description
                  Z.mays mRNA for putative MADS-domain transcription factor,
                  ZMM7
                  294084
Seq. No.
                  LIB3067-049-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q462195
BLAST score
                  364
E value
                  1.0e-34
Match length
                  109
% identity
                  65
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi_100682_pir__S21636 GOS2 protein - rice
                  >gi_20238_emb_CAA36190 (X51910) GOS2 [Oryza sativa]
                  >gi 3789950 (AF094774) translation initiation factor [Oryza
                  sativa]
                  294085
Seq. No.
Seq. ID
                  LIB3067-049-Q1-K1-G11
Method
                  BLASTX
                  g3386615
NCBI GI
```

BLAST score 160 E value 7.0e-11 Match length 45 % identity 62

NCBI Description (AC004665) putative phosphomannomutase [Arabidopsis

thalianal

Seq. No.

294086

Seq. ID

LIB3067-050-Q1-K1-A8

Method

BLASTX



```
NCBI GI
                  g3582332
BLAST score
                  189
E value
                  3.0e-14
Match length
                  78
% identity
                  42
                  (AC005496) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  294087
                  LIB3067-050-Q1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3163946
BLAST score
                  356
E value
                  7.0e - 34
Match length
                  93
% identity
NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]
Seq. No.
                  294088
Seq. ID
                  LIB3067-050-Q1-K1-F7
Method
                  BLASTN
NCBI GI
                  q939784
BLAST score
                  125
E value
                  7.0e-64
Match length
                  165
                  95
% identity
NCBI Description Zea mays MADS-box protein (ZAP1) mRNA, complete cds
                  294089
Seq. No.
Seq. ID
                  LIB3067-050-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  q3024363
BLAST score
                  396
E value
                  1.0e-38
Match length
                  95
% identity
                  79
                  PHENYLALANINE AMMONIA-LYASE >gi 1483610 emb CAA68036
NCBI Description
                  (X99705) phenylalanine ammonia-lyase [Triticum aestivum]
                  294090
Seq. No.
Seq. ID
                  LIB3067-051-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  g3738297
BLAST score
                  154
                  4.0e-10
E value
Match length
                  32
                  75
% identity
NCBI Description
                  (AC005309) unknown protein [Arabidopsis thaliana]
                  294091
Seq. No.
                  LIB3067-051-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914685
BLAST score
                  285
                  2.0e-25
E value
Match length
                  95
```

% identity 65
NCBI Description 60S RIBOSOMAL PROTEIN L17 >gi 2668748 (AF034948) ribosomal

NCBI Description



protein L17 [Zea mays]

```
294092.
Seq. No.
                  LIB3067-051-Q1-K1-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g585551
BLAST score
                  543
                  9.0e-56
E value
                  107
Match length
                  96
% identity
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                  >gi_629798_pir__S43330 nucleoside-diphosphate kinase (EC
                  2.7.4.6) - rice >gi 303849_dbj_BAA03798_ (D16292)
                  nucleoside diphosphate kinase [Oryza sativa]
                  294093
Seq. No.
Seq. ID
                  LIB3067-051-Q1-K1-D9
                  BLASTX
Method
                  g1658193
NCBI GI
BLAST score
                  372
E value
                  1.0e-35
Match length
                  133
% identity
                   61
                  (U74319) obtusifoliol 14-alpha demethylase CYP51 [Sorghum
NCBI Description
                  bicolor]
                   294094
Seq. No.
                  LIB3067-051-Q1-K1-F1
Seq. ID
                  BLASTX
Method
                   g4567249
NCBI GI
BLAST score
                   246
E value
                   6.0e-21
Match length
                   58
% identity
                   76
                  (AC007070) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   294095
Seq. No.
Seq. ID
                   LIB3067-051-Q1-K1-G6
                   BLASTX
Method
                   q4567247
NCBI GI
BLAST score
                   160
E value
                   8.0e-11
Match length
                   122
% identity
                  (AC007070) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   294096
Seq. ID
                   LIB3067-051-Q1-K1-H2
Method
                   BLASTX
NCBI GI
                   g132964
BLAST score
                   145
                   2.0e-09
E value
Match length
                   52
% identity
                   52
```

(X60744) ribosomal protein [Rattus norvegicus]

60S RIBOSOMAL PROTEIN L29 (P23) >gi 71376 pir R6RT43

ribosomal protein RL43 - rat >gi 57145 emb CAA43146





>gi 312208_emb_CAA48344_ (X68283) rat ribosomal protein L29 [Rattus norvegicus]

294097 Seq. No. Seq. ID LIB3067-051-Q1-K1-H7 Method BLASTX NCBI GI g3914935 BLAST score 158 2.0e-22 E value 99 Match length 50 % identity NCBI Description

40S RIBOSOMAL PROTEIN SA (P40) >qi 3204099 emb CAA07226

(AJ006759) ribosome-associated protein p40 [Cicer

arietinum]

294098 Seq. No.

Seq. ID LIB3067-052-Q1-K1-A6 BLASTX Method

NCBI GI q4049341 BLAST score 181 1.0e-13 E value 82 Match length 51 % identity

NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

294099 Seq. No.

Seq. ID LIB3067-052-Q1-K1-B10

Method BLASTX NCBI GI g3355483 BLAST score 253 E value 1.0e-21 Match length 62 % identity 68

(AC004218) gibberellin-regulated protein (GASA5)-like NCBI Description

[Arabidopsis thaliana]

Seq. No. 294100

LIB3067-052-Q1-K1-B3 Seq. ID

Method BLASTN NCBI GI g1906603 BLAST score 77 3.0e-35 E value Match length 109 % identity 92

Zea mays ACCase gene, intron containing colonist1 and NCBI Description

colonist2 retrotransposons and reverse transcriptase

pseudogene, complete sequence

294101 Seq. No.

LIB3067-052-Q1-K1-B6 Seq. ID

Method BLASTX NCBI GI q3869280 BLAST score 218 4.0e-20 E value Match length 70 73 % identity

(AF064786) beta-galactosidase precursor [Carica papaya] NCBI Description

Method

NCBI GI

E value

BLAST score

BLASTX

169

g4586021

7.0e-12



```
294102
 Seq. No.
 Seq. ID
                   LIB3067-052-Q1-K1-C3
 Method
                   BLASTN
 NCBI GI
                    g4007864
 BLAST score
                   153
                    1.0e-80
 E value
                    309
 Match length
 % identity
                    28
 NCBI Description Zea mays HRGP gene, AC1503 line
                    294103
 Seq. No.
                   LIB3067-052-Q1-K1-E1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q482985
 BLAST score
                    213
 E value
                    2.0e-17
 Match length
                    33
 % identity
                    100
 NCBI Description chitinase (EC 3.2.1.14) precursor - maize (fragment)
 Seq. No.
                    294104
                    LIB3067-052-Q1-K1-E5
 Seq. ID
 Method
                    BLASTN
                    g3821780
 NCBI GI
. BLAST score
                    36
                    8.0e-11
 E value
 Match length
                    36
                    100
 % identity
 NCBI Description Xenopus laevis cDNA clone 27A6-1
                    294105
 Seq. No.
                    LIB3067-052-Q1-K1-G7
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4103243
                    198
 BLAST score
                    2.0e-15
 E value
 Match length
                    65
 % identity
                    57
 NCBI Description (AF022368) BIPOSTO [Arabidopsis thaliana]
                    294106
 Seq. No.
                    LIB3067-052-Q1-K1-H3
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g3821780
 BLAST score
                    36
                    8.0e-11
 E value
 Match length
                    48
 % identity
                    67
 NCBI Description Xenopus laevis cDNA clone 27A6-1
                    294107
 Seq. No.
                    LIB3067-053-Q1-K1-A11
 Seq. ID
```



Match length 54 % identity 63

NCBI Description (AC007170) putative cytoplasmic aconitate hydratase

[Arabidopsis thaliana]

Seq. No. 294108

Seq. ID LIB3067-053-Q1-K1-A2

Method BLASTX
NCBI GI g118104
BLAST score 581
E value 4.0e-60
Match length 125
% identity 89

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)

>gi 68408 pir CSZM peptidylprolyl isomerase (EC 5.2.1.8) -

maize >gi 168461 (M55021) cyclophilin [Zea mays]

>gi 829148 emb CAA48638 (X68678) cyclophilin [Zea mays]

Seq. No. 294109

Seq. ID LIB3067-053-Q1-K1-B5

Method BLASTX
NCBI GI g4090257
BLAST score 143
E value 5.0e-09
Match length 88
% identity 43

NCBI Description (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]

Seq. No. 294110

Seq. ID LIB3067-053-Q1-K1-D1

Method BLASTX
NCBI GI g2462746
BLAST score 185
E value 7.0e-14
Match length 108
% identity 41

NCBI Description (AC002292) Similar to ATP-citrate-lyase [Arabidopsis

thaliana]

Seq. No. 294111

Seq. ID LIB3067-053-Q1-K1-E5

Method BLASTX
NCBI GI g2290780
BLAST score 150
E value 6.0e-10
Match length 57
% identity 54

NCBI Description (AF002667) heat shock cognate protein [Solanum commersonii]

Seq. No. 294112

Seq. ID LIB3067-053-Q1-K1-G10

Method BLASTX
NCBI GI g3036810
BLAST score 214
E value 3.0e-17
Match length 72



% identity 58

NCBI Description (AL022373) putative Myc-type transcription factor

[Arabidopsis thaliana]

Seq. No. 294113

Seq. ID LIB3067-053-Q1-K1-G6

Method BLASTN
NCBI GI g444046
BLAST score 43
E value 6.0e-15
Match length 103
% identity 85

NCBI Description Z.mays OBF1 mRNA for ocs-element binding factor

Seq. No.

Seq. ID LIB3067-053-Q1-K1-H11

294114

Method BLASTX
NCBI GI g2832694
BLAST score 263
E value 6.0e-23
Match length 143
% identity 13

NCBI Description (AL021713) putative protein [Arabidopsis thaliana]

Seq. No. 294115

Seq. ID LIB3067-054-Q1-K1-C7

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 9.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 294116

Seq. ID LIB3067-054-Q1-K1-D10

Method BLASTN
NCBI GI g1914844
BLAST score 53
E value 4.0e-21
Match length 167
% identity 86

NCBI Description Zea mays liquleless1 protein (liquleless1) mRNA, complete

cds

Seq. No. 294117

Seq. ID LIB3067-054-Q1-K1-H7

Method BLASTN
NCBI GI g4416300
BLAST score 75
E value 4.0e-34
Match length 147
% identity 89

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster

region, complete sequence

Seq. No. 294118



```
LIB3067-054-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245118
                  197
BLAST score
                  3.0e-15
E value
Match length
                  59
% identity
NCBI Description (297343) hypothetical protein [Arabidopsis thaliana]
                  294119
Seq. No.
Seq. ID
                  LIB3067-055-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  g2414681
                  174
BLAST score
                  1.0e-12
E value
                  38
Match length
% identity
                  82
NCBI Description (Z99174) cysteine proteinase precursor [Vicia narbonensis]
                  294120
Seq. No.
Seq. ID
                  LIB3067-055-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g2497748
BLAST score
                  162
                  3.0e-11
E value
                  53
Match length
                  55
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 4 PRECURSOR (LTP 4)
NCBI Description
                  >qi 902058 (U29176) lipid transfer protein precursor [Oryza
                  satīva]
                  294121
Seq. No.
Seq. ID
                  LIB3067-055-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g2911280
BLAST score
                  317
E value
                  3.0e-29
Match length
                  122
                  53
% identity
                  (U73937) PK12 protein kinase [Nicotiana tabacum]
NCBI Description
Seq. No.
                  294122
                  LIB3067-055-Q1-K1-C3
Seq. ID
Method
                  BLASTX
                  g2935342
NCBI GI
BLAST score
                  412
                  2.0e-40
E value
Match length
                  105
                  72
% identity
                  (AF044216) steroid 22-alpha-hydroxylase; DWF4; CYP90B1
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  294123
                  LIB3067-055-Q1-K1-C7
Seq. ID
```

41073

BLASTX

337

g1703199

Method

NCBI GI BLAST score

% identity



```
E value
                  8.0e-32
Match length
                  97
                  64
% identity
                  PROTEIN KINASE AFC1 >gi 601787 (U16176) protein kinase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  294124
Seq. ID
                  LIB3067-055-Q1-K1-D9
                  BLASTX
Method
                  q282994
NCBI GI
BLAST score
                  204
                  1.0e-16
E value
Match length
                  58
                  72
% identity
NCBI Description Sip1 protein - barley >gi_167100 (M77475) seed imbibition
                  protein [Hordeum vulgare]
                  294125
Seq. No.
                  LIB3067-055-Q1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4585995
BLAST score
                  241
E value
                  2.0e-20
Match length
                  65
                  71
% identity
NCBI Description (AC005287) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  294126
                  LIB3067-055-Q1-K1-E3
Seq. ID
Method
                  BLASTX
                  g3757520
NCBI GI
BLAST score
                  161
E value
                  3.0e-11
                  48
Match length
% identity
NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]
Seq. No.
                  294127
                  LIB3067-055-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4099406
BLAST score
                  151
E value
                   4.0e-12
Match length
                  41
% identity
                  (U86762) gamma-type tonoplast intrinsic protein [Triticum
NCBI Description
                  aestivum]
Seq. No.
                  294128
                  LIB3067-055-Q1-K1-H11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g22237
BLAST score
                  71
                  7.0e-32
E value
Match length
                  218
                  84
```

41074

NCBI Description Maize mRNA for cytosolic GAPDH (GapC)

Method

BLASTN



glyceraldehyde-3-phosphate dehydrogenase

```
294129
Seq. No.
                  LIB3067-056-Q1-K1-D5
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3821780
BLAST score
                  33
                  5.0e-09
E value
                  37
Match length
                  97
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  294130
Seq. No.
                  LIB3067-056-Q1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g70753
BLAST score
                  191
                  1.0e-14
E value
                  61
Match length
% identity
                  66
                  histone H3 - garden pea >gi 82610_pir__S00373 histone H3 -
NCBI Description
                  wheat
                  294131
Seq. No.
Seq. ID
                  LIB3067-056-Q1-K1-F7
                  BLASTN
Method
                  g1244652
NCBI GI
BLAST score
                  104
                  1.0e-51
E value
                  198
Match length
% identity
                  97
                  Zea mays copia-type retroelement PREM-2 gag gene, complete
NCBI Description
                  294132
Seq. No.
Seq. ID
                  LIB3067-057-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g1143864
BLAST score
                  331
E value
                  2.0e-33
Match length
                  106
% identity
                  74
                  (U28047) beta glucosidase [Oryza sativa]
NCBI Description
Seq. No.
                  294133
                  LIB3067-057-Q1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2982289
BLAST score
                   140
                   8.0e-09
E value
Match length
                   47
% identity
                   64
                  (AF051229) 60S ribosomal protein L17 [Picea mariana]
NCBI Description
                   294134
Seq. No.
                  LIB3067-057-Q1-K1-C11
Seq. ID
```

% identity

62



```
NCBI GI
                  g2668739
BLAST score
                   47
                   2.0e-17
E value
                  107
Match length
% identity
                   87
                  Zea mays translation initiation factor GOS2 (TIF) mRNA,
NCBI Description
                  complete cds
                  294135
Seq. No.
Seq. ID
                  LIB3067-057-Q1-K1-D12
Method
                  BLASTX
                  g4262186
NCBI GI
BLAST score
                  199
                   8.0e-16
E value
                   70
Match length
                   57
% identity
NCBI Description (AC005508) Highly similar to cullin 3 [Arabidopsis
                   thaliana]
                   294136
Seq. No.
                  LIB3067-057-Q1-K1-E11
Seq. ID
Method
                  BLASTX
                   g2668742
NCBI GI
                   385
BLAST score
                   2.0e-37
E value
                   84
Match length
% identity
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]
Seq. No.
                   294137
Seq. ID
                   LIB3067-057-Q1-K1-E9
Method
                   BLASTX
NCBI GI
                   q3138799
BLAST score
                   568
E value
                   1.0e-58
Match length
                   134
% identity
                   82
                  (AB014058) beta 6 subunit of 20S proteasome [Oryza sativa]
NCBI Description
                   294138
Seq. No.
                   LIB3067-057-Q1-K1-G4
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4007864
BLAST score
                   198
                   1.0e-107
E value
                   302
Match length
                   31
% identity
NCBI Description Zea mays HRGP gene, AC1503 line
                   294139
Seq. No.
                   LIB3067-058-Q1-K1-C5
Seq. ID
Method
                   BLASTX
                   g4039152
NCBI GI
BLAST score
                   166
                   1.0e-11
E value
Match length
                   52
```



(AF104221) low temperature and salt responsive protein LTI6B [Arabidopsis thaliana] >gi_4325219_gb_AAD17303_(AF122006) hydrophobic protein [Arabidopsis thaliana]

Seq. No. 294140

NCBI Description

Seq. ID LIB3067-058-Q1-K1-D4

Method BLASTX
NCBI GI g4038044
BLAST score 452
E value 4.0e-45
Match length 130
% identity 59

NCBI Description (AC005936) unknown protein [Arabidopsis thaliana]

>gi_4406788_gb_AAD20098_ (AC006532) unknown protein

[Arabidopsis thaliana]

Seq. No. 294141

Seq. ID LIB3067-058-Q1-K1-H9

Method BLASTX
NCBI GI g3915866
BLAST score 509
E value 9.0e-52
Match length 125
% identity 73

NCBI Description GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)

>gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine

synthetase [Lupinus luteus]

Seq. No. 294142

Seq. ID LIB3067-059-Q1-K1-C2

Method BLASTX
NCBI GI g2618699
BLAST score 146
E value 2.0e-09
Match length 93
% identity 31

NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No. 294143

Seq. ID LIB3067-059-Q1-K1-C6

Method BLASTX
NCBI GI g951172
BLAST score 459
E value 6.0e-46
Match length 108
% identity 85

NCBI Description (U31521) MADS box protein [Zea mays]

>gi_1001934_emb_CAA56504_ (X80206) ZAG2 [Zea mays]

Seq. No. 294144

Seq. ID LIB3067-059-Q1-K1-E1

Method BLASTX
NCBI GI g4056486
BLAST score 189
E value 2.0e-14
Match length 116
% identity 40

Seq. ID

Method



NCBI Description



(AC005896) hypothetical protein [Arabidopsis thaliana]

```
Seq. No.
                  294145
Seq. ID
                  LIB3067-059-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                   q4056486
BLAST score
                   177
E value
                   6.0e-13
Match length
                   106
% identity
                   39
NCBI Description (AC005896) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   294146
                  LIB3067-059-Q1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q548851
BLAST score
                   251
E value
                   1.0e-21
Match length
                   87
                   62
% identity
                   40S RIBOSOMAL PROTEIN S20 >qi 481226 pir S38356 ribosomal
NCBI Description
                   protein S20 - rice >gi 391875 dbj BAA02157 (D12632) 40S
                   subunit ribosomal protein [Oryza sativa]
Seq. No.
                   294147
Seq. ID
                   LIB3067-059-Q1-K1-G6
Method
                   BLASTN
NCBI GI
                   g1213276
BLAST score
                   55
                   5.0e-22
E value
Match length
                   63
% identity
                   97
NCBI Description Z.mays ZEMa gene
Seq. No.
                   294148
Seq. ID
                   LIB3067-060-Q1-K1-D2
Method
                   BLASTX
NCBI GI
                   g2984709
BLAST score
                   151
E value
                   4.0e-10
Match length
                   44
% identity
                   68
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
NCBI Description
                   294149
Seq. No.
                   LIB3067-060-Q1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3114966
BLAST score
                   156
E value
                   1.0e-10
Match length
                   48
% identity
                   54
NCBI Description (Y14996) prolidase [Suberites domuncula]
                   294150
Seq. No.
```

41078

LIB3067-060-Q1-K1-E7

BLASTX

```
NCBI GI
                  q3461848
BLAST score
                  151
                  2.0e-11
E value
                  64
Match length
% identity
NCBI Description
                  (AC005315) putative ATPase [Arabidopsis thaliana]
                  294151
Seq. No.
                  LIB3067-060-Q1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4056437
BLAST score
                  312
E value
                  1.0e-28
Match length
                  75
                  80
% identity
NCBI Description
                  (AC005990) Strong similarity to PFAM PF 00069 Eukaryotic
                  protein kinase domain. [Arabidopsis thaliana]
Seq. No.
                  294152
Seq. ID
                  LIB3067-060-Q1-K1-F6
Method
                  BLASTN
NCBI GI
                  q829147
BLAST score
                  134
                  2.0e-69
E value
                  154
Match length
                  97
% identity
NCBI Description Z.mays gene for cyclophilin
                  294153
Seq. No.
Seq. ID
                  LIB3067-060-Q1-K1-F9
Method
                  BLASTX
                  g119355
NCBI GI
BLAST score
                  242
E value
                  6.0e-21
Match length
                  73
                  70
% identity
NCBI Description
                  ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                  >gi 100869 pir S16257 phosphopyruvate hydratase (EC
                  4.2.1.11) - maize >gi 22273 emb CAA39454 (X55981) enolase
                  [Zea mays]
Seq. No.
                  294154
Seq. ID
                  LIB3067-060-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  q2462748
BLAST score
                  209
E value
                  1.0e-16
Match length
                  122
% identity
                  39
                  (AC002292) putative Clathrin Coat Assembly protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  294155
                  LIB3068-001-Q1-K1-A10
Seq. ID
```

Method BLASTX NCBI GI g3882173



```
BLAST score
                  1.0e-56
E value
                  139
Match length
                  77
% identity
NCBI Description (AB018269) KIAA0726 protein [Homo sapiens]
                  294156
Seq. No.
Seq. ID
                  LIB3068-001-Q1-K1-A12
                  BLASTX
Method
                  q3831580
NCBI GI
BLAST score
                  190
                  2.0e-14
E value
                  37
Match length
% identity
                  (AF061934) regulator of G-protein signaling 11; RGS11 [Mus
NCBI Description
                  musculus]
                  294157
Seq. No.
                  LIB3068-001-Q1-K1-A3
Seq. ID
```

Method BLASTX NCBI GI q321328 BLAST score 671 9.0e-71 E value

128 Match length 99 % identity

N-methyl-D-aspartate receptor 1G precursor - rat >gi_475568 NCBI Description (U08268) N-methyl-D-aspartate receptor NMDAR1-4b subunit

[Rattus norvegicus]

294158 Seq. No.

LIB3068-001-Q1-K1-A9 Seq. ID

Method BLASTX NCBI GI g3514097 209 BLAST score 1.0e-35 E value 119 Match length 72 % identity

(AF084260) signalosome subunit 2 [Homo sapiens] NCBI Description

>gi 3639069 gb AAC36309.1 (AF087688) alien-like protein

[Mus musculus]

Seq. No. 294159

Seq. ID LIB3068-001-Q1-K1-B1

Method BLASTX NCBI GI q4262600 BLAST score 155 E value 3.0e-10 86 Match length % identity 40

(AF125956) similar to vertebrate galactoside-binding NCBI Description

lectins (Pfam: PF00337, Score=76.8, E=1.5e-21, N=1)

[Caenorhabditis elegans]

Seq. No. 294160

LIB3068-001-Q1-K1-B11 Seq. ID

Method BLASTX NCBI GI q1220311

Match length

% identity

82 91



```
BLAST score
                  7.0e-39
E value
                  89
Match length
                  91
% identity
NCBI Description (L10340) elongation factor-1 alpha [Homo sapiens]
Seq. No.
                  294161
                  LIB3068-001-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2599500
BLAST score
                  583
E value
                  2.0e-60
                  108
Match length
                  99
% identity
NCBI Description (AF029250) alpha-tubulin [Danio rerio]
                  294162
Seq. No.
Seq. ID
                  LIB3068-001-Q1-K1-C12
Method
                  BLASTN
                  g162786
NCBI GI
BLAST score
                  185
                  1.0e-99
E value
Match length
                  185
                  100
% identity
                  B.taurus cAMP-dependent protein kinase beta2-catalytic
NCBI Description
                  subunit (C-beta2) mRNA, complete cds
Seq. No.
                  294163
                  LIB3068-001-Q1-K1-C6
Seq. ID
Method
                  BLASTN
                  g1066270
NCBI GI
BLAST score
                   82
                   3.0e-38
E value
                  154
Match length
                   89
% identity
NCBI Description H.sapiens mRNA for Pr22 protein
Seq. No.
                   294164
Seq. ID
                   LIB3068-001-Q1-K1-C7
Method
                   BLASTX
NCBI GI
                   q3282515
BLAST score
                   434
E value
                   6.0e-43
Match length
                   135
% identity
                   (AF025771) C2H2 zinc finger protein splicing variant b2
NCBI Description
                   [Homo sapiens] >gi 3294542 (U95991) C2H2-type zinc finger
                  protein [Homo sapiens]
                   294165
Seq. No.
                   LIB3068-001-Q1-K1-D10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4049331
BLAST score
                   54
                   7.0e-22
E value
```

41081

.





NCBI Description Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence [Homo sapiens]

Seq. No. 294166

Seq. ID LIB3068-001-Q1-K1-D6

Method BLASTX
NCBI GI g246796
BLAST score 456
E value 1.0e-45
Match length 129
% identity 73

NCBI Description major centromere protein, CENP-B [human, Peptide, 594 aa]

Seq. No. 294167

Seq. ID LIB3068-001-Q1-K1-E10

Method BLASTX
NCBI GI g585911
BLAST score 540
E value 1.0e-55
Match length 108
% identity 100

NCBI Description HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K (HNRNP K)

(DC-STRETCH BINDING PROTEIN) (CSBP) (TRANSFORMATION

UPREGULATED NUCLEAR PROTEIN) (TUNP) >gi_284150_pir__A42058 heterogeneous nuclear ribonucleoprotein complex K, hnRNP K - human >gi_543380_pir__S41495 dC stretch-binding protein CSBP - rat >gi_241478_bbs_74679 (S74678) heterogeneous nuclear ribonucleoprotein complex K, hnRNP K [human, Peptide, 463 aa] [Homo sapiens] >gi_409389_dbj_BAA04566_ (D17711) dC-stretch binding protein (CSBP) [Rattus rattus]

Seq. No. 294168

Seq. ID LIB3068-001-Q1-K1-E11

Method BLASTN
NCBI GI g178845
BLAST score 40
E value 4.0e-13
Match length 68
% identity 90

NCBI Description Human apolipoprotein D gene, exon 4

Seq. No. 294169

Seq. ID LIB3068-001-Q1-K1-E3

Method BLASTN
NCBI GI g404675
BLAST score 84
E value 2.0e-39
Match length 120
% identity 93

NCBI Description Bos taurus (clones pCLYSI8 and pCMG1) lysozyme mRNA,

complete cds

Seq. No. 294170

Seq. ID LIB3068-001-Q1-K1-F10

Method BLASTN NCBI GI g399575 BLAST score 38



3.0e-12 E value Match length 70 % identity 89

NCBI Description Bos taurus myelin/oligodendrocyte glycoprotein mRNA

sequence

Seq. No.

294171

Seq. ID

LIB3068-001-Q1-K1-F4

Method BLASTX NCBI GI g2506439 BLAST score 612 E value 8.0e-64 Match length 124 % identity 97

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (GAPDH)

Seq. No.

294172

Seq. ID Method

LIB3068-001-Q1-K1-G10

BLASTX NCBI GI q3255965 BLAST score 152 E value 4.0e-10 30 Match length % identity

NCBI Description (Z70200) U5 snRNP-specific 200kD protein [Homo sapiens]

Seq. No.

294173

Seq. ID LIB3068-001-Q1-K1-G12 Method BLASTX NCBI GI g321323 BLAST score 408 E value 3.0e-40Match length 84 % identity 94

N-methyl-D-aspartate receptor 1B precursor - rat NCBI Description

>gi 56765 emb CAA46335 (X65227) NMDA receptor subunit, type NMDAR1-LL [Rattus norvegicus] >gi_256031_bbs_113946 (S44967) N-methyl-D-aspartate receptor subunit, NMDA-R1B [rats, Peptide, 959 aa] [Rattus sp.] >gi_475558 (U08263) N-methyl-D-aspartate receptor NMDAR1-1b subunit [Rattus

norvegicus]

Seq. No. 294174

Seq. ID LIB3068-001-Q1-K1-G2

Method BLASTN NCBI GI g4507098 BLAST score 231 E value 1.0e-127 Match length 351 91 % identity

Homo sapiens synaptosomal-associated protein, 25kD (SNAP25) NCBI Description

mRNA >gi 2373387 dbj D21267 D21267 Homo sapiens mRNA,

complete cds

294175 Seq. No.

Seq. ID LIB3068-001-Q1-K1-G3

Method BLASTN



```
g559331
NCBI GI
BLAST score
                  67
E value
                  1.0e-29
Match length
                  178
% identity
                  93
NCBI Description Human mRNA for KIAA0080 gene, partial cds
                  294176
Seq. No.
                  LIB3068-001-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1942133
BLAST score
                  387
E value
                  2.0e-37
Match length
                  92
% identity
                  83
NCBI Description
                  Chain A, S100b (S100beta) Nmr Data Was Collected From A
                  Sample Of Calcium Free Protein At Ph 6.3 And A Temperature
                  Of 311 K And 1.7-6.9 Mm Concentration, 25 Structures
                  >qi 1942134 pdb 1CFP B Chain B, S100b (S100beta) Nmr Data
                  Was Collected From A Sample Of Calcium Free Protein At Ph
                  6.3 And A Temperature Of 311 K And 1.7-6.9 Mm
                  Concentration, 25 Structures >gi 554574 (J03742)
                  calcium-modulated protein S100-beta [Artificial gene]
Seq. No.
                  294177
Seq. ID
                  LIB3068-001-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  g1498227
BLAST score
                  199
E value
                  1.0e-15
Match length
                  39
% identity
                  100
NCBI Description (Y07570) PHAPI2b protein [Homo sapiens]
                  294178
Seq. No.
                  LIB3068-001-Q1-K1-G9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g193411
BLAST score
                  35
E value
                  4.0e-10
Match length
                  47
                  94
% identity
NCBI Description Mus musculus GABA transporter mRNA sequence
                  294179
Seq. No.
                  LIB3068-001-Q1-K1-H3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4020145
BLAST score
                  34
                  2.0e-09
E value
Match length
                  58
% identity
                  90
NCBI Description Homo sapiens clone BAC 9H13 chromosome 8 map 8q21, complete
                  sequence [Homo sapiens]
```

Seq. No. 294180

Seq. ID LIB3068-001-Q1-K1-H4



```
Method
                  q1526419
NCBI GI
                  543
BLAST score
                  7.0e-56
E value
Match length
                  110
% identity
                  95
NCBI Description (D50366) KAP3A [Mus musculus]
                  294181
Seq. No.
                  LIB3068-002-Q1-K1-A12
Seq. ID
Method
                  BLASTX
                  q2062169
NCBI GI
                  506
BLAST score
                  2.0e-51
E value
                  139
Match length
% identity
                  (ACO01645) ABC transporter (PDR5-like) isolog [Arabidopsis
NCBI Description
                  thaliana]
                   294182
Seq. No.
                  LIB3068-002-Q1-K1-D3
Seq. ID
Method
                  BLASTX
                  q312179
NCBI GI
                   575
BLAST score
                   2.0e-59
E value
                   113
Match length
% identity
                   (X73151) glyceraldehyde 3-phosphate dehydrogenase
NCBI Description
                   (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic
                   glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]
                   >gi_1185554 (U45858) glyceraldehyde-3-phosphate
                   dehydrogenase [Zea mays]
                   294183
Seq. No.
Seq. ID
                   LIB3068-002-Q1-K1-F4
Method
                   BLASTX
NCBI GI
                   g464863
BLAST score
                   197
                   9.0e-16
E value
Match length
                   60
                   75
% identity
                   26S PROTEASE REGULATORY SUBUNIT 8 (TAT-BINDING PROTEIN
NCBI Description
                   HOMOLOG 10) >gi_422297_pir__JN0610 probable transcription
                   factor DdTBP10 - slime mold (Dictyostelium discoideum)
                   (fragment) >gi_290057 (L16579) HIV1 TAT-binding protein
                   [Dictyostelium discoideum]
Seq. No.
                   294184
                   LIB3068-002-Q1-K1-G4
Seq. ID
                   BLASTX
Method
                   g1498388
NCBI GI
                   378
BLAST score
```

1.0e-36 E value Match length 88 85 % identity

NCBI Description (U60510) actin [Zea mays]



```
Seq. No.
                  294185
                  LIB3068-003-Q1-K1-A12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  34
E value
                  7.0e-10
Match length
                  34
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  294186
Seq. ID
                  LIB3068-003-Q1-K1-B1
Method
                  BLASTN
NCBI GI
                  q22268
BLAST score
                  126
E value
                  1.0e-64
Match length
                  234
% identity
                  90
                  Maize (strain E41) mRNA for cell wall glycoprotein
NCBI Description
                  (partial) >gi 168458 gb M36914 MZECWAC Z.mays cell wall
                  protein mRNA, 3' end
                  294187
Seq. No.
Seq. ID
                  LIB3068-003-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  g729882
BLAST score
                  549
E value
                  2.0e-56
Match length
                  111
% identity
                  88
                  CASEIN KINASE II BETA' CHAIN (CK II)
NCBI Description
                  >gi 1076300 pir S47968 casein kinase II (EC 2.7.1.-) beta
                  chain CKB2 - Arabidopsis thaliana >qi 467975 (U03984)
                  casein kinase II beta subunit CKB2 [Arabidopsis thaliana]
                  >qi 2245122 emb CAB10544 (Z97343) unnamed protein product
                   [Arabidopsis thaliana]
                  294188
Seq. No.
                  LIB3068-003-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3860247
                  147
BLAST score
E value
                  3.0e-09
Match length
                  54
% identity
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  294189
                  LIB3068-003-Q1-K1-E9
Seq. ID
Method
                  BLASTN
```

Method BLASTN
NCBI GI g2062705
BLAST score 36
E value 8.0e-11
Match length 36
% identity 100

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds



```
Seq. No.
                  LIB3068-003-Q1-K1-F1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3292827
                  388
BLAST score
                  1.0e-37
E value
                  92
Match length
% identity
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
                  294191
Seq. No.
                  LIB3068-003-Q1-K1-H7
Seq. ID
                  BLASTN
Method
NCBI GI
                   q4206305
                  291
BLAST score
                   1.0e-163
E value
                   395
Match length
                   94
% identity
NCBI Description Zea mays retrotransposon Cinful-1, complete sequence
                   294192
Seq. No.
                   LIB3068-004-Q1-K1-B10
Seq. ID
                   BLASTX
Method
                   g2760334
NCBI GI
BLAST score
                   194
                   3.0e-15
E value
                   50
Match length
% identity
                   64
NCBI Description (AC002130) F1N21.5 [Arabidopsis thaliana]
                   294193
Seq. No.
                   LIB3068-004-Q1-K1-C12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g168445
                   194
BLAST score
                   4.0e-15
E value
                   71
Match length
% identity
NCBI Description (L00973) acidic class I chitinase [Zea mays]
                   294194
Seq. No.
Seq. ID
                   LIB3068-004-Q1-K1-D5
                   BLASTX
Method
NCBI GI
                   q3024122
                   206
BLAST score
                   8.0e-17
E value
Match length
                   45
                   89
% identity
                   S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821
                   (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]
```

Seq. No. 294195

Seq. ID LIB3068-004-Q1-K1-G9

Method BLASTN
NCBI GI g7228263
BLAST score 36



```
8.0e-11
E value
Match length
                  68
% identity
                  88
NCBI Description
                  F.hygrometrica gene for 18S rRNA, 5.8S rRNA and 25S rRNA
Seq. No.
                  294196
                  LIB3068-005-Q1-K1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q169818
BLAST score
                  42
E value
                  8.0e-15
Match length
                  134
                  83
% identity
NCBI Description Rice 25S ribosomal RNA gene
Seq. No.
                  294197
                  LIB3068-005-Q1-K1-C10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q7228263
BLAST score
                  42
E value
                  2.0e-14
Match length
                  102
% identity
                  85
NCBI Description F.hygrometrica gene for 18S rRNA, 5.8S rRNA and 25S rRNA
Seq. No.
                  294198
Seq. ID
                  LIB3068-005-Q1-K1-C6
Method
                  BLASTN
NCBI GI
                  q3290005
BLAST score
                  106
E value
                  6.0e-53
Match length
                  161
% identity
                  91
                  Zea mays pathogenesis related protein-5 (PR-5) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  294199
                  LIB3068-005-Q1-K1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g169818
BLAST score
                  74
E value
                  2.0e-33
Match length
                  277
% identity
                  82
NCBI Description Rice 25S ribosomal RNA gene
                  294200
Seq. No.
```

LIB3068-005-Q1-K1-H11 Seq. ID

Method BLASTN NCBI GI g2138080 BLAST score 37 E value 8.0e-12 Match length 77 88 % identity

NCBI Description Agelanthus sansibaricus 18S ribosomal RNA gene, partial

sequence



Seq. No. 29420

Seq. ID LIB3068-006-Q1-K1-C7

Method BLASTX
NCBI GI g542175
BLAST score 604
E value 6.0e-63
Match length 119
% identity 91

NCBI Description endoxyloglucan transferase - wheat >gi_469511_dbj_BAA03924_

(D16457) endo-xyloglucan transferase [Triticum aestivum]

Seq. No. 294202

Seq. ID LIB3068-007-Q1-K1-E12

Method BLASTN
NCBI GI 9747914
BLAST score 40
E value 2.0e-13
Match length 64
% identity 91

NCBI Description Z.mays CaM1 mRNA for calmodulin

Seq. No. 294203

Seq. ID LIB3068-007-Q1-K1-E8

Method BLASTX
NCBI GI g587564
BLAST score 270
E value 6.0e-24
Match length 76
% identity 67

NCBI Description (X80235) mitochondrial processing peptidase [Solanum

tuberosum]

Seq. No. 294204

Seq. ID LIB3068-007-Q1-K1-F1

Method BLASTN
NCBI GI g22332
BLAST score 199
E value 1.0e-108
Match length 357
% identity 89

NCBI Description Z.mays HRGP gene

Seq. No. 294205

Seq. ID LIB3068-007-Q1-K1-F11

Method BLASTN
NCBI GI g22292
BLAST score 44
E value 7.0e-16
Match length 104
% identity 86

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 294206

Seq. ID LIB3068-007-Q1-K1-H10

Method BLASTX NCBI GI g283045 BLAST score 160



E value 3.0e-11 Match length 59 % identity 58

NCBI Description hydroxyproline-rich glycoprotein - maize

>gi_22333_emb_CAA44844_ (X63134) hydroxyproline-rich
glycoprotein [Zea mays] >gi_228936_prf__1814452A Hyp-rich

glycoprotein [Zea mays]

Seq. No. 294207

Seq. ID LIB3068-007-Q1-K1-H8

Method BLASTN
NCBI GI g257040
BLAST score 133
E value 1.0e-68
Match length 344
% identity 29

NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No. 294208

Seq. ID LIB3068-008-Q1-K1-A11

Method BLASTX
NCBI GI g114193
BLAST score 273
E value 3.0e-24
Match length 77
% identity 66

NCBI Description PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 1 PRECURSOR

(PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 1) (DAHP

SYNTHETASE 1) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE

SYNTHASE 1) >gi 170225 (M64261)

3-deoxy-D-arabino-heptulosonate 7-phosphate synthase

[Nicotiana tabacum] >gi_228697_prf__1808327A

deoxyheptulosonate phosphate synthase [Nicotiana tabacum]

Seq. No. 294209

Seq. ID LIB3068-008-Q1-K1-A6

Method BLASTX
NCBI GI g2058706
BLAST score 211
E value 9.0e-17
Match length 114
% identity 39

NCBI Description (U95008) Rb7 [Lycopersicon esculentum]

Seq. No. 294210

Seq. ID LIB3068-008-Q1-K1-H2

Method BLASTX
NCBI GI g312179
BLAST score 557
E value 2.0e-57
Match length 107
% identity 99

NCBI Description (X73151) glyceraldehyde 3-phosphate dehydrogenase

(phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]

>gi_1185554 (U45858) glyceraldehyde-3-phosphate

dehydrogenase [Zea mays]

Match length

% identity

63

67



```
294211
Seq. No.
Seq. ID
                  LIB3068-008-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  g2190992
BLAST score
                  208
E value
                  2.0e-16
                  69
Match length
                  55
% identity
NCBI Description (AF004358) glutathione S-transferase TSI-1 [Aegilops
                  tauschii]
                  294212
Seq. No.
Seq. ID
                  LIB3068-009-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g2326947
BLAST score
                  350
E value
                  2.0e-33
Match length
                  100
% identity
                  72
NCBI Description (Z50801) Chlorophyll a/b-binding protein CP29 precursor
                  [Zea mays]
Seq. No.
                  294213
Seq. ID
                  LIB3068-009-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  g548605
BLAST score
                  262
E value
                  7.0e-23
                  75
Match length
% identity
                  79
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
                  - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
Seq. No.
                  294214
Seq. ID
                  LIB3068-009-Q1-K1-F5
                  BLASTN
Method
                  g11957
NCBI GI
BLAST score
                  91
E value
                  9.0e-44
Match length
                  135
% identity
                  46
NCBI Description Rice complete chloroplast genome
                  294215
Seq. No.
Seq. ID
                  LIB3068-009-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g115815
BLAST score
                  196
E value
                  2.0e-15
```

~:. .

41091

(CAB-M9) (LHCP) >qi 100866 pir S13098 chlorophyll

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR



a/b-binding protein precursor - maize >gi 22355 emb CAA39376 (X55892) light-harvesting chlorophyll a/b binding protein [Zea mays]

Seq. No. 294216 LIB3068-009-Q1-K1-H11 Seq. ID Method BLASTX

NCBI GI g283045 BLAST score 176 E value 6.0e-13 Match length 80 % identity 49

NCBI Description hydroxyproline-rich glycoprotein - maize

> >gi 22333 emb CAA44844 (X63134) hydroxyproline-rich glycoprotein [Zea mays] >gi_228936_prf__1814452A Hyp-rich

glycoprotein [Zea mays]

Seq. No. 294217

Seq. ID LIB3068-010-Q1-K1-A8

Method BLASTN NCBI GI q19655 BLAST score 38 E value 5.0e-12Match length 62 % identity 90

NCBI Description M.sativa 26S rRNA

Seq. No. 294218

Seq. ID LIB3068-010-Q1-K1-B10

Method BLASTX NCBI GI q232031 BLAST score 274 E value 3.0e-24Match length 74

% identity 72

NCBI Description ELONGATION FACTOR 1 BETA' >qi 322851 pir S29224

translation elongation factor eEF-1 beta chain - rice >gi_218161_dbj_BAA02253 (D12821) elongation factor 1 beta'

[Oryza sativa]

Seq. No. 294219

LIB3068-010-Q1-K1-C7 Seq. ID

Method BLASTX NCBI GI q283045 BLAST score 236 5.0e-20 E value Match length 68 % identity 63

NCBI Description hydroxyproline-rich glycoprotein - maize

> >gi 22333 emb CAA44844 (X63134) hydroxyproline-rich glycoprotein [Zea mays] >gi_228936_prf__1814452A Hyp-rich

glycoprotein [Zea mays]

Seq. No. 294220

Seq. ID LIB3068-010-Q1-K1-C8

Method BLASTX NCBI GI g3645898



```
BLAST score
                  1.0e-59
E value
Match length
                  144
                  78
% identity
NCBI Description
                  (U68408) in-frame stop codon; possibly a post-transposition
                  mutation [Zea mays]
Seq. No.
                  294221
                  LIB3068-010-Q1-K1-E1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g551482
BLAST score
                  78
                  8.0e-36
E value
Match length
                  156
                  89
% identity
NCBI Description
                  Zea mays ABA- and ripening-inducible-like protein mRNA,
                  complete cds
                  294222
Seq. No.
Seq. ID
                  LIB3068-010-Q1-K1-H11
Method
                  BLASTN
NCBI GI
                   q556559
BLAST score
                  33
E value
                   4.0e-09
Match length
                   65
                   88
% identity
                  Rice mRNA for homologue of Tat binding protein, complete
NCBI Description
Seq. No.
                   294223
Seq. ID
                  LIB3068-011-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                   q1335862
BLAST score
                   219
E value
                   7.0e-18
Match length
                  119
% identity
                  (U42608) clathrin heavy chain [Glycine max]
NCBI Description
                   294224
Seq. No.
Seq. ID
                   LIB3068-011-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   g1498597
                   158
BLAST score
                   1.0e-10
E value
Match length
                   88
% identity
                   42
```

(U66105) phospholipid transfer protein [Zea mays] NCBI Description

294225 Seq. No.

LIB3068-011-Q1-K1-B7 Seq. ID

Method BLASTX g4586242 NCBI GI BLAST score 206 8.0e-17 E value Match length 60 % identity 67



NCBI Description (AL049640) putative protein (fragment) [Arabidopsis thaliana]

Seq. No. 294226
Seq. ID LIB3068-011-Q1-K1-F10

Method BLASTX
NCBI GI g4154352
BLAST score 242
E value 1.0e-20
Match length 115
% identity 48

NCBI Description (AF110333) PrMC3 [Pinus radiata]

Seq. No. 294227

Seq. ID LIB3068-011-Q1-K1-G11

Method BLASTN
NCBI GI 9425799
BLAST score 99
E value 2.0e-48
Match length 210
% identity 87

NCBI Description Rice mRNA for 17S ribosomal RNA (gene name AD486), partial

sequence

Seq. No. 294228

Seq. ID LIB3068-012-Q1-K1-B2

Method BLASTX
NCBI GI g3080420
BLAST score 147
E value 3.0e-09
Match length 93
% identity 43

NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis

thaliana]

Seq. No. 294229

Seq. ID LIB3068-012-Q1-K1-B5

Method BLASTX
NCBI GI g114649
BLAST score 160
E value 3.0e-11
Match length 81
% identity 46

NCBI Description ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III)

>gi_67899_pir__LWLVA H+-transporting ATP synthase (EC
3.6.1.34) lipid-binding protein - liverwort (Marchantia
polymorpha) chloroplast >gi 11653 emb CAA28066 (X04465)

atpH [Marchantia polymorpha]

Seq. No. 294230

Seq. ID LIB3068-012-Q1-K1-D6

Method BLASTN
NCBI GI g169818
BLAST score 125
E value 7.0e-64
Match length 256
% identity 88



```
NCBI Description Rice 25S ribosomal RNA gene
                  294231
Seq. No.
                  LIB3068-012-Q1-K1-D7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22091
BLAST score
                  242
                  1.0e-133
E value
                  279
Match length
                  97
% identity
                  Z.diploperennis gene for hydroxyproline-rich glycoprotein
NCBI Description
                  294232
Seq. No.
                  LIB3068-012-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2499708
BLAST score
                  279
                  7.0e-26
E value
                  101
Match length
% identity
                  63
                  PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
NCBI Description
                  (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                  >gi_1020409_dbj_BAA11135_ (D73410) phospholipase D [Zea
                  mays]
                  294233
Seq. No.
Seq. ID
                  LIB3068-012-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  g627304
BLAST score
                  164
E value
                  1.0e-11
                  73
Match length
% identity
                  59
                  actin beta - goose >qi 213273 (M26111) beta-actin [Anser
NCBI Description
                  anser]
Seq. No.
                  294234
Seq. ID
                  LIB3068-012-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  q2499709
BLAST score
                  265
E value
                  1.0e-23
Match length
                  70
% identity
                  PHOSPHOLIPASE D 1 PRECURSOR (PLD 1) (CHOLINE PHOSPHATASE 1)
NCBI Description
                   (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D 1)
                  >qi 1020415 dbj BAA11136 (D73411) phospholipase D [Oryza
                   sativa] >gi_1902903_dbj_BAA19467_ (AB001920) phospholipase
                   D [Oryza sativa]
```

Seq. No. 294235 LIB3068-012-Q1-K1-G10 Seq. ID

Method BLASTN NCBI GI g168608 BLAST score 141 2.0e-73 E value Match length 185

% identity NCBI Description Maize 17S ribosomal RNA gene and flanks Seq. No. 294236 Seq. ID LIB3068-012-Q1-K1-H4 Method BLASTN NCBI GI g12888 BLAST score 287 E value 1.0e-160 Match length 342 % identity 96 Maize mitochondrial gene for cytochrome c oxidase subunit I NCBI Description (COX I) Seq. No. 294237 Seq. ID LIB3068-012-Q1-K1-H8 Method BLASTX NCBI GI q400872 BLAST score 171 E value 4.0e-12 Match length 36 % identity 97 PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-I) NCBI Description >gi_1363532_pir__S58561 photosystem I protein psaI - maize

chloroplast >gi 12433 emb CAA43491 (X61188) photosystem I subunit [Zea mays] >qi 902231 emb CAA60295 (X86563) psaI [Zea mays] >gi 444322 prf 1906371A psaI gene [Zea mays]

294238 Seq. No. LIB3068-013-Q1-K1-B10 Seq. ID BLASTX

Method NCBI GI q531829 BLAST score 141 8.0e-09 E value Match length 68 49 % identity

(U12390) beta-galactosidase alpha peptide [cloning vector NCBI Description

pSport1]

294239 Seq. No.

LIB3068-013-Q1-K1-B11 Seq. ID

Method BLASTX g2668742 NCBI GI BLAST score 412 2.0e-40 E value Match length 86 % identity 94

(AF034945) glycine-rich RNA binding protein [Zea mays] NCBI Description

294240 Seq. No.

LIB3068-013-Q1-K1-C10 Seq. ID

Method BLASTN g2062705 NCBI GI BLAST score 36 1.0e-10 E value Match length 36 % identity 100

Seq. No.

Seq. ID

294246

LIB3068-014-Q1-K1-B8





```
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  294241
Seq. No.
Seq. ID
                  LIB3068-013-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  q3377836
BLAST score
                  233
E value
                  2.0e-19
Match length
                  100
                  50
% identity
NCBI Description
                  (AF075598) contains similarity to reverse transcriptases
                  [Arabidopsis thaliana]
Seq. No.
                  294242
Seq. ID
                  LIB3068-013-Q1-K1-E4
Method
                  BLASTN
NCBI GI
                  q546034
BLAST score
                  40
E value
                  3.0e-13
Match length
                  108
% identity
                  84
NCBI Description
                  IRF170=rps operon {RNA editing, unspliced} [corn,
                  seedlings, mRNA Chloroplast, 261 nt, segment 1 of 3]
Seq. No.
                  294243
Seq. ID
                  LIB3068-013-Q1-K1-E6
Method
                  BLASTN
NCBI GI
                  q902200
BLAST score
                  349
E value
                  0.0e + 00
Match length
                  378
% identity
                  98
NCBI Description Z.mays complete chloroplast genome
Seq. No.
                  294244
                  LIB3068-013-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1184123
BLAST score
                  275
E value
                  2.0e-24
Match length
                  126
% identity
                  43
                  (U20809) auxin-induced protein [Vigna radiata]
NCBI Description
                  294245
Seq. No.
                  LIB3068-014-Q1-K1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2995383
BLAST score
                  117
                  2.0e-59
E value
Match length
                  161
% identity
                  93
NCBI Description
                  Zea mays mays mRNA for cytochrome P450 monooxygenase,
                  partial
```



```
Method
                    BLASTX
                    g409007
NCBI GI
BLAST score
                    140
                    7.0e-09
E value
Match length
                    36
                    67
% identity
                    BBI-M=Bowman-Birk trypsin inhibitor-related protein [Zea
NCBI Description
                    mays=corn, Peptide, 102 aa] >gi 447268 prf 1914141A
                    trypsin inhibitor-related protein [Zea mays]
                    294247
Seq. No.
                    LIB3068-014-Q1-K1-C10
Seq. ID
Method
                    BLASTN
NCBI GI
                    g22091
BLAST score
                    274
E value
                    1.0e-153
                    323
Match length
                    97
% identity
NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein
Seq. No.
                    294248
                    LIB3068-014-Q1-K1-G12
Seq. ID
Method
                    BLASTX
                    g3393062
NCBI GI
BLAST score
                    196
                    2.0e-15
E value
Match length
                    57
% identity
                    68
                    (Y17386) putative In2.1 protein [Triticum aestivum]
NCBI Description
                    294249
Seq. No.
                    LIB3068-014-Q1-K1-H9
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2668742
BLAST score
                    326
                    2.0e-30
E value
Match length
                    85
                    78
% identity
                   (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
Seq. No.
                    294250
                    LIB3068-015-Q1-K1-A11
Seq. ID
Method
                    BLASTX
                    g133999
NCBI GI
BLAST score
                    256
E value
                    2.0e-22
Match length
                    82
                    68
% identity
NCBI Description
                    CHLOROPLAST 30S RIBOSOMAL PROTEIN S7 >gi 70904 pir R3RZ7
                    ribosomal protein S7 - rice chloroplast
                    >gi_12037_emb_CAA33942 (X15901) ribosomal protein S7
[Oryza sativa] >gi_12065_emb_CAA33919_ (X15901) ribosomal
protein S7 [Oryza sativa] >gi_226657_prf__1603356CH
```

Seq. No. 294251

Seq. ID LIB3068-015-Q1-K1-B7

ribosomal protein S7 [Oryza sativa]



```
Method
NCBI GI
                  g3290006
BLAST score
                  188
                  3.0e-14
E value
Match length
                  65
% identity
                  63
NCBI Description (U82201) pathogenesis related protein-5 [Zea mays]
                  294252
Seq. No.
Seq. ID
                  LIB3068-015-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g115786
BLAST score
                  450
E value
                  7.0e-45
                  102
Match length
% identity
                  84
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB) (LHCP) >gi_82680_pir__A29119 chlorophyll a/b-binding
                  protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea
                  mays]
Seq. No.
                  294253
Seq. ID
                  LIB3068-015-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  g1076746
BLAST score
                  349
E value
                  4.0e-42
                  109
Match length
% identity
                  84
NCBI Description
                  heat shock protein 70 - rice (fragment)
                  >gi 763160 emb CAA47948 (X67711) heat shock protein 70
                  [Oryza sativa]
Seq. No.
                  294254
Seq. ID
                  LIB3068-015-Q1-K1-D8
Method
                  BLASTN
NCBI GI
                  g22192
BLAST score
                  66
E value
                  1.0e-28
Match length
                  122
% identity
                  89
NCBI Description Z.mays B-I gene for B transcriptional activator
                  294255
Seq. No.
                  LIB3068-015-Q1-K1-F7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2995383
BLAST score
                  69
E value
                  9.0e-31
Match length
                  185
% identity
                  84
```

NCBI Description Zea mays mays mRNA for cytochrome P450 monooxygenase,

partial

Seq. No. 294256

Seq. ID LIB3068-015-Q1-K1-G2

Method BLASTX



q4539665 NCBI GI BLAST score 356 E value 9.0e-34 Match length 135 % identity 53

(AF061282) polyprotein [Sorghum bicolor] NCBI Description

Seq. No.

294257

Seq. ID

LIB3068-015-Q1-K1-G6

Method BLASTX NCBI GI g3769673 BLAST score 268 E value 2.0e-23 Match length 122 % identity 39

NCBI Description (AF095285) Tic20 [Pisum sativum]

Seq. No.

294258

Seq. ID

LIB3068-016-Q1-K1-C2

Method BLASTN NCBI GI q22091 BLAST score 172 E value 3.0e-92 Match length 205 % identity 96

NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No.

294259

Seq. ID

LIB3068-016-Q1-K1-D3

Method BLASTX NCBI GI g1172861 BLAST score 222 E value 7.0e-20 Match length 107 % identity 52

NCBI Description

RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR

(RUBISCO LARGE SUBUNIT) >gi 1363613 pir S58560

ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain

- maize chloroplast >gi 18036 emb CAA78027 (Z11973)

Ribulose bisphosphate carboxylase [Zea mays]

>gi 902230 emb CAA60294 (X86563) rubisco large subunit

[Zea mays]

Seq. No.

294260

Seq. ID

LIB3068-016-Q1-K1-E8

Method BLASTN NCBI GI g2995383 BLAST score 84 E value 1.0e-39 188

Match length % identity 87

NCBI Description Zea mays mays mRNA for cytochrome P450 monooxygenase,

partial

Seq. No.

294261

Seq. ID

LIB3068-016-Q1-K1-F8

Method

BLASTX



NCBI GI g1172995 BLAST score 141 E value 9.0e-09 Match length 70 % identity 41

NCBI Description 60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal

protein L22 - rat >gi_710295_emb_CAA55204_ (X78444)

ribosomal protein L22 [Rattus norvegicus]

>gi_1093952 prf 2105193A ribosomal protein L22 [Rattus

norvegicus]

Seq. No. 294262

Seq. ID LIB3068-016-Q1-K1-G1

Method BLASTX
NCBI GI g3292824
BLAST score 395
E value 2.0e-38
Match length 126
% identity 63

NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 294263

Seq. ID LIB3068-016-Q1-K1-G12

Method BLASTX
NCBI GI g131281
BLAST score 381
E value 8.0e-37
Match length 117
% identity 66

NCBI Description PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN)

(CP43)

Seq. No. 294264

Seq. ID LIB3068-016-Q1-K1-H8

Method BLASTN
NCBI GI g1546918
BLAST score 37
E value 2.0e-11
Match length 115
% identity 88

NCBI Description Z.mays mRNA for translation initiation factor 5A

Seq. No. 294265

Seq. ID LIB3068-017-Q1-K1-A12

Method BLASTN
NCBI GI g2832242
BLAST score 212
E value 1.0e-116
Match length 396
% identity 49

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No.

294266

Seq. ID LIB3068-017-Q1-K1-C2

Method BLASTX
NCBI GI g2995384
BLAST score 220



```
E value
                   3.0e-18
Match length
                   60
% identity
                  75
NCBI Description
                  (AJ004810) cytochrome P450 monooxygenase [Zea mays]
Seq. No.
                  294267
                  LIB3068-017-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q728882
BLAST score
                  336
E value
                  1.0e-31
Match length
                  90
% identity
                  73
                  ADP-RIBOSYLATION FACTOR 3 >gi_541846_pir__$41938
NCBI Description
                  ADP-ribosylation factor 3 - Arabidopsis Thaliana
                  \geqgi_453191_emb_CAA54564_ (X77385) ADP-ribosylation factor 3
                   [Arabidopsis thaliana]
Seq. No.
                  294268
Seq. ID
                  LIB3068-018-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  q3063465
BLAST score
                  174
E value
                  2.0e-12
Match length
                  151
% identity
                  32
NCBI Description
                  (AC003981) F22013.27 [Arabidopsis thaliana]
Seq. No.
                  294269
Seq. ID
                  LIB3068-018-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g3402754
BLAST score
                  203
E value
                  6.0e-16
Match length
                  64
% identity
                  58
                  (AL031187) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  294270
Seq. ID
                  LIB3068-018-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  q2995384
BLAST score
                  153
E value
                  4.0e-10
Match length
                  62
% identity
                  48
NCBI Description
                  (AJ004810) cytochrome P450 monooxygenase [Zea mays]
                  294271
Seq. No.
Seq. ID
                  LIB3068-019-Q1-K1-D5
```

Method BLASTX
NCBI GI g3415115
BLAST score 166
E value 1.0e-13
Match length 81
% identity 52

NCBI Description (AF081202) villin 2 [Arabidopsis thaliana]



```
294272
Seq. No.
                  LIB3068-019-Q1-K1-E2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q902200
BLAST score
                  99
                  2.0e-48
E value
                  275
Match length
                  85
% identity
                  Z.mays complete chloroplast genome
NCBI Description
                  294273
Seq. No.
                  LIB3068-019-Q1-K1-H3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2062705
BLAST score
                  35
E value
                   3.0e-10
Match length
                   35
                   100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                   294274
                  LIB3068-019-Q1-K1-H8
Seq. ID
Method
                  BLASTN
NCBI GI
                   g22336
BLAST score
                   85
E value
                   4.0e-40
                   137
Match length
% identity
NCBI Description Maize mRNA for an 18kDa heat shock protein
                   294275
Seq. No.
                   LIB3068-020-Q1-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3482915
BLAST score
                   186
E value
                   5.0e-14
Match length
                   77
% identity
                   53
                   (AC003970) Similar to 12-oxophytodienoate reductase,
NCBI Description
                   gi 2765083 and old-yellow-enzyme homolog, gi_2232254
                   [Arabidopsis thaliana]
                   294276
Seq. No.
                   LIB3068-020-Q1-K1-B10
Seq. ID
                   BLASTX
Method
                   g2687358
NCBI GI
BLAST score
                   242
                   2.0e-20
E value
Match length
                   46
                   100
% identity
                   (AF033263) nonphototropic hypocotyl 1 [Zea mays]
NCBI Description
```

Seq. No.

Seq. ID LIB3068-020-Q1-K1-D1

294277

Method BLASTX NCBI GI g3256035



```
BLAST score
E value
                  8.0e-38
Match length
                  117
% identity
                  66
NCBI Description
                  (Y14274) putative serine/threonine protein kinase [Sorghum
                  bicolor
Seq. No.
                  294278
Seq. ID
                  LIB3068-020-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  g1352440
BLAST score
                  261
                  1.0e-22
E value
                  50
Match length
                  96
% identity
NCBI Description
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E)
                  (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT)
                  (EIF-4F P26 SUBUNIT) >gi_1002915 (U34597) p26 [Oryza
                  sativa]
                  294279
Seq. No.
Seq. ID
                  LIB3068-020-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g2493650
                  533
BLAST score
E value
                  2.0e-54
Match length
                  116
% identity
                  91
                  RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD
NCBI Description
                  CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)
                  >gi 1167858 emb CAA93139 (Z68903) chaperonin [Secale
                  cereale
Seq. No.
                  294280
Seq. ID
                  LIB3068-020-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  g2995384
BLAST score
                  181
E value
                  1.0e-13
Match length
                  82
% identity
NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]
                  294281
Seq. No.
                  LIB3068-020-Q1-K1-G11
Seq. ID
Method
                  BLASTX
                  g3236259
NCBI GI
```

BLAST score 227 4.0e-28 E value 89 Match length 75 % identity

NCBI Description

(AC004684) putative alcohol dehydrogenase [Arabidopsis

thaliana]

294282 Seq. No.

LIB3068-020-Q1-K1-H10 Seq. ID

Method BLASTX

```
NCBI GI
                  g3451070
BLAST score
                  151
E value
                  4.0e-10
Match length
                  46
% identity
NCBI Description
                  (AL031326) putative protein [Arabidopsis thaliana]
Seq. No.
                  294283
Seq. ID
                  LIB3068-021-Q1-K1-A11
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
E value
                  8.0e-11
Match length
                  48
% identity
                  67
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  294284
Seq. ID
                  LIB3068-021-Q1-K1-B3
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
E value
                  7.0e-11
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
```

Seq. No. 294285 Seq. ID LIB3068-021-Q1-K1-C4 Method BLASTX NCBI GI q2494128 BLAST score 202 E value 4.0e-16

Match length 57 % identity

NCBI Description (AC002376) EST gb T43244 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 294286

Seq. ID LIB3068-021-Q1-K1-D5

Method BLASTN NCBI GI g3821780 BLAST score 36 E value 4.0e-11 Match length 36 % identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 294287

Seq. ID LIB3068-021-Q1-K1-D6

Method BLASTN NCBI GI g296179 BLAST score 60 E value 2.0e-25 Match length 112 88 % identity

NCBI Description Z.mays mRNA for wound induced protein



```
Seq. No.
                  294288
Seq. ID
                  LIB3068-021-Q1-K1-D8
Method
                  BLASTN
NCBI GI
                  g459169
BLAST score
                  41
E value
                  3.0e-14
Match length
                  61
                  93
% identity
                  Zea mays B73 antifungal zeamatin-like protein mRNA,
NCBI Description
                  complete cds
                  294289
Seq. No.
Seq. ID
                  LIB3068-021-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  g2245128
BLAST score
                  232
E value
                  3.0e-19
                  90
Match length
% identity
                  48
NCBI Description (Z97344) peroxidase [Arabidopsis thaliana]
                  294290
Seq. No.
Seq. ID
                  LIB3068-021-Q1-K1-G3
Method
                  BLASTN
NCBI GI
                  g551482
BLAST score
                  64
E value
                  1.0e-27
Match length
                  179
% identity
                  92
NCBI Description
                  Zea mays ABA- and ripening-inducible-like protein mRNA,
                  complete cds
Seg. No.
                  294291
                  LIB3068-022-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g22465
BLAST score
                  266
                  1.0e-23
E value
Match length
                  58
% identity
                  93
                  (Y00322) ribulose 1,5-bisphosphate carboxylase/oxygenase
NCBI Description
                  [Zea mays]
Seq. No.
                  294292
                  LIB3068-022-Q1-K1-A8
Seq. ID
Method
                  BLASTX
                  g3004950
NCBI GI
BLAST score
                  319
                  6.0e-30
E value
Match length
                  67
                  97
% identity
NCBI Description
                  (AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays]
```

41106

294293

BLASTX

LIB3068-022-Q1-K1-C1

Seq. No.

Seq. ID Method



```
NCBI GI
                  q3560680
BLAST score
                  297
E value
                  7.0e-27
Match length
                  121
% identity
                  49
NCBI Description
                  (AF074149) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  [Dichaea riopalenquensis]
                  294294
Seq. No.
Seq. ID
                  LIB3068-022-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g3386614
BLAST score
                  199
E value
                  1.0e-15
Match length
                  89
% identity
                  48
NCBI Description
                  (AC004665) putative transcription factor SF3 [Arabidopsis
                  thaliana]
Seq. No.
                  294295
Seq. ID
                  LIB3068-023-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  q4388728
BLAST score
                  163
                  2.0e-11
E value
Match length
                  57
% identity
                  56
                  (AC006413) putative grr1-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  294296
Seq. ID
                  LIB3068-023-Q1-K1-C5
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
E value
                  9.0e-11
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  294297
                  LIB3068-024-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3915009
BLAST score
                  192
E value
                  4.0e-15
Match length
                  84
% identity
                  62
                  ARGININE DECARBOXYLASE (ARGDC) (ADC) >gi 1163181 (U35367)
NCBI Description
                  arginine decarboxylase [Glycine max]
                  294298
Seq. No.
Seq. ID
                  LIB3068-024-Q1-K1-B3
```

Method BLASTN
NCBI GI g257040
BLAST score 152
E value 6.0e-80



Match length 273
% identity 97
NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
Seq. No. 294299
Seq. ID LIB3068-024-Q1-K1-D11

Method BLASTX
NCBI GI g2995384
BLAST score 253
E value 6.0e-22
Match length 78
% identity 69

NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No. 294300

Seq. ID LIB3068-024-Q1-K1-E5

Method BLASTN
NCBI GI g22332
BLAST score 200
E value 1.0e-108
Match length 402
% identity 94

NCBI Description Z.mays HRGP gene

Seq. No. 294301

Seq. ID LIB3068-024-Q1-K1-F11

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 294302

Seq. ID LIB3068-025-Q1-K1-B5

Method BLASTX
NCBI GI g135417
BLAST score 291
E value 2.0e-26
Match length 60
% identity 92

NCBI Description TUBULIN ALPHA-3 CHAIN >gi 100946 pir JN0105 tubulin

alpha-3 chain - maize >gi_22150_emb_CAA44861_ (X63176) Alpha-tubulin #3 [Zea mays] >qi 485377 (M60171) alpha-3

tubulin [Zea mays]

Seq. No. 294303

Seq. ID LIB3068-025-Q1-K1-D7

Method BLASTX
NCBI GI g3851333
BLAST score 300
E value 2.0e-27
Match length 108
% identity 63

NCBI Description (Y09302) putative MADS-domain transcription factor [Zea

mays]



```
294304
Seq. No.
                  LIB3068-025-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4033424
BLAST score
                  364
E value
                  8.0e-35
Match length
                  102
                  72
% identity
NCBI Description
                  SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
                  PHOSPHO-HYDROLASE) (PPASE) >gi 2668746 (AF034947) inorganic
                  pyrophosphatase [Zea mays]
Seq. No.
                  294305
Seq. ID
                  LIB3068-025-Q1-K1-E6
Method
                  BLASTN
NCBI GI
                  q169818
BLAST score
                  66
                   1.0e-28
E value
                  229
Match length
                  83
% identity
NCBI Description Rice 25S ribosomal RNA gene
                                                                          ÷.
                  294306
Seq. No.
                  LIB3068-025-Q1-K1-G3
Seq. ID
Method
                  BLASTN
NCBI GI
                   q22312
BLAST score
                   134
E value
                   2.0e-69
Match length
                   190
% identity
                   93
                  Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                   abscisic acid)
                   294307
Seq. No.
                   LIB3068-026-Q1-K1-C9
Seq. ID
Method
                   BLASTX
                   g2505876
NCBI GI
BLAST score
                   279
E value
                   6.0e-25
Match length
                   81
% identity
                   64
                  (Y12776) MYB-related protein [Arabidopsis thaliana]
NCBI Description
                   294308
Seq. No.
                   LIB3068-026-Q1-K1-D1
Seq. ID
                   BLASTX
Method
                   g3193284
NCBI GI
                   260
BLAST score
                   1.0e-22
E value
                   123
Match length
% identity
                   46
NCBI Description (AF069298) No definition line found [Arabidopsis thaliana]
```

Seq. No. 294309

Seq. ID LIB3068-026-Q1-K1-D10

Method BLASTX



```
g2773154
NCBI GI
BLAST score
                  149
E value
                  1.0e-09
Match length
                  54
% identity
                  50
                  (AF039573) abscisic acid- and stress-inducible protein
NCBI Description
                  [Oryza sativa]
                  294310
Seq. No.
Seq. ID
                  LIB3068-026-Q1-K1-F7
Method
                  BLASTX
                  g122022
NCBI GI
                  365
BLAST score
                  6.0e-35
E value
                  80
Match length
% identity
                  93
NCBI Description
                  HISTONE H2B >gi 283025 pir S22323 histone H2B - wheat
                  >gi 21801 emb CAA42530 (X59873) histone H2B [Triticum
                  aestivum]
Seq. No.
                  294311
Seq. ID
                  LIB3068-026-Q1-K1-F8
Method
                  BLASTX
                  g399853
NCBI GI
BLAST score
                  194
                  4.0e-15
E value
Match length
                  64
% identity
                  64
                  HISTONE H2B.1 >gi 283041 pir S28048 histone H2B - maize
NCBI Description
                  >gi 22323 emb CAA40564 (X57312) H2B histone [Zea mays]
                  294312
Seq. No.
Seq. ID
                  LIB3068-027-Q1-K1-B11
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
% identity
                  100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  294313
Seq. ID
                  LIB3068-027-Q1-K1-B9
Method
                  BLASTN
                  g168462
NCBI GI
                  103
BLAST score
                  1.0e-50
E value
Match length
                  258
% identity
                  89
                  Zea mays defective suppressor-mutator from the
NCBI Description
                  brittle-1-mutable allele
```

Seq. No. 294314

Seq. ID LIB3068-027-Q1-K1-D2

Method BLASTX
NCBI GI g3122071
BLAST score 365



E value 4.0e-35 77 Match length 91 % identity ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) NCBI Description >gi_2130148_pir__S66339 translation elongation factor eEF-1 alpha chain - maize >gi_1321656_dbj_BAA08249_ (D45408) alpha subunit of tlanslation elongation factor 1 [Zea mays] 294315 Seq. No. LIB3068-027-Q1-K1-F8 Seq. ID BLASTX

Method BLASTX
NCBI GI g3600032
BLAST score 310
E value 1.0e-28
Match length 107
% identity 55

NCBI Description (AF080119) contains similarity to tropomyosin (Pfam: Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam: ATP-synt B.hmm, score: 10.89) [Arabidopsis thaliana]

 Seq. No.
 294316

 Seq. ID
 LIB3068-027-Q1-K1-G4

 Method
 BLASTX

 NCBI GI
 g860676

NCBI Description (U24188) calcium/calmodulin-dependent protein kinase

[Lilium longiflorum] >gi 1097385_prf__2113422A

Ca/calmodulin-dependent protein kinase [Lilium longiflorum]

Seq. No. 294317

Seq. ID LIB3068-027-Q1-K1-H3

Method BLASTN
NCBI GI g169818
BLAST score 95
E value 3.0e-46
Match length 222
% identity 87

NCBI Description Rice 25S ribosomal RNA gene

Seq. No. 294318

Seq. ID LIB3068-028-Q1-K1-F11

Method BLASTN
NCBI GI g342676
BLAST score 318
E value 1.0e-179
Match length 338
% identity 99

NCBI Description Maize (cms-T) mitochondrial TURF 2H3 sequence containing 2

ORFs

Seq. No. 294319

Seq. ID LIB3068-028-Q1-K1-F3

Method BLASTX NCBI GI g1076758



BLAST score 3.0e-21 E value 53 Match length % identity heat-shock protein precursor - rye >gi_2130093_pir__\$65776 NCBI Description heat-shock protein, 82K, precursor - rye >gi 556673 emb_CAA82945_ (Z30243) heat-shock protein [Secale cereale] 294320 Seq. No. Seq. ID LIB3068-028-Q1-K1-F8 BLASTX Method g2623310 NCBI GI 180 BLAST score 9.0e-14 E value 50 Match length 62 % identity (AC002409) unknown protein [Arabidopsis thaliana] NCBI Description >gi 3402721 (AC004261) unknown protein [Arabidopsis thaliana] 294321 Seq. No. LIB3068-029-Q1-K1-B1 Seq. ID BLASTX Method q2668742 NCBI GI 280 BLAST score 3.0e-25 E value Match length 70 % identity NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays] 294322 Seq. No. Seq. ID LIB3068-029-Q1-K1-F11 BLASTX Method q3970797 NCBI GI BLAST score 153 1.0e-10 E value Match length 44 % identity (Y13766) polynucleotide phosphorylase [Staphylococcus NCBI Description aureus] Seq. No. 294323 Seq. ID LIB3068-030-Q1-K1-A10 Method BLASTN NCBI GI q2773153 BLAST score 73 6.0e-33 E value Match length 141 88 % identity NCBI Description Oryza sativa abscisic acid- and stress-inducible protein

Seq. No. 294324

Seq. ID LIB3068-030-Q1-K1-B12

Method BLASTX NCBI GI g115771

41112

(Asr1) mRNA, complete cds



BLAST score 342 E value 3.0e-32 Match length 83 % identity 82

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >gi 82682 pir S04453 chlorophyll

a/b-binding protein precursor - maize

>gi 22224 emb CAA32900 (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No. 294325

Seq. ID LIB3068-030-Q1-K1-F12

Method BLASTN
NCBI GI g1498596
BLAST score 69
E value 1.0e-30
Match length 69
% identity 100

NCBI Description Zea mays phospholipid transfer protein mRNA, complete cds

Seq. No.

Seq. ID LIB3068-031-Q1-K1-A4

294326

Method BLASTX
NCBI GI g2109457
BLAST score 369
E value 2.0e-35
Match length 117
% identity 61

NCBI Description (AF001501) chitinase [Oryza sativa]

Seq. No. 294327

Seq. ID LIB3068-031-Q1-K1-C5

Method BLASTN
NCBI GI g902200
BLAST score 52
E value 7.0e-21
Match length 88
% identity 90

NCBI Description Z.mays complete chloroplast genome

Seq. No. 294328

Seq. ID LIB3068-031-Q1-K1-D10

Method BLASTX
NCBI GI g548770
BLAST score 313
E value 8.0e-29
Match length 62
% identity 98

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal

protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)

ribosomal protein L3 [Oryza sativa]

Seq. No. 294329

Seq. ID LIB3068-031-Q1-K1-D3

Method BLASTN NCBI GI g642261 BLAST score 39



E value 6.0e-13

Match length 77 % identity 87

NCBI Description P.racemosum ITS2 and 28S rRNA gene (partial)

Seq. No. 294330

Seq. ID LIB3068-032-Q1-K1-H5

Method BLASTX
NCBI GI g4567232
BLAST score 286
E value 1.0e-25
Match length 68
% identity 82

NCBI Description (AC007119) putative 40S ribosomal protein S25 [Arabidopsis

thaliana]

Seq. No. 294331

Seq. ID LIB3068-033-Q1-K1-A7

Method BLASTN
NCBI GI g2921303
BLAST score 203
E value 1.0e-110
Match length 281
% identity 95

NCBI Description Zea mays herbicide safener binding protein (SBP1) mRNA,

complete cds

Seq. No. 294332

Seq. ID LIB3068-033-Q1-K1-B2

Method BLASTN

NCBI GI g902200

BLAST score 193

E value 1.0e-104

Match length 218

% identity 96

NCBI Description Z.mays complete chloroplast genome

Seq. No. 294333

Seq. ID LIB3068-033-Q1-K1-B3

Method BLASTX
NCBI GI g115771
BLAST score 676
E value 3.0e-71
Match length 127
% identity 98

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll

a/b-binding protein precursor - maize

>gi 22224 emb CAA32900 (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No. 294334

Seq. ID LIB3068-033-Q1-K1-B8

Method BLASTX
NCBI GI g3851333
BLAST score 251
E value 1.0e-21



```
Match length
                  110
                   55
% identity
                   (Y09302) putative MADS-domain transcription factor [Zea
NCBI Description
                  mays]
                   294335
Seq. No.
                  LIB3068-033-Q1-K1-C2
Seq. ID
Method
                  BLASTN
                  g902200
NCBI GI
                  122
BLAST score
                   2.0e-62
E value
                   210
Match length
                   90
% identity
NCBI Description Z.mays complete chloroplast genome
                   294336
Seq. No.
                   LIB3068-033-Q1-K1-D3
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2687430
                   55
BLAST score
                   4.0e-22
E value
Match length
                   191
                   82
% identity
                   Acorus gramineus large subunit 26S ribosomal RNA gene,
NCBI Description
                   partial sequence
                   294337
Seq. No.
                   LIB3068-033-Q1-K1-E7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g115815
BLAST score
                   561
                   8.0e-58
E value
Match length
                   129
                   83
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-M9) (LHCP) >gi_100866_pir__S13098 chlorophyll
                   a/b-binding protein precursor - maize
                   >gi 22355 emb CAA39376 (X55892) light-harvesting
                   chlorophyll a/b binding protein [Zea mays]
                   294338
Seq. No.
Seq. ID
                   LIB3068-033-Q1-K1-F10
                   BLASTX
Method
NCBI GI
                   g2760324
                   281
BLAST score
                   6.0e-25
E value
                   128
Match length
% identity
                   46
                   (AC002130) F1N21.9 [Arabidopsis thaliana]
NCBI Description
                   294339
Seq. No.
                   LIB3068-033-Q1-K1-G10
```

Seq. ID

Method BLASTX NCBI GI q133724 BLAST score 162 3.0e-11 E value Match length 97



Method BLASTN
NCBI GI g257040
BLAST score 109
E value 2.0e-54
Match length 225
% identity 88

NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No. 294341

Seq. ID LIB3068-034-Q1-K1-B3

Method BLASTN
NCBI GI g22553
BLAST score 55
E value 3.0e-22
Match length 119
% identity 87

NCBI Description Tomato 25S ribosomal RNA gene

Seq. No. 294342

Seq. ID LIB3068-034-Q1-K1-E4

Method BLASTN
NCBI GI g169818
BLAST score 59
E value 2.0e-24
Match length 150
% identity 87

NCBI Description Rice 25S ribosomal RNA gene

Seq. No. 294343

Seq. ID LIB3068-034-Q1-K1-F6

Method BLASTN
NCBI GI g169818
BLAST score 49

E value 1.0e-18
Match length 205
% identity 81

NCBI Description Rice 25S ribosomal RNA gene

Seq. No. 294344

Seq. ID LIB3068-034-Q1-K1-G12

Method BLASTN
NCBI GI g12888
BLAST score 170
E value 1.0e-90
Match length 181
% identity 99

NCBI Description Maize mitochondrial gene for cytochrome c oxidase subunit I

(COX I)

NCBI GI

E value

BLAST score



```
294345
Seq. No.
                  LIB3068-035-Q1-K1-C2
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
                  36
BLAST score
                  9.0e-11
E value
                  36
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  294346
Seq. No.
                  LIB3068-035-Q1-K1-E11
Seq. ID
                  BLASTN
Method
NCBI GI
                   g22332
                   308
BLAST score
                   1.0e-173
E value
Match length
                   418
% identity
                   94
NCBI Description Z.mays HRGP gene
Seq. No.
                   294347
                   LIB3068-035-Q1-K1-G11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2369714
                   410
BLAST score
                   9.0e-41
E value
                   128
Match length
                   70
% identity
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]
                   294348
Seq. No.
                   LIB3068-035-Q1-K1-G2
Seq. ID
                   BLASTN
Method
                   g3821780
NCBI GI
                   36
BLAST score
                   6.0e-11
E value
                   36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   294349
Seq. No.
Seq. ID
                   LIB3068-035-Q1-K1-G6
Method
                   BLASTX
NCBI GI
                   g4102839
                   197
BLAST score
                   4.0e-15
E value
                   99
Match length
% identity
                  (AF016713) LeOPT1 [Lycopersicon esculentum]
NCBI Description
                   294350
Seq. No.
Seq. ID
                   LIB3068-036-Q1-K1-A10
Method
                   BLASTX
```

q1747296

2.0e-37

385

BLAST score

Match length

% identity

E value

211

78

3.0e-17



```
Match length
                  110
                  77
% identity
                  (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
NCBI Description
                  >gi 3298476_dbj_BAA31524_ (AB012766) ovp2 [Oryza sativa]
Seq. No.
                  LIB3068-036-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g116329
BLAST score
                  139
                  5.0e-09
E value
                  48
Match length
% identity
                  58
                  ENDOCHITINASE A PRECURSOR (SEED CHITINASE A) >gi 168441
NCBI Description
                  (M84164) chitinase A [Zea mays]
Seq. No.
                  294352
Seq. ID
                  LIB3068-036-Q1-K1-B5
Method
                  BLASTN
NCBI GI
                  g169818
BLAST score
                  59
E value
                  2.0e-24
Match length
                  162
% identity
                  85
NCBI Description Rice 25S ribosomal RNA gene
Seq. No.
                  294353
                  LIB3068-036-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3341695
                  382
BLAST score
                  8.0e-37
E value
Match length
                  144
                  53
% identity
                  (AC003672) putative thiamin pyrophosphokinase [Arabidopsis
NCBI Description
                  thaliana]
                  294354
Seq. No.
                  LIB3068-036-Q1-K1-G12
Seq. ID
Method
                  BLASTX
                  g3176661
NCBI GI
BLAST score
                  451
                  7.0e-45
E value
Match length
                  150
% identity
                   64
                   (AC004393) Similar to putative DNA polymerase gb M29683
NCBI Description
                  from S. cerevisiae. [Arabidopsis thaliana]
Seq. No.
                  294355
Seq. ID
                  LIB3068-036-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g1351856
```

41118

NCBI Description ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)



(ACONITASE) >gi 868003_dbj_BAA06108_ (D29629) aconitase [Cucurbita sp.]

294356 Seq. No.

Seq. ID LIB3068-036-Q1-K1-G9

Method BLASTX NCBI GI g1345683 BLAST score 180 2.0e-13 E value 113 Match length % identity

CATALASE ISOZYME 3 >gi 487045 pir_ S37379 catalase (EC NCBI Description

1.11.1.6) 3 - maize $>g\bar{i}$ 168437 (LO5934) catalase [Zea mays]

Seq. No.

294357

Seq. ID LIB3068-037-Q1-K1-B7

Method BLASTN NCBI GI g4580745 35 BLAST score 4.0e-10 E value Match length 59 90 % identity

Arabidopsis thaliana chromosome 1 BAC F1003 sequence, NCBI Description

complete sequence

Seq. No. 294358

Seq. ID LIB3068-037-Q1-K1-D10

Method BLASTX NCBI GI g3334115 BLAST score 158 E value 3.0e-11 Match length 48 % identity 69

ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) NCBI Description

(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium

hirsutum]

Seq. No. 294359

LIB3068-037-Q1-K1-E5 Seq. ID

Method BLASTX q3004547 NCBI GI BLAST score 413 2.0e-40 E value 99 Match length 79 % identity

(AC003673) unknown protein [Arabidopsis thaliana] NCBI Description

>gi 4185150 (AC005724) unknown protein [Arabidopsis

thaliana]

294360 Seq. No.

LIB3068-037-Q1-K1-F12 Seq. ID

Method BLASTN g169818 NCBI GI BLAST score 175 9.0e-94 E value 343 Match length

NCBI Description



```
% identity
NCBI Description Rice 25S ribosomal RNA gene
                  294361
Seq. No.
Seq. ID
                  LIB3068-038-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g168570
BLAST score
                  170
                  3.0e-14
E value
                  59
Match length
% identity
NCBI Description (M95077) phenylalanine ammonia lyase [Zea mays]
                  294362
Seq. No.
Seq. ID
                  LIB3068-038-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  g2914710
BLAST score
                  212
E value
                  4.0e-20
                  112
Match length
% identity
                  (AC003974) putative beta-D-galactosidase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  294363
Seq. ID
                  LIB3068-038-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g506629
BLAST score
                  174
                  9.0e-13
E value
Match length
                  88
% identity
                  47
                  (U01964) photosystem II type I chlorophyll a/b-binding
NCBI Description
                  protein [Glycine max]
                  294364
Seq. No.
Seq. ID
                  LIB3068-038-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  q1872521
BLAST score
                  229
E value
                  5.0e-19
Match length
                  78
% identity
NCBI Description
                  (U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana]
                  >qi 1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis
                  thaliana]
Seq. No.
                  294365
Seq. ID
                  LIB3068-038-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g82696
BLAST score
                  147
E value
                  2.0e-09
Match length
                  88
% identity
                   44
```

(X61121) glycine-rich protein [Zea mays]

glycine-rich protein - maize >gi_22293 emb CAA43431



```
Seq. No.
                  294366
Seq. ID
                  LIB3068-038-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  q133852
BLAST score
                  186
E value
                  9.0e-17
Match length
                  66
                  67
% identity
NCBI Description
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S19 >gi 71030 pir R3ZM19
                  ribosomal protein S19 - maize chloroplast
                  >gi 1208517 emb CAA60374 (X86563) ribosomal protein S19
                  [Zea mays] >gi 2654314 emb CAA60326 (X86563) ribosomal
                  protein S19 [Zea mays]
Seq. No.
                  294367
Seq. ID
                  LIB3068-038-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  g2326947
BLAST score
                  329
E value
                  8.0e-31
Match length
                  85
% identity
NCBI Description
                  (Z50801) Chlorophyll a/b-binding protein CP29 precursor
                  [Zea mays]
Seq. No.
                  294368
Seq. ID
                  LIB3068-038-Q1-K1-G11
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  5.0e-11
Match length
                  48
% identity
                  67
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  294369
                  LIB3068-038-Q1-K1-G3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22320
BLAST score
                  373
                  0.0e+00
E value
Match length
                  399
% identity
                  98
NCBI Description Maize H1 mRNA for H1 histone
```

Seq. No.

294370

Seq. ID LIB3068-038-Q1-K1-G5

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 294371



```
LIB3068-039-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2109457
BLAST score
                  265
E value
                  2.0e-23
Match length
                  70
% identity
NCBI Description
                 (AF001501) chitinase [Oryza sativa]
Seq. No.
                  294372
Seq. ID
                  LIB3068-039-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  g115771
BLAST score
                  328
                  1.0e-30
E value
Match length
                  71
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-1) (LHCP) >gi 82682 pir S04453 chlorophyll
                  a/b-binding protein precursor - maize
                  >gi 22224 emb CAA32900 (X14794) chlorophyll a/b-binding
                  preprotein (AA 1 - 262) [Zea mays]
                  294373
Seq. No.
Seq. ID
                  LIB3068-039-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  g4467111
BLAST score
                  294
E value
                  2.0e-26
Match length
                  117
% identity
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]
Seq. No.
                  294374
Seq. ID
                  LIB3068-039-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  g3702340
BLAST score
                  172
E value
                  3.0e-12
Match length
                  113
% identity
NCBI Description
                  (AC005397) hypothetical protein [Arabidopsis thaliana]
                  294375
Seq. No.
                  LIB3068-039-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3913464
BLAST score
                  151
```

E value 1.0e-14 Match length 81 % identity 48

NCBI Description BETAINE-ALDEHYDE DEHYDROGENASE (BADH)

>gi 2244604 dbj BAA21098 (AB001348) betaine aldehyde

dehydrogenase [Oryza sativa]

Seq. No. 294376

Seq. ID LIB3068-039-Q1-K1-D12

```
Method
NCBI GI
                   g1871182
BLAST score
                   150
E value
                   5.0e-13
Match length
                   114
% identity
                   45
                  (U90439) phospholipase D isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   294377
Seq. ID
                  LIB3068-039-Q1-K1-E2
Method
                  BLASTN
                  g169818
```

Method BLASTN
NCBI GI g169818
BLAST score 151
E value 2.0e-79
Match length 243
% identity 91

NCBI Description Rice 25S ribosomal RNA gene

 Seq. No.
 294378

 Seq. ID
 LIB3068-039-Q1-K1-F12

 Method
 BLASTX

 NCBI GI
 g2369714

 BLAST score
 482

 E value
 4.0e-56

 Match length
 136

82

NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

 Seq. No.
 294379

 Seq. ID
 LIB3068-039-Q1-K1-F2

 Method
 BLASTX

 NCBI GI
 g1895084

 BLAST score
 263

BLAST score 263 E value 3.0e-23 Match length 69 % identity 72

% identity

NCBI Description (U89897) golgi associated protein se-wap41 [Zea mays]

Seq. No. 294380

Seq. ID LIB3068-039-Q1-K1-F4

Method BLASTX
NCBI GI g2109457
BLAST score 144
E value 4.0e-09
Match length 82
% identity 39

NCBI Description (AF001501) chitinase [Oryza sativa]

Seq. No. 294381

Seq. ID LIB3068-039-Q1-K1-H10

Method BLASTN
NCBI GI g454880
BLAST score 46
E value 8.0e-17
Match length 128
% identity 91

NCBI Description Rice mRNA for WSI724 protein induced by water stress,

NCBI Description



complete cds

```
Seq. No.
                  294382
Seq. ID
                  LIB3068-039-Q1-K1-H11
Method
                  BLASTN
NCBI GI
                  g2331140
BLAST score
                   46
E value
                   6.0e-17
Match length
                  74
                   92
% identity
NCBI Description
                  Oryza sativa water-stress inducible protein (WSI) mRNA,
                  complete cds
Seq. No.
                  294383
Seq. ID
                  LIB3068-040-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  g2811026
BLAST score
                  290
                   4.0e-26
E value
                  80
Match length
                  70
% identity
NCBI Description
                  TCP1-CHAPERONIN COFACTOR A HOMOLOG >gi 1946375 (U93215)
                  TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana]
                  >gi 2347204 (AC002338) TCP1-chaperonin cofactor A isolog
                   [Arabidopsis thaliana]
Seq. No.
                  294384
Seq. ID
                  LIB3068-041-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  g3747026
BLAST score
                  216
E value
                  2.0e-17
Match length
                  78
% identity
NCBI Description
                  (AF093244) import protein Tim9p [Saccharomyces cerevisiae]
Seq. No.
                  294385
Seq. ID
                  LIB3068-041-Q1-K1-A8
Method
                  BLASTN
NCBI GI
                  q168406
BLAST score
                  36
E value
                  8.0e-11
Match length
                  77
% identity
                  87
NCBI Description
                  Z.mays alcohol dehydrogenase (ADH-1 C-m allele) gene,
                  complete cds
Seq. No.
                  294386
Seq. ID
                  LIB3068-041-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g1729980
BLAST score
                  201
E value
                  9.0e-16
Match length
                  110
% identity
                  47
```

THAUMATIN-LIKE PROTEIN PRECURSOR >gi_2129751_pir__S71175 thaumatin-like protein - Arabidopsis thaliana >gi_536825

Seq. No.



(L34693) thaumatin-like protein [Arabidopsis thaliana] >gi_1094863_prf__2106421A thaumatin-like protein [Arabidopsis thaliana]

Seq. No. 294387 Seq. ID LIB3068-041-Q1-K1-D2 Method BLASTX NCBI GI g4559384 BLAST score 156 E value 2.0e-10 Match length 72 43 % identity NCBI Description (AC006526) unknown protein [Arabidopsis thaliana] 294388 Seq. No. Seq. ID LIB3068-041-Q1-K1-F4 Method BLASTX NCBI GI g3242715 254 BLAST score E value 6.0e-22 122 Match length % identity 48 (AC003040) hypothetical protein [Arabidopsis thaliana] NCBI Description 294389 Seq. No. Seq. ID LIB3068-041-Q1-K1-G4 Method BLASTN NCBI GI g4007864 BLAST score 151 E value 2.0e-79 249 Match length 25 % identity NCBI Description Zea mays HRGP gene, AC1503 line Seq. No. 294390 Seq. ID LIB3068-042-Q1-K1-A3 Method BLASTN NCBI GI g2995383 BLAST score 40 E value 2.0e-13 Match length 76 % identity 89 NCBI Description Zea mays mays mRNA for cytochrome P450 monooxygenase, partial 294391 Seq. No. LIB3068-042-Q1-K1-B8 Seq. ID Method BLASTX g4504909 NCBI GI BLAST score 205 5.0e-16 E value Match length 111 % identity 38 karyopherin (importin) beta 3 >gi 2102696 (U72761) NCBI Description

294392

karyopherin beta 3 [Homo sapiens]



```
LIB3068-042-Q1-K1-C10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2773154
BLAST score
                  192
                  1.0e-14
E value
                  51
Match length
                  71
% identity
                  (AF039573) abscisic acid- and stress-inducible protein
NCBI Description
                  [Oryza sativa]
                  294393
Seq. No.
                  LIB3068-043-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82696
BLAST score
                  333
                  3.0e-31
E value
                  82
Match length
                  78
% identity
                  glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
Seq. No.
                  294394
                  LIB3068-043-Q1-K1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2995383
BLAST score
                  75
                   2.0e-34
E value
Match length
                  107
% identity
                   93
                  Zea mays mays mRNA for cytochrome P450 monooxygenase,
NCBI Description
                  partial
                   294395
Seq. No.
Seq. ID
                  LIB3068-043-Q1-K1-C6
Method
                  BLASTX
                   g3785996
NCBI GI
                   242
BLAST score
                   2.0e-20
E value
Match length
                   85
% identity
                  (AC005499) putative annexin [Arabidopsis thaliana]
NCBI Description
                   294396
Seq. No.
Seq. ID
                   LIB3068-043-Q1-K1-E5
Method
                   BLASTX
NCBI GI
                   g131271
BLAST score
                   203
                   6.0e-24
E value
                   108
Match length
                   56
% identity
                   PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47
NCBI Description
                   PROTEIN) >gi 72705_pir__QJRZ6A photosystem II chlorophyll
```

a-binding protein psbB - rice chloroplast

>gi_12013_emb_CAA33973_ (X15901) PSII 47kDa protein [Oryza

sativa] >gi_226634_prf__1603356BH photosystem II 47kD

protein [Oryza sativa]



```
Seq. No.
                  294397
                  LIB3068-043-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827699
BLAST score
                  193
E value
                  1.0e-14
Match length
                  85
% identity
                  55
NCBI Description
                  (AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.
                  294398
                  LIB3068-043-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112994
BLAST score
                  425
E value
                  6.0e-42
Match length
                  86
% identity
                  98
NCBI Description
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
                  >gi 82685 pir S04536 embryonic abundant protein,
                  glycine-rich - maize >gi 22313 emb CAA31077 (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi 226091 prf 1410284A abscisic acid inducible gene [Zea
                  mays]
Seq. No.
                  294399
Seq. ID
                  LIB3068-043-Q1-K1-F3
Method
                  BLASTN
NCBI GI
                  g902200
BLAST score
                  93
E value
                  5.0e-45
Match length
                  117
                  95
% identity
NCBI Description Z.mays complete chloroplast genome
Seq. No.
                  294400
                  LIB3068-043-Q1-K1-G7
Seq. ID
Method
                  BLASTX
                  g282994
NCBI GI
BLAST score
                  244
E value
                  1.0e-20
                  106
Match length
% identity
                  55
NCBI Description Sipl protein - barley >gi 167100 (M77475) seed imbibition
                  protein [Hordeum vulgare]
                  294401
Seq. No.
Seq. ID
                  LIB3068-043-Q1-K1-H6
Method
                  BLASTX
                  g3717987
                  209
```

NCBI GI BLAST score E value 1.0e-16 Match length 80 56 % identity

NCBI Description (AJ005899) G subunit of Vacuolar-type H+-ATPase [Nicotiana

tabacum]

Match length

NCBI Description

% identity

199



```
294402
Seq. No.
Seq. ID
                  LIB3068-044-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g1703374
BLAST score
                  317
                  3.0e-29
E value
                  79
Match length
                  76
% identity
                  ADP-RIBOSYLATION FACTOR 1 >gi 2129457 pir S66337
NCBI Description
                  ADP-ribosylation factor 1 - Chlamydomonas reinhardtii
                  >qi 861205 (U27120) ADP-ribosylation factor [Chlamydomonas
                  reinhardtii]
Seq. No.
                  294403
Seq. ID
                  LIB3068-044-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  g1703380
BLAST score
                  287
                  1.0e-25
E value
                  98
Match length
% identity
                  62
NCBI Description ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760)
                  ADP-ribosylation factor [Oryza sativa]
                  294404
Seq. No.
Seq. ID
                  LIB3068-044-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                  g3309243
                  159
BLAST score
E value
                  3.0e-11
Match length
                  52
% identity
                  65
NCBI Description
                  (AF073507) aconitase-iron regulated protein 1 [Citrus
                  limon]
Seg. No.
                  294405
Seq. ID
                  LIB3068-044-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  g3080393
BLAST score
                  165
E value
                  9.0e-12
Match length
                  82
% identity
NCBI Description
                  (AL022603) NADH dehydrogenase like protein [Arabidopsis
                  thaliana]
Seq. No.
                  294406
Seq. ID
                  LIB3068-044-Q1-K1-B1
Method
                  BLASTN
NCBI GI
                  g169819
BLAST score
                  47
E value
                  2.0e-17
```

5.8S, complete; 25S, 5' end

Rice gene encoding three ribosomal RNA's: the 17S, 3' end;



```
Seq. No.
                   294407
                  LIB3068-044-Q1-K1-B10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g347843
BLAST score
                  68
E value
                  9.0e-30
Match length
                  273
% identity
                  82
NCBI Description
                  Zea mays globulin-1 gene, promoter region
Seq. No.
                  294408
Seq. ID
                  LIB3068-044-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  q66009
BLAST score
                  232
E value
                   1.0e-19
Match length
                  85
% identity
                   58
NCBI Description
                  glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C,
                  cytosolic - maize >gi 22238 emb CAA30151 (X07156) GADPH
                   (AA 1-337) [Zea mays]
Seq. No.
                   294409
Seq. ID
                  LIB3068-044-Q1-K1-D10
Method
                  BLASTN
NCBI GI
                  q2995383
BLAST score
                  108
E value
                   1.0e-53
Match length
                   383
% identity
                   83
NCBI Description
                  Zea mays mays mRNA for cytochrome P450 monooxygenase,
Seq. No.
                  294410
Seq. ID
                  LIB3068-044-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  g595775
BLAST score
                  161
E value
                  5.0e-11
Match length
                  58
% identity
                   60
NCBI Description
                  (U13869) lacZ alpha peptide [Cloning vector]
Seq. No.
                  294411
                  LIB3068-044-Q1-K1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2921303
BLAST score
                  67
                  3.0e-29
                  261
% identity
                  80
NCBI Description
                  Zea mays herbicide safener binding protein (SBP1) mRNA,
                  complete cds
```

E value Match length

Seq. No.

294412

Seq. ID

LIB3068-044-Q1-K1-F6

Method BLASTN



```
NCBI GI
                   g2995383
BLAST score
                   102
E value
                   3.0e-50
Match length
                   233
% identity
                   82
                   Zea mays mays mRNA for cytochrome P450 monooxygenase,
NCBI Description
                   partial
Seq. No.
                   294413
Seq. ID
                   LIB3068-044-Q1-K1-F7
Method
                   BLASTN
NCBI GI
                   g169818
BLAST score
                   104
E value
                   2.0e-51
Match length
                   302
% identity
                   83
NCBI Description Rice 25S ribosomal RNA gene
                   294414
Seq. No.
Seq. ID
                   LIB3068-044-Q1-K1-H1
Method
                   BLASTN
NCBI GI
                   g1777706
BLAST score
                  89
E value
                  2.0e-42
Match length
                  247
% identity
                  79
NCBI Description Zea mays 18S ribosomal RNA gene, partial sequence
                  294415
Seq. No.
Seq. ID
                  LIB3068-045-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  q409007
BLAST score
                  175
E value
                  7.0e-13
Match length
                  88
% identity
                  49
NCBI Description
                  BBI-M=Bowman-Birk trypsin inhibitor-related protein [Zea
                  mays=corn, Peptide, 102 aa] >gi 447268 prf 1914141A
                  trypsin inhibitor-related protein [Zea mays]
Seq. No.
                  294416
Seq. ID
                  LIB3068-045-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  g1806140
BLAST score
                  629
E value
                  8.0e-66
Match length
                  128
% identity
                  91
NCBI Description (X97314) cdc2MsC [Medicago sativa]
Seq. No.
                  294417
Seq. ID
                  LIB3068-045-Q1-K1-G4
```

Method BLASTX NCBI GI g1172836 BLAST score 168 E value 3.0e-18 Match length 60



% identity 59

NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi_496272 (L16787)

small ras-related protein [Nicotiana tabacum]

24

Seq. No. 294418

Seq. ID LIB3068-045-Q1-K1-G9

Method BLASTN
NCBI GI g2687433
BLAST score 57
E value 2.0e-23
Match length 139
% identity 86

NCBI Description Tragopogon dubius large subunit 26S ribosomal RNA gene,

partial sequence

Seq. No. 294419

Seq. ID LIB3068-045-Q1-K1-H6

Method BLASTN
NCBI GI g3821780
BLAST score 33
E value 4.0e-09
Match length 33

% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 294420

Seq. ID LIB3068-045-Q1-K1-H9

Method BLASTX
NCBI GI g4455356
BLAST score 348
E value 6.0e-33
Match length 128

% identity 52

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 294421

Seq. ID LIB3068-046-Q1-K1-B5

Method BLASTN
NCBI GI g22332
BLAST score 221
E value 1.0e-121
Match length 361
% identity 91

NCBI Description Z.mays HRGP gene

Seq. No. 294422

Seq. ID LIB3068-046-Q1-K1-C5

Method BLASTN
NCBI GI g2995383
BLAST score 87
E value 2.0e-41
Match length 136
% identity 93

NCBI Description Zea mays mays mRNA for cytochrome P450 monooxygenase,

partial

Seq. No. 294423



```
LIB3068-046-Q1-K1-F6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22263
                  34
BLAST score
                  2.0e-09
E value
Match length
                  58
% identity
                  90
                  Z.mays Ds insertion element
NCBI Description
                  294424
Seq. No.
                  LIB3068-046-Q1-K1-F7
Seq. ID
Method
                  BLASTN
                  g2687433
NCBI GI
BLAST score
                  34
                  7.0e-10
E value
                  50
Match length
                  92
% identity
                  Tragopogon dubius large subunit 26S ribosomal RNA gene,
NCBI Description
                  partial sequence
Seq. No.
                  294425
Seq. ID
                  LIB3068-046-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  q2832643
BLAST score
                  212
E value
                   4.0e-17
                  55
Match length
                  71
% identity
NCBI Description (ALO21710) hypothetical protein [Arabidopsis thaliana]
                   294426
Seq. No.
Seq. ID
                  LIB3068-047-Q1-K1-A12
Method
                  BLASTN
NCBI GI
                   g3821780
BLAST score
                  37
E value
                  1.0e-11
                  37
Match length
% identity
                  100
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   294427
Seq. No.
Seq. ID
                  LIB3068-047-Q1-K1-B12
Method
                  BLASTN
                   g22229
NCBI GI
BLAST score
                   33
E value
                   4.0e-09
Match length
                   61
                   89
% identity
NCBI Description
                  Z.mays cab-m7 gene for light harvesting chlorophyll a/b
                  binding protein
                   294428
Seq. No.
Seq. ID
                   LIB3068-047-Q1-K1-D4
Method
                  BLASTX
```

Method BLASTX NCBI GI g99898 BLAST score 289 E value 6.0e-26

```
Match length
% identity
                  DNA-directed RNA polymerase (EC 2.7.7.6) largest chain
NCBI Description
                  (isoform B1) - soybean (fragment)
                  294429
Seq. No.
Seq. ID
                  LIB3068-047-Q1-K1-D7
                  BLASTN
Method
                  g169818
NCBI GI
                  50
BLAST score
                  3.0e-19
E value
                  126
Match length
                  86
% identity
NCBI Description Rice 25S ribosomal RNA gene
                  294430
Seq. No.
                  LIB3068-047-Q1-K1-E8
Seq. ID
Method
                  BLASTN
                  g1220422
NCBI GI
                  117
BLAST score
                   3.0e-59
E value
                  125
Match length
% identity
                   98
NCBI Description Zea mays ubiquitin (MUB14) mRNA, 3' end
                   294431
Seq. No.
                  LIB3068-047-Q1-K1-G8
Seq. ID
                  BLASTN
Method
                   g3452305
NCBI GI
                   109
BLAST score
                   2.0e-54
E value
Match length
                   192
                   90
% identity
```

NCBI Description Zea mays retrotransposon Opie-3 3' LTR, partial sequence

 Seq. No.
 294432

 Seq. ID
 LIB3068-047-Q1-K1-H7

 Method
 BLASTN

NCBI GI g2062705
BLAST score 36
E value 9.0e-11
Match length 36
% identity 100

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 294433

Seq. ID LIB3068-048-Q1-K1-G11

Method BLASTX
NCBI GI g2980770
BLAST score 227
E value 9.0e-19
Match length 106
% identity 45

NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 294434

Seq. ID LIB3068-049-Q1-K1-F10



```
Method
                  BLASTX
NCBI GI
                  g2995384
BLAST score
                  255
                  3.0e-22
E value
                  85
Match length
                  65
% identity
NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]
                  294435
Seq. No.
Seq. ID
                  LIB3068-049-Q1-K1-H10
                  BLASTN
Method
NCBI GI
                  g3821780
                  36
BLAST score
E value
                  1.0e-10
                  36
Match length
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  294436
Seq. No.
Seq. ID
                  LIB3068-049-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  g1168470
BLAST score
                  400
E value
                  4.0e-39
                  119
Match length
                  63
% identity
                  PROTEIN KINASE APK1A >gi_282877_pir_S28615 protein kinase,
NCBI Description
                  tyrosine/serine/threonine-specific (EC 2.7.1.-) -
                  Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522)
                  protein tyrosine-serine-threonine kinase [Arabidopsis
                  thaliana]
                  294437
Seq. No.
                  LIB3068-050-Q1-K1-C8
Seq. ID
Method
                  BLASTN
                  q257040
NCBI GI
BLAST score
                  116
                  4.0e-59
E value
Match length
                  116
% identity
                  100
NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
                  294438
Seq. No.
Seq. ID
                  LIB3068-050-Q1-K1-D11
                  BLASTX
Method
                  q3482933
NCBI GI
BLAST score
                  300
                   3.0e-27
E value
Match length
                  127
% identity
                   49
                   (AC003970) Similar to cdc2 protein kinases [Arabidopsis
NCBI Description
```

thaliana]

Seq. No. 294439

Seq. ID LIB3068-050-Q1-K1-E4

Method BLASTX NCBI GI g3135543

BLAST score

E value

227

1.0e-18



```
BLAST score
                  1.0e-25
E value
                  90
Match length
% identity
NCBI Description
                  (AF062393) aquaporin [Oryza sativa]
Seq. No.
                  294440
                  LIB3068-050-Q1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q552736
BLAST score
                  267
E value
                  2.0e-23
                  88
Match length
                  61
% identity
NCBI Description (M11203) P700 chlorophyll a-protein PSI-A2 [Zea mays]
Seq. No.
                  294441
Seq. ID
                  LIB3068-050-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  g4455171
BLAST score
                  153
                  1.0e-10
E value
Match length
                  66
                  55
% identity
NCBI Description (AL035521) hypothetical protein [Arabidopsis thaliana]
                  294442
Seq. No.
                  LIB3068-050-Q1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112994
BLAST score
                  282
                  3.0e-25
E value
Match length
                  82
                  72
% identity
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >qi 82685 pir S04536 embryonic abundant protein,
                   glycine-rich - maize >gi 22313_emb_CAA31077_ (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi 226091 prf 1410284A abscisic acid inducible gene [Zea
                  mays]
Seq. No.
                   294443
Seq. ID
                  LIB3068-050-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                   g2109457
BLAST score
                   366
E value
                   5.0e-35
Match length
                   124
% identity
                   60
                  (AF001501) chitinase [Oryza sativa]
NCBI Description
                   294444
Seq. No.
                   LIB3068-051-Q1-K1-B1
Seq. ID
Method
                   BLASTX
                   g4454032
NCBI GI
```



```
Match length 79
% identity 49
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
Seq. No. 294445
Seq. ID LIB3068-051-Q1-K1-D10
```

Method BLASTX
NCBI GI g1001430
BLAST score 528
E value 5.0e-54
Match length 133
% identity 71

NCBI Description (D63999) ORF1 [Synechocystis sp.]

Seq. No. 294446

Seq. ID LIB3068-051-Q1-K1-D6

Method BLASTX
NCBI GI g3645898
BLAST score 551
E value 1.0e-56
Match length 151
% identity 71

NCBI Description (U68408) in-frame stop codon; possibly a post-transposition

mutation [Zea mays]

Seq. No. 294447

Seq. ID LIB3068-051-Q1-K1-F2

Method BLASTX
NCBI GI g133414
BLAST score 417
E value 5.0e-41
Match length 92
% identity 89

NCBI Description DNA-DIRECTED RNA POLYMERASE BETA CHAIN >gi_66971_pir__RNZMB

DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - maize chloroplast >gi_12480_emb_CAA35195_ (X17318) RNA polymerase

beta subunit (AA 1-1075) [Zea mays]

>qi 902212 emb CAA60276 (X86563) RNA polymerase beta

subunit [Zea mays]

Seq. No. 294448

Seq. ID LIB3068-051-Q1-K1-F9

Method BLASTN
NCBI GI g257040
BLAST score 267
E value 1.0e-148
Match length 400
% identity 23

NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No. 294449

Seq. ID LIB3068-052-Q1-K1-B9

Method BLASTX
NCBI GI g4586031
BLAST score 172
E value 3.0e-12
Match length 64

NCBI Description

Seq. No.

294455



```
% identity
                  (AC007109) unknown protein [Arabidopsis thaliana]
NCBI Description
                   294450
Seq. No.
                  LIB3068-052-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g310940
                  152
BLAST score
                   2.0e-10
E value
                  55
Match length
% identity
                  (L20756) ABA- and ripening-induced protein [Solanum
NCBI Description
                   lycopersicum]
                   294451
Seq. No.
                   LIB3068-052-Q1-K1-D12
Seq. ID
                   BLASTN
Method
NCBI GI
                   g169818
                   116
BLAST score
E value
                   2.0e-58
                   288
Match length
                   85
% identity
NCBI Description Rice 25S ribosomal RNA gene
                   294452
Seq. No.
                   LIB3068-052-Q1-K1-G12
Seq. ID
                   BLASTX
Method
                   g2369714
NCBI GI
BLAST score
                   221
                   5.0e-18
E value
                   131
Match length
                   44
% identity
                  (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                   294453
Seq. No.
Seq. ID
                   LIB3068-052-Q1-K1-G5
                   BLASTX
Method
NCBI GI
                   g2352492
                   363
BLAST score
                   1.0e-34
E value
                   146
Match length
% identity
                   48
                   (AF005047) transport inhibitor response 1 [Arabidopsis
NCBI Description
                   thalianal >gi 2352494 (AF005048) transport inhibitor
                   response 1 [Arabidopsis thaliana]
                   294454
Seq. No.
                   LIB3068-052-Q1-K1-G6
Seq. ID
Method
                   BLASTX
                   g2995384
NCBI GI
BLAST score
                   290
                   3.0e-26
E value
Match length
                   74
% identity
                   74
```

41137

(AJ004810) cytochrome P450 monooxygenase [Zea mays]



```
LIB3068-053-Q1-K1-C1
Seq. ID
                  BLASTX
Method
                  q4455159
NCBI GI
                  237
BLAST score
                  8.0e-20
E value
Match length
                  120
% identity
                  (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
                  294456
Seq. No.
                  LIB3068-053-Q1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2344818
                  202
BLAST score
                  6.0e-16
E value
                  54
Match length
% identity
                  (AJ001268) basic pathogenesis-related protein PR5 [Hordeum
NCBI Description
                  vulgare]
                  294457
Seq. No.
Seq. ID
                  LIB3068-053-Q1-K1-H5
                  BLASTN
Method
                  g170767
NCBI GI
                  41
BLAST score
                   9.0e-14
E value
                   49
Match length
                   96
% identity
NCBI Description Wheat Nor-D3 locus ribosomal RNA gene
                   294458
Seq. No.
                  LIB3068-054-Q1-K1-A10
Seq. ID
Method
                  BLASTN
                   g248338
NCBI GI
                   65
BLAST score
                   5.0e-28
E value
                   249
Match length
% identity
                   55
NCBI Description polyubiquitin [maize, Genomic, 3439 nt]
Seq. No.
                   294459
                   LIB3068-054-Q1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131772
BLAST score
                   408
                   5.0e-40
E value
Match length
                   93
% identity
                   88
                   40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
NCBI Description
                   >gi 82723 pir A30097 ribosomal protein S14 (clone MCH1) -
                   maize
Seq. No.
                   294460
                   LIB3068-054-Q1-K1-G10
Seq. ID
                   BLASTX
Method
```

41138

g115771

603

NCBI GI BLAST score



8.0e-63 E value Match length 115 % identity 99 CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description (CAB-1) (LHCP) >gi 82682 pir S04453 chlorophyll a/b-binding protein precursor - maize >gi 22224 emb CAA32900 (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays] 294461 Seq. No. Seq. ID LIB3068-054-Q1-K1-H4 Method BLASTN g3821780 NCBI GI 35 BLAST score 2.0e-10 E value Match length 35 % identity 100 NCBI Description Xenopus laevis cDNA clone 27A6-1 294462 Seq. No. LIB3068-055-Q1-K1-C6 Seq. ID Method BLASTN q2737881 NCBI GI 63 BLAST score 4.0e-27 E value 83 Match length % identity NCBI Description Saccharum sp. polyphenol oxidase mRNA, complete cds Seq. No. 294463 LIB3068-055-Q1-K1-E8 Seq. ID Method BLASTX NCBI GI q4432864 BLAST score 240 E value 4.0e-20 Match length 127 % identity (AC006300) hypothetical protein [Arabidopsis thaliana] NCBI Description 294464 Seq. No. LIB3068-056-Q1-K1-C4 Seq. ID BLASTX Method g1184077 NCBI GI BLAST score 195 6.0e-15 E value 131 Match length % identity NCBI Description (U42445) Cf-2.2 [Lycopersicon pimpinellifolium] 294465 Seq. No. LIB3068-057-Q1-K1-A3 Seq. ID

Method BLASTX
NCBI GI g3056595
BLAST score 156
E value 2.0e-10
Match length 91
% identity 42



```
(AC004255) T1F9.16 [Arabidopsis thaliana]
NCBI Description
                  294466
Seq. No.
                  LIB3068-057-Q1-K1-C3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168608
                  54
BLAST score
                  9.0e-22
E value
                  190
Match length
                  82
% identity
NCBI Description Maize 17S ribosomal RNA gene and flanks
                  294467
Seq. No.
                  LIB3068-057-Q1-K1-G11
Seq. ID
                  BLASTN
Method
NCBI GI
                  q22332
BLAST score
                  156
                   3.0e-82
E value
                   343
Match length
                   93
% identity
NCBI Description Z.mays HRGP gene
                   294468
Seq. No.
                  LIB3068-058-Q1-K1-C3
Seq. ID
                  BLASTX
Method
                   g3643605
NCBI GI
BLAST score
                   183
E value
                   1.0e-13
                   113
Match length
% identity
                  (AC005395) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   294469
                   LIB3068-058-Q1-K1-D1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g169818
BLAST score
                   72
                   2.0e-32
E value
Match length
                   116
% identity
                   91
NCBI Description Rice 25S ribosomal RNA gene
Seq. No.
                   294470
                   LIB3068-058-Q1-K1-D5
Seq. ID
                   BLASTN
Method
                   g1498596
NCBI GI
BLAST score
                   46
                   5.0e-17
E value
```

94 Match length 87 % identity

NCBI Description

Zea mays phospholipid transfer protein mRNA, complete cds

Seq. No.

294471

LIB3068-058-Q1-K1-D7 Seq. ID

BLASTX Method g1498597 NCBI GI BLAST score 179

Match length

48



```
2.0e-13
E value
                  63
Match length
% identity
                  (U66105) phospholipid transfer protein [Zea mays]
NCBI Description
Seq. No.
                  294472
                  LIB3068-058-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132897
                  298
BLAST score
                  5.0e-27
E value
Match length
                  57
                  98
% identity
                  CHLOROPLAST 50S RIBOSOMAL PROTEIN L33 >gi 71355_pir_ R5ZM33
NCBI Description
                  ribosomal protein L33 - maize chloroplast
                  >gi_12449_emb_CAA39995_ (X56673) chloroplast ribosomal
                  protein L33 [Zea mays] >gi 902242 emb CAA60306_ (X86563)
                  ribosomal protein L33 [Zea mays]
                  294473
Seq. No.
                  LIB3068-058-Q1-K1-G10
Seq. ID
                  BLASTN
Method
NCBI GI
                  g169818
BLAST score
                  79
                  2.0e-36
E value
                  235
Match length
                  84
% identity
NCBI Description Rice 25S ribosomal RNA gene
                  294474
Seq. No.
                  LIB3068-058-Q1-K1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2501986
BLAST score
                  288
                   8.0e-26
E value
                  142
Match length
                   47
% identity
NCBI Description (AF022178) TAFII250 transcription factor [Mus musculus]
                   294475
Seq. No.
Seq. ID
                   LIB3068-059-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   q464470
BLAST score
                   290
E value
                   3.0e-26
Match length
                   90
% identity
                   67
                  PROFILIN 3 >gi 422033 pir S35798 profilin 3 - maize
NCBI Description
                   >gi 313142 emb_CAA51720_ (X73281) profilin 3 [Zea mays]
                   294476
Seq. No.
                   LIB3068-059-Q1-K1-A8
Seq. ID
Method
                   BLASTX
                   q464470
NCBI GI
BLAST score
                   144
                   2.0e-09
E value
```



% identity 62 NCBI Description PROFILIN 3 >gi_422033 pir_ S35798 profilin 3 - maize >gi_313142 emb_CAA51720_ (X73281) profilin 3 [Zea mays]

Seq. No. 294477

Seq. ID LIB3068-059-Q1-K1-B12

Method BLASTN
NCBI GI g1657763
BLAST score 36
E value 6.0e-11
Match length 36
% identity 100

NCBI Description Zea mays retrotransposon Ji-3 5' LTR and primer binding

site DNA sequence

Seq. No. 294478

Seq. ID LIB3068-059-Q1-K1-D4

Method BLASTX
NCBI GI g2668742
BLAST score 176
E value 7.0e-13
Match length 77
% identity 53

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 294479

Seq. ID LIB3068-059-Q1-K1-F4

Method BLASTN
NCBI GI g551482
BLAST score 92
E value 2.0e-44
Match length 207
% identity 86

NCBI Description Zea mays ABA- and ripening-inducible-like protein mRNA,

complete cds

Seq. No. 294480

Seq. ID LIB3068-059-Q1-K1-F7

Method BLASTX
NCBI GI g567890
BLAST score 160
E value 8.0e-11
Match length 84
% identity 42

NCBI Description (L37352) beta-galactosidase-complementation protein

[Cloning vector]

Seq. No. 294481

Seq. ID LIB3068-059-Q1-K1-G6

Method BLASTX
NCBI GI g3241943
BLAST score 449
E value 1.0e-44
Match length 102
% identity 77

NCBI Description (AC004625) hypothetical protein [Arabidopsis thaliana]



```
294482
Seq. No.
                  LIB3068-059-Q1-K1-G9
Seq. ID
                  BLASTX
Method
                  g2668742
NCBI GI
BLAST score
                  351
E value
                  2.0e-33
                  87
Match length
% identity
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]
Seq. No.
                  294483
                  LIB3068-059-Q1-K1-H2
Seq. ID
                  BLASTX
Method
                   q3334411
NCBI GI
                   308
BLAST score
E value
                   3.0e-28
Match length
                   87
                   71
% identity
                  VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
NCBI Description
                   >gi 1263911_emb_CAA65581_ (X96785) vacuolar H(+)-ATPase
                   [Spinacia oleracea]
                   294484
Seq. No.
                   LIB3068-060-Q1-K1-A9
Seq. ID
                   BLASTX
Method
                   g2129630
NCBI GI
BLAST score
                   185
                   1.0e-13
E value
                   91
Match length
% identity
                   lamin - Arabidopsis thaliana >gi_1262754_emb_CAA65750
NCBI Description
                   (X97023) lamin [Arabidopsis thaliana] >gi 3395760 (U77721)
                   unknown [Arabidopsis thaliana]
Seq. No.
                   294485
                   LIB3068-060-Q1-K1-C3
Seq. ID
Method
                   BLASTN
                   g169818
NCBI GI
BLAST score
                   162
E value
                   4.0e-86
Match length
                   222
% identity
                   94
NCBI Description Rice 25S ribosomal RNA gene
                   294486
Seq. No.
                   LIB3068-060-Q1-K1-C5
Seq. ID
                   BLASTN
Method
                   g169818
NCBI GI
BLAST score
                   64
                   1.0e-27
E value
                   176
Match length
                   85
% identity
NCBI Description Rice 25S ribosomal RNA gene
```

41143

294487

BLASTX

LIB3068-060-Q1-K1-E11

Seq. No.

Seq. ID Method

NCBI GI

E value

BLAST score

q3894191

1.0e-10

157



```
g3057120
NCBI GI
                  222
BLAST score
                  9.0e-27
E value
                  130
Match length
                  52
% identity
NCBI Description (AF023159) starch synthase DULL1 [Zea mays]
                  294488
Seq. No.
                  LIB3068-060-Q1-K1-E2
Seq. ID
                  BLASTN
Method
                  q1272684
NCBI GI
BLAST score
                  140
                  5.0e-73
E value
                  244
Match length
                  89
% identity
NCBI Description Z.mays mRNA for acetyl CoA carboxylase (partial)
Seq. No.
                  294489
Seq. ID
                  LIB3068-060-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  g1709001
                  182
BLAST score
                  4.0e-19
E value
Match length
                  85
                  66
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_2129888_pir__S66351 methionine adenosyltransferase (EC
                  2.5.1.6) 1 - garden pea (fragment) >gi_609223_emb_CAA57580_
                   (X82076) methionine adenosyltransferase [Pisum sativum]
                  294490
Seq. No.
                  LIB3068-060-Q1-K1-G3
Seq. ID
                  BLASTN
Method
                  g3452290
NCBI GI
BLAST score
                  69
                  2.0e-30
E value
                  155
Match length
% identity
                  87
NCBI Description Zea mays retrotransposon Huck-1 5' LTR, partial sequence
                   294491
Seq. No.
Seq. ID
                  LIB3068-060-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g2213643
BLAST score
                   339
                   4.0e-32
E value
                   88
Match length
% identity
NCBI Description
                  (U57338) glossyl homolog [Oryza sativa]
                   294492
Seq. No.
Seq. ID
                   LIB3068-060-Q1-K1-H11
Method
                   BLASTX
```



```
Match length 41
% identity 68
NCBI Description (AC005662) unknown protein [Arabidopsis thaliana]
Seq. No. 294493
Seq. ID LIB3068-061-Q1-K1-A4
Method BLASTN
MCBI CI g1498596
```

NCBI GI g1498596 BLAST score 56 E value 7.0e-23 Match length 128 % identity 86

NCBI Description Zea mays phospholipid transfer protein mRNA, complete cds

 Seq. No.
 294494

 Seq. ID
 LIB3068-061-Q1-K1-B10

 Method
 BLASTX

 NCBI GI
 g2995384

 BLAST score
 238

 E value
 2.0e-20

E value 2.0e-2
Match length 76
% identity 66

NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]

 Seq. No.
 294495

 Seq. ID
 LIB3068-061-Q1-K1-C2

 Method
 BLASTX

NCBI GI g1362086
BLAST score 141
E value 3.0e-09
Match length 68
% identity 49

NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>qi 2129919 pir S65957

5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase

[Catharanthus roseus]

Seq. No. 294496

Seq. ID LIB3068-061-Q1-K1-D10

Method BLASTN
NCBI GI g551482
BLAST score 56
E value 8.0e-23
Match length 137
% identity 91

NCBI Description Zea mays ABA- and ripening-inducible-like protein mRNA,

complete cds

Seq. No. 294497

Seq. ID LIB3068-061-Q1-K1-E2

Method BLASTX
NCBI GI g1905944
BLAST score 201
E value 1.0e-15



Match length 72 % identity 61

NCBI Description (U49734) MADS box transcription factor SbMADS1 [Sorghum

bicolor]

Seq. No. 294498

Seq. ID LIB3068-061-Q1-K1-G11

Method BLASTN
NCBI GI g169818
BLAST score 57
E value 2.0e-23
Match length 149
% identity 85

NCBI Description Rice 25S ribosomal RNA gene

Seq. No. 294499

Seq. ID LIB3068-062-Q1-K1-E8

Method BLASTN
NCBI GI g902200
BLAST score 142
E value 5.0e-74
Match length 310
% identity 86

NCBI Description Z.mays complete chloroplast genome

Seq. No. 294500

Seq. ID LIB3068-062-Q1-K1-F1

Method BLASTN
NCBI GI g4007864
BLAST score 153
E value 1.0e-80
Match length 326
% identity 37

NCBI Description Zea mays HRGP gene, AC1503 line

Seq. No. 294501

Seq. ID LIB3069-001-Q1-K1-C3

Method BLASTX
NCBI GI g2842744
BLAST score 141
E value 7.0e-09
Match length 34
% identity 74

NCBI Description ENHANCER OF RUDIMENTARY HOMOLOG >gi 1595812 (U67398)

enhancer of rudimentary homolog ATER [Arabidopsis thaliana]

Seq. No. 294502

Seq. ID LIB3069-001-Q1-K1-C8

Method BLASTX
NCBI GI g3128171
BLAST score 156
E value 2.0e-11
Match length 100
% identity 43

NCBI Description (AC004521) putative proteinase [Arabidopsis thaliana]

Seq. No. 294503



```
LIB3069-001-Q1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2673906
                  230
BLAST score
                  5.0e-19
E value
                  62
Match length
% identity
                  (AC002561) putative DNA polymerase delta small subunit
NCBI Description
                  [Arabidopsis thaliana]
                  294504
Seq. No.
Seq. ID
                  LIB3069-001-Q1-K1-H9
                  BLASTX
Method
NCBI GI
                  q3882329
BLAST score
                  508
                  1.0e-51
E value
                  120
Match length
% identity
                  86
NCBI Description (AB018347) KIAA0804 protein [Homo sapiens]
                  294505
Seq. No.
                  LIB3069-002-Q1-K1-A4
Seq. ID
                  BLASTN
Method
NCBI GI
                  g168500
                  57
BLAST score
                  9.0e-24
E value
                  93
Match length
                   90
% identity
NCBI Description Maize (Zea mays) histone H4 gene (H4C14), complete cds
                   294506
Seq. No.
Seq. ID
                  LIB3069-002-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                   g3025299
BLAST score
                   144
                   5.0e-09
E value
                   61
Match length
                   52
% identity
NCBI Description HYPOTHETICAL 62.3 KD PROTEIN T29M21.25 >gi 2088660
                   (AF002109) ABC1 isolog [Arabidopsis thaliana]
                   294507
Seq. No.
Seq. ID
                   LIB3069-002-Q1-K1-C1
Method
                   BLASTX
                   g3776567
NCBI GI
BLAST score
                   381
                   8.0e-37
E value
                   127
Match length
% identity
                   65
                   (AC005388) Strong similarity to F21B7.33 gi_2809264 from A.
NCBI Description
                   thaliana BAC qb AC002560. EST qb N65119 comes from this
```

gene. [Arabidopsis thaliana]

Seq. No. 294508

Seq. ID LIB3069-002-Q1-K1-D12

Method BLASTX NCBI GI g3522931



```
585
BLAST score
                   1.0e-60
E value
Match length
                   135
                   79
% identity
                   (AC002535) putative Na+/Ca2+ exchanger [Arabidopsis
NCBI Description
                   thaliana]
                   294509
Seq. No.
                   LIB3069-002-Q1-K1-D4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
                   8.0e-11
E value
Match length
                   36
% identity
                   100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   294510
Seq. No.
                   LIB3069-002-Q1-K1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2688842
BLAST score
                   146
E value
                   2.0e-09
Match length
                   63
                   51
% identity
                   (AF004830) serine palmitoyltransferase LCB2 subunit
NCBI Description
                   [Cricetulus griseus]
                   294511
Seq. No.
                   LIB3069-002-Q1-K1-E4
Seq. ID
Method
                   BLASTX
                   g3193284
NCBI GI
                   158
BLAST score
                   2.0e-13
E value
                   73
Match length
% identity
                   53
                   (AF069298) No definition line found [Arabidopsis thaliana]
NCBI Description
                   294512
Seq. No.
                   LIB3069-002-Q1-K1-G9
Seq. ID
                   BLASTX
Method
                   g1705659
NCBI GI
                   248
BLAST score
                   3.0e-21
E value
                   88
Match length
% identity
                   62
                   CCAAT-BINDING FACTOR (CBF) >gi 2137192 pir JC6067
NCBI Description
                   CCAAT-binding factor CBF1 - mouse >gi \overline{7}905\overline{75} (U19891)
                   putative CCAAT binding factor 1; alternatively spliced
                   transcript mCBF1 [Mus musculus]
                   294513
Seq. No.
```

Seq. ID LIB3069-002-Q1-K1-H3

Method BLASTN
NCBI GI g4206305
BLAST score 36
E value 1.0e-10

NCBI Description



```
Match length
                  96
                  84
% identity
                  Zea mays retrotransposon Cinful-1, complete sequence
NCBI Description
                  294514
Seq. No.
                  LIB3069-002-Q1-K1-H7
Seq. ID
Method
                  BLASTX
                  g4538978
NCBI GI
                  163
BLAST score
                  1.0e-11
E value
                  84
Match length
                  40
% identity
                  (ALO49487) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  294515
Seq. No.
                  LIB3069-003-Q1-K1-A12
Seq. ID
Method
                  BLASTX
                  g4099919
NCBI GI
BLAST score
                  172
                  1.0e-12
E value
                  87
Match length
                   43
% identity
                  (U91981) pollen allergen homolog [Triticum aestivum]
NCBI Description
                   294516
Seq. No.
                  LIB3069-003-Q1-K1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3046696
BLAST score
                   207
                   2.0e-16
E value
                   113
Match length
% identity
                   42
                  (AL022224) CTP synthase like protein [Arabidopsis thaliana]
NCBI Description
                   294517
Seq. No.
Seq. ID
                   LIB3069-003-Q1-K1-B7
Method
                   BLASTX
NCBI GI
                   g82694
BLAST score
                   146
                   2.0e-09
E value
                   50
Match length
% identity
                   70
                   glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) 2 -
NCBI Description
                   maize (fragment) >gi 293889 (L13432)
                   glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
Seq. No.
                   294518
                   LIB3069-003-Q1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115794
BLAST score
                   193
E value
                   6.0e-15
Match length
                   88
% identity
                   51
```

41149

protein type III precursor (cab-13) - tomato

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR

(CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding



```
>gi_19277_emb_CAA42818_ (X60275) LHCII type III
[Lycopersicon esculentum]
```

Seq. No. 294519

Seq. ID LIB3069-003-Q1-K1-C10

Method BLASTX
NCBI GI g3281861
BLAST score 398
E value 1.0e-38
Match length 157
% identity 50

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 294520

Seq. ID LIB3069-003-Q1-K1-C3

Method BLASTX
NCBI GI g3551960
BLAST score 235
E value 8.0e-20
Match length 107
% identity 47

NCBI Description (AF082033) senescence-associated protein 15 [Hemerocallis

hybrid cultivar]

Seq. No. 294521

Seq. ID LIB3069-003-Q1-K1-D4

Method BLASTX
NCBI GI g2129851
BLAST score 219
E value 1.0e-17
Match length 146
% identity 39

NCBI Description tRNA adenylyltransferase (EC 2.7.7.25) - white lupine

>gi 1139585 (U15930) tRNA nucleotidyltransferase [Lupinus

albus]

Seq. No. 294522

Seq. ID LIB3069-003-Q1-K1-D5

Method BLASTX
NCBI GI g3123908
BLAST score 279
E value 6.0e-25
Match length 115
% identity 49

NCBI Description (AF038392) pre-mRNA splicing factor [Homo sapiens]

Seq. No. 294523

Seq. ID LIB3069-003-Q1-K1-D6

Method BLASTX
NCBI GI g2494320
BLAST score 155
E value 7.0e-11
Match length 64
% identity 55

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5)

>gi_1806575_emb_CAA67868_ (X99517) Eukaryotic initiation

factor-5 [Zea mays]



```
294524
Seq. No.
Seq. ID
                  LIB3069-003-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g1619602
BLAST score
                  241
                  2.0e-20
E value
                  81
Match length
% identity
NCBI Description (Y08726) MtN3 [Medicago truncatula]
                  294525
Seq. No.
                  LIB3069-003-Q1-K1-E10
Seq. ID
                  BLASTX
Method
                   g82040
NCBI GI
BLAST score
                   688
E value
                   1.0e-72
Match length
                   153
                   26
% identity
                  ubiquitin precursor - flax (fragment) >gi_168304 (M57895)
NCBI Description
                   ubiquitin [Linum usitatissimum]
                   294526
Seq. No.
                   LIB3069-003-Q1-K1-E11
Seq. ID
                   BLASTX
Method
                   g1200205
NCBI GI
BLAST score
                   166
                   2.0e-11
E value
                   66
Match length
% identity
NCBI Description (X95753) DAG [Antirrhinum majus]
Seq. No.
                   294527
                   LIB3069-003-Q1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2497748
BLAST score
                   146
                   2.0e-09
E value
Match length
                   60
                   47
% identity
                   NONSPECIFIC LIPID-TRANSFER PROTEIN 4 PRECURSOR (LTP 4)
NCBI Description
                   >gi_902058 (U29176) lipid transfer protein precursor [Oryza
                   sativa]
Seq. No.
                   294528
                   LIB3069-003-Q1-K1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1708107
BLAST score
                   310
                   1.0e-28
E value
Match length
                   92
                   75
% identity
                  HISTONE H2B >gi_473605 (U08226) histone H2B [Zea mays]
NCBI Description
```

41151

294529

BLASTX

LIB3069-003-Q1-K1-H4

Seq. No.

Seq. ID Method



```
q2924508
NCBI GI
                  241
BLAST score
                  6.0e-21
E value
                  62
Match length
% identity
                  (AL022023) actin depolymerizing factor - like protein
NCBI Description
                  [Arabidopsis thaliana]
                  294530
Seq. No.
                  LIB3069-004-Q1-K1-A11
Seq. ID
                  BLASTX
Method
                  g3522942
NCBI GI
BLAST score
                  191
                  1.0e-14
E value
                  82
Match length
% identity
NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]
                  294531
Seq. No.
                  LIB3069-004-Q1-K1-A3
Seq. ID
Method
                  BLASTX
                  g3650036
NCBI GI
                  144
BLAST score
E value
                  6.0e-09
                  123
Match length
% identity
                  36
NCBI Description (AC005396) putative transposase [Arabidopsis thaliana]
                  294532
Seq. No.
Seq. ID
                  LIB3069-004-Q1-K1-A9
                  BLASTX
Method
NCBI GI
                  g1352081
                  732
BLAST score
                   7.0e-78
E value
                  138
Match length
                   99
% identity
                  BETA-GLUCOSIDASE, CHLOROPLAST PRECURSOR (GENTIOBIASE)
NCBI Description
                   (CELLOBIASE) (BETA-D-GLUCOSIDE GLUCOHYDROLASE) >gi 799377
                   (U25157) beta-D-glucosidase [Zea mays] >gi_1399390 (U44773)
                   beta-D-glucosidase [Zea mays] >gi 4096602 (U33816)
                   beta-D-glucosidase [Zea mays]
                   294533
Seq. No.
Seq. ID
                   LIB3069-004-Q1-K1-B4
                   BLASTX
Method
                   q3420054
NCBI GI
BLAST score
                   199
                   2.0e-15
E value
Match length
                   113
% identity
                  (AC004680) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   294534
                   LIB3069-004-Q1-K1-D7
Seq. ID
Method
                   BLASTX
                   q4335724
NCBI GI
```

192

BLAST score



2.0e-14 E value Match length 97 % identity (AC006248) putative RING-H2 finger protein [Arabidopsis NCBI Description thaliana] 294535 Seq. No. LIB3069-004-Q1-K1-E7 Seq. ID Method BLASTX NCBI GI g2160319 166 BLAST score 6.0e-12 E value 62 Match length % identity 56 NCBI Description (D25240) possible SEC18 coding sequence [Oryza sativa] Seq. No. 294536 LIB3069-004-Q1-K1-F1 Seq. ID Method BLASTX NCBI GI g1432058 151 BLAST score E value 5.0e-10 55 Match length % identity NCBI Description (U58540) WRKY2 [Petroselinum crispum] 294537 Seq. No. LIB3069-004-Q1-K1-F12 Seq. ID Method BLASTX NCBI GI g1362162 191 BLAST score 7.0e-15 E value 82 Match length % identity 46 beta-glucosidase BGQ60 precursor - barley >gi 804656 NCBI Description (L41869) beta-glucosidase [Hordeum vulgare] 294538 Seq. No. Seq. ID LIB3069-004-Q1-K1-F5 BLASTX Method q4507229 NCBI GI 179 BLAST score 2.0e-13 E value Match length 85 % identity 48 Succinic semialdehyde dehydrogenase NCBI Description >gi_3766467_emb_CAA72076 (Y11192) NAD+ dependent succinic semialdehyde dehydrogenase [Homo sapiens] >gi 4164365 emb CAA20248 (AL031230) dJ73M23.2 (NAD+-dependent succinic semialdehyde dehydrogenase (SSADH, EC 1.2.1.24)) [Homo sapiens] 294539 Seq. No.

Seq. ID LIB3069-004-Q1-K1-G11

Method BLASTN NCBI GI g1532072 BLAST score 106



```
1.0e-52
E value
                  126
Match length
                  96
% identity
NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase
                  294540
Seq. No.
                  LIB3069-004-Q1-K1-H11
Seq. ID
Method
                  BLASTX
                  q3785995
NCBI GI
                  339
BLAST score
                   5.0e-32
E value
Match length
                  99
                   71
% identity
NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]
                  294541
Seq. No.
Seq. ID
                  LIB3069-004-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                   g2315449
BLAST score
                   169
                   7.0e-12
E value
                   116
Match length
                   37
% identity
                  (AF016448) similar to Saccharomyces cerevisiae nuclear
NCBI Description
                   protein SNF7 (SP:P39929)in one region and the chromosome
                   segregation protein SMC2 (SP:P38989) in another
                   [Caenorhabditis elegans]
                   294542
Seq. No.
Seq. ID
                   LIB3069-004-Q1-K1-H9
                   BLASTX
Method
                   q3643593
NCBI GI
BLAST score
                   170
                   4.0e-12
E value
                   59
Match length
                   59
% identity
                  (AC005395) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   294543
Seq. No.
                   LIB3069-005-Q1-K1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2191187
BLAST score
                   294
                   2.0e-26
E value
                   137
Match length
% identity
                   46
                   (AF007271) contains similarity to a DNAJ-like domain
NCBI Description
                   [Arabidopsis thaliana]
                   294544
Seq. No.
                   LIB3069-005-Q1-K1-B1
Seq. ID
                   BLASTX
Method
                   g2194125
NCBI GI
                   232
BLAST score
                   3.0e-19
E value
```

55

71

Match length % identity



```
(AC002062) ESTs gb_R30459,gb_N38441 come from this gene.
NCBI Description
                  [Arabidopsis thaliana]
                  294545
Seq. No.
Seq. ID
                  LIB3069-005-Q1-K1-G2
Method
                  BLASTX
                  q118104
NCBI GI
                  500
BLAST score
                  7.0e-51
E value
Match length
                  106
% identity
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                  (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi 68408_pir _CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi 168461 (M55021) cyclophilin [Zea mays]
                  >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]
                  294546
Seq. No.
Seq. ID
                  LIB3069-005-Q1-K1-H5
                  BLASTX
Method
NCBI GI
                  q3218543
BLAST score
                  146
                   3.0e-09
E value
                  118
Match length
                   32
% identity
                  (AB004813) alternative oxidase [Oryza sativa]
NCBI Description
                   >gi 3218548 dbj BAA28774 (AB004865) alternative oxidase
                   [Oryza sativa]
Seq. No.
                   294547
                   LIB3069-005-Q1-K1-H6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4539312
                   200
BLAST score
                   2.0e-20
E value
                   68
Match length
                   74
% identity
                   (AL035679) putative ubiquitin-dependent proteolytic protein
NCBI Description
                   [Arabidopsis thaliana]
                   294548
Seq. No.
                   LIB3069-006-Q1-K1-B12
Seq. ID
Method .
                   BLASTX
                   q450880
NCBI GI
                   201
BLAST score
                   7.0e-16
E value
                   95
Match length
                   51
% identity
                   (X77199) heat shock cognate 70-1 [Arabidopsis thaliana]
NCBI Description
                   294549
 Seq. No.
                   LIB3069-006-Q1-K1-C11
 Seq. ID
Method
                   BLASTX
                   g3482928
NCBI GI
                   307
 BLAST score
```

41155

4.0e-28

82

E value

Match length



% identity

% identity

46

```
(AC003970) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  >qi 3929586 (AF100166) phytochrome interacting factor 3
                  [Arabidopsis thaliana]
                  294550
Seq. No.
Seq. ID
                  LIB3069-006-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  g3894214
BLAST score
                  160
                  4.0e-11
E value
Match length
                  58
                  47
% identity
                  (D83726) elongation factor 1 beta 2 [Oryza sativa]
NCBI Description
                  >gi 3894216_dbj_BAA34599_ (D83727) elongation factor 1 beta
                  2 [Oryza sativa]
Seq. No.
                  294551
Seq. ID
                  LIB3069-006-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g2668742
                  177
BLAST score
E value
                   6.0e-13
                  86
Match length
                   51
% identity
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]
                  294552
Seq. No.
Seq. ID
                  LIB3069-006-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                   q3885882
BLAST score
                  171
E value
                   6.0e-27
                   79
Match length
% identity
                  (AF093629) inorganic pyrophosphatase [Oryza sativa]
NCBI Description
Seq. No.
                   294553
                   LIB3069-006-Q1-K1-G11
Seq. ID
                  BLASTX
Method
                   q2961384
NCBI GI
BLAST score
                   258
E value
                   3.0e-22
Match length
                   118
                   47
% identity
                   (AL022141) aldehyde dehydrogenase like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   294554
Seq. ID
                   LIB3069-006-Q1-K1-G12
Method
                   BLASTX
NCBI GI
                   g1362190
BLAST score
                   141
E value
                   9.0e-09
Match length
                   82
```

NCBI Description calcium-dependent protein kinase - maize (fragment)



>gi_506413 (L15390) calcium-dependent protein kinase [Zea
mays]

Seq. No. 294555

Seq. ID LIB3069-006-Q1-K1-G6

Method BLASTX
NCBI GI g2583121
BLAST score 161
E value 5.0e-11
Match length 47

% identity 66 NCBI Description (AC002387) putative phosphotransferase [Arabidopsis

thaliana]

Seq. No. 294556

Seq. ID LIB3069-006-Q1-K1-G7

Method BLASTX
NCBI GI g1351974
BLAST score 151
E value 8.0e-10
Match length 43

% identity 72

NCBI Description ADP-RIBOSYLATION FACTOR >gi_1076788_pir__S49325

ADP-ribosylation factor - maize >gi_1076789_pir__S53486 ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_

(X80042) ADP-ribosylation factor [Zea mays]

Seq. No. 294557

Seq. ID LIB3069-006-Q1-K1-H12

Method BLASTN
NCBI GI g3132824
BLAST score 85
E value 2.0e-40
Match length 129

% identity 91

NCBI Description Zea mays putative cytosine-5 DNA methyltransferase (ZMET1)

gene, complete cds

Seq. No. 294558

Seq. ID LIB3069-008-Q1-K1-A11

Method BLASTX
NCBI GI g404466
BLAST score 179
E value 2.0e-13
Match length 48
% identity 85

NCBI Description (S64499) H3 histone [Styela plicata, sperm, Peptide, 136

aa] [Styela plicata]

Seq. No. 294559

Seq. ID LIB3069-008-Q1-K1-A8

Method BLASTX
NCBI GI g1168191
BLAST score 217
E value 4.0e-18
Match length 65
% identity 71



```
14-3-3-LIKE PROTEIN 4 (PBLT4) >gi 1362089 pir__S57272
NCBI Description
                  14-3-3 brain protein homolog (clone pBLT4) - tomato
                  >gi_466336 (L29150) 14-3-3 protein homologue [Solanum
                  lycopersicum] >gi_1090847_prf__2019487B 14-3-3 protein
                  [Lycopersicon esculentum]
                  294560
Seq. No.
                  LIB3069-008-Q1-K1-A9
Seq. ID
                  BLASTX
Method
                  g1620982
NCBI GI
                  180
BLAST score
                  8.0e-14
E value
                  47
Match length
                  77
% identity
                  (Y08860) 40S ribosomal protein S5 [Nicotiana
NCBI Description
                  plumbaginifolia]
                  294561
Seq. No.
                  LIB3069-008-Q1-K1-D3
Seq. ID
                  BLASTX
Method
                  q1498342
NCBI GI
BLAST score
                  165
                   5.0e-12
E value
                  72
Match length
% identity
                   53
NCBI Description (U60504) actin [Glycine max]
                   294562
Seq. No.
                  LIB3069-008-Q1-K1-D4
Seq. ID
                  BLASTX
Method
                   g3549626
NCBI GI
BLAST score
                   186
                   3.0e-14
E value
                   77
Match length
% identity
NCBI Description (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
                   294563
Seq. No.
Seq. ID
                   LIB3069-008-Q1-K1-E5
                   BLASTX
Method
                   q2880043
NCBI GI
BLAST score
                   298
                   5.0e-27
E value
Match length
                   106
% identity
                   58
                   (AC002340) putative 3-hydroxyisobutyryl-coenzyme A
NCBI Description
                   hydrolase [Arabidopsis thaliana]
Seq. No.
                   294564
                   LIB3069-009-Q1-K1-A3
Seq. ID
                   BLASTX
Method
                   q3540195
NCBI GI
```

Method BLASTX
NCBI GI g3540195
BLAST score 272
E value 6.0e-24
Match length 80
% identity 32

NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]

% identity

NCBI Description



```
294565
Seq. No.
                  LIB3069-009-Q1-K1-C9
Seq. ID
                  BLASTX
Method
                  g1717870
NCBI GI
BLAST score
                  152
                  3.0e-10
E value
                  91
Match length
                  35
% identity
                  PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C8A4.01C
NCBI Description
                   (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING
                  PROTEASE) (DEUBIQUITINATING ENZYME)
                  294566
Seq. No.
                  LIB3069-009-Q1-K1-E12
Seq. ID
                  BLASTX
Method
                  g136632
NCBI GI
BLAST score
                  243
                  4.0e-23
E value
Match length
                  84
                  68
% identity
                  UBIQUITIN-ACTIVATING ENZYME E1 1 >gi 100841 pir A38373
NCBI Description
                  ubiquitin--protein ligase (EC 6.3.2.19) E1 - wheat
                  >gi_285451_pir__A42873 ubiquitin-activating enzyme E1, UBA1
                   - Wheat >gi 170780 (M55604) ubiquitin-activating enzyme E1
                   [Triticum aestivum]
                   294567
Seq. No.
                  LIB3069-009-Q1-K1-F3
Seq. ID
                  BLASTX
Method
                   g4522008
NCBI GI
BLAST score
                   175
                   6.0e-13
E value
Match length
                   66
% identity
NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]
                   294568
Seq. No.
                   LIB3069-009-Q1-K1-F7
Seq. ID
                   BLASTX
Method
                   q2894534
NCBI GI
BLAST score
                   329
E value
                   9.0e-31
Match length
                   80
% identity
                  (AJ224327) aquaporin [Oryza sativa]
NCBI Description
                   294569
Seq. No.
Seq. ID
                   LIB3069-009-Q1-K1-G1
Method
                   BLASTX
                   g4140398
NCBI GI
BLAST score
                   294
E value
                   7.0e-27
Match length
                   81
```

(AF081794) sterol-C5(6)-desaturase [Nicotiana tabacum]

Method

NCBI GI

BLASTX

g2511531



```
Seq. No.
                  294570
                  LIB3069-009-Q1-K1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1495251
                  231
BLAST score
E value
                  4.0e-24
Match length
                  119
                  54
% identity
NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana]
                  294571
Seq. No.
Seq. ID
                  LIB3069-009-Q1-K1-H2
                  BLASTX
Method
                  g1076797
NCBI GI
                  206
BLAST score
                  5.0e-22
E value
Match length
                  84
                  74
% identity
                  cysteine proteinase inhibitor precursor - maize
NCBI Description
                  >gi 809608 emb_CAA60610_ (X87126) cysteine proteinase
                  inhibitor [Zea mays]
                  294572
Seq. No.
                  LIB3069-009-Q1-K1-H3
Seq. ID
                  BLASTX
Method
                  g1076739
NCBI GI
                  315
BLAST score
                   4.0e-29
E value
                   86
Match length
                   74
% identity
                  box protein - rice >gi_508577 (L34271) box protein [Oryza
NCBI Description
                   sativa]
                   294573
Seq. No.
Seq. ID
                   LIB3069-010-Q1-K1-A7
                   BLASTX
Method
NCBI GI
                   g2102691
BLAST score
                   164
E value
                   2.0e-11
Match length
                 . 53
% identity
NCBI Description (U64817) fructokinase [Lycopersicon esculentum]
Seq. No.
                   294574
                   LIB3069-010-Q1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3176725
BLAST score
                   241
                   2.0e-20
E value
                   109
Match length
% identity
                   41
                  (AC002392) unknown protein [Arabidopsis thaliana]
NCBI Description
                   294575
Seq. No.
                   LIB3069-010-Q1-K1-C12
Seq. ID
```



```
BLAST score
                  3.0e-49
E value
Match length
                  93
                  97
% identity
                  (AF008120) alpha tubulin 1 [Eleusine indica]
NCBI Description
                  >gi 3163944 emb CAA06618_ (AJ005598) alpha-tubulin 1
                  [Eleusine indica]
Seq. No.
                  294576
Seq. ID
                  LIB3069-010-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  g3273202
BLAST score
                  142
E value
                  1.0e-08
Match length
                  40
% identity
NCBI Description (AB010918) responce reactor4 [Arabidopsis thaliana]
Seq. No.
                  294577
                  LIB3069-010-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q730456
BLAST score
                  230
E value
                  3.0e-19
Match length
                  45
% identity
                   91
NCBI Description 40S RIBOSOMAL PROTEIN S19
                   294578
Seq. No.
Seq. ID
                  LIB3069-010-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                   g2773154
BLAST score
                  167
E value
                   9.0e-12
Match length
                   60
% identity
                   55
                   (AF039573) abscisic acid- and stress-inducible protein
NCBI Description
                   [Oryza sativa]
                   294579
Seq. No.
Seq. ID
                  LIB3069-010-Q1-K1-G4
                  BLASTX
Method
NCBI GI
                   g3024657
BLAST score
                   226
                   9.0e-19
E value
Match length
                   65
                   74
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                   >gi 2668740 (AF034944) translation initiation factor; GOS2
                   [Zea mays]
```

Seq. No. 294580

Seq. ID LIB3069-010-Q1-K1-H3

Method BLASTX
NCBI GI g2435519
BLAST score 386
E value 2.0e-37



```
Match length
                  106
                  71
% identity
                   (AF024504) similar to mouse MEM3 (GB:U47024 and S.
NCBI Description
                  cerevisiae vacuolar sorting protein 35 (SW; P34110)
                   [Arabidopsis thaliana]
Seq. No.
                  294581
Seq. ID
                  LIB3069-011-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  g4204759
                  272
BLAST score
E value
                  5.0e-24
                  86
Match length
                  59
% identity
NCBI Description (U51191) peroxidase precursor [Glycine max]
                  294582
Seq. No.
Seq. ID
                  LIB3069-011-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                  g3414809
BLAST score
                  145
                   4.0e-09
E value
Match length
                  82
% identity
                   38
NCBI Description (AF061529) rjs [Mus musculus]
                  294583
Seq. No.
Seq. ID
                  LIB3069-011-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                   g733454
BLAST score
                   158
E value
                   1.0e-10
Match length
                   147
% identity
                   35
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
Seq. No.
                   294584
Seq. ID
                   LIB3069-012-Q1-K1-A11
Method
                   BLASTX
NCBI GI
                   q1084457
BLAST score
                   280
E value
                   8.0e-25
Match length
                   88
% identity
                   64
                  elongation factor 1-beta - Rice >gi 432368 dbj BAA04903
NCBI Description
                   (D23674) elongation factor 1 beta [Oryza sativa]
                   294585
Seq. No.
                   LIB3069-012-Q1-K1-B3
Seq. ID
```

Method BLASTX
NCBI GI g1172553
BLAST score 282
E value 1.0e-25
Match length 65
% identity 80

NCBI Description OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN

% identity

NCBI Description

88

protein mRNA, 3' end



(VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) >gi_456672_emb_CAA54788_ (X77733) voltage dependent anion channel (VDAC) [Triticum aestivum]

```
294586
Seq. No.
                  LIB3069-012-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4585985
BLAST score
                  185
E value
                  9.0e-14
Match length
                  123
                  37
% identity
NCBI Description (AC005287) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  294587
                  LIB3069-012-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3786011
BLAST score
                  211
E value
                  8.0e-17
Match length
                  56
                  82
% identity
                   (AC005499) putative elongation factor [Arabidopsis
NCBI Description
                   thaliana]
                   294588
Seq. No.
                  LIB3069-012-Q1-K1-D3
Seq. ID
Method
                  BLASTX
                   g4335735
NCBI GI
BLAST score
                   306
                   4.0e-28
E value
                  115
Match length
                   48
% identity
                  (AC006248) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   294589
Seq. No.
Seq. ID
                  LIB3069-012-Q1-K1-D6
                   BLASTX
Method
NCBI GI
                   g4371293
BLAST score
                   150
                   9.0e-10
E value
                   127
Match length
% identity
                  (AC006260) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   294590
Seq. No.
                   LIB3069-012-Q1-K1-H7
Seq. ID
                   BLASTN
Method
NCBI GI
                   g22268
                   271
BLAST score
                   1.0e-151
E value
                   338
Match length
```

Maize (strain E41) mRNA for cell wall glycoprotein

(partial) >gi_168458_gb_M36914_MZECWAC Z.mays cell wall

St.



```
294591
Seq. No.
                  LIB3069-013-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1899175
BLAST score
                  148
                  2.0e-09
E value
                  98
Match length
% identity
                  39
                  (U90262) calcium-dependent calmodulin-independent protein
NCBI Description
                  kinase CDPK [Cucurbita pepo]
                  294592
Seq. No.
                  LIB3069-015-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2833348
BLAST score
                  338
E value
                  7.0e-32
Match length
                  85
% identity
                  80
                  INTERFERON-INDUCED PROTEIN 6-16 PRECURSOR (IFI-6-16)
NCBI Description
                  >gi 218574 dbj BAA01980 (D11384) ORF [Pan troglodytes]
                  294593
Seq. No.
                  LIB3069-015-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1644368
                  225
BLAST score
                  1.0e-18
E value
                  87
Match length
% identity
                  55
NCBI Description (U72661) ninjurin1 [Homo sapiens] >gi_3077899 (U91512)
                  ninjurin [Homo sapiens]
                  294594
Seq. No.
                  LIB3069-015-Q1-K1-B7
Seq. ID
Method
                  BLASTX
                   q4006835
NCBI GI
                   201
BLAST score
                   1.0e-15
E value
Match length
                   92
% identity
NCBI Description (AC005970) hypothetical protein [Arabidopsis thaliana]
                   294595
Seq. No.
                   LIB3069-015-Q1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2262176
BLAST score
                   156
                   2.0e-10
E value
Match length
                   59
                   47
% identity
                   (AC002329) putative RING zinc-finger protein [Arabidopsis
NCBI Description
                   thaliana] >gi_3790573 (AF078824) RING-H2 finger protein
                   RHA3a [Arabidopsis thaliana]
```

Seq. No. 294596

Seq. ID LIB3069-015-Q1-K1-C10



```
BLASTX
Method
NCBI GI
                  g2996636
BLAST score
                  447
E value
                  2.0e-44
                  113
Match length
                  75
% identity
NCBI Description
                  (AC004503) BIGH3 [Homo sapiens]
                  294597
Seq. No.
Seq. ID
                  LIB3069-015-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  q584908
BLAST score
                  468
E value
                  5.0e-47
                  96
Match length
                  91
% identity
                  COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN
NCBI Description
                  FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
                  >gi_625235_pir__BBHU complement factor B precursor - human
                  >gi_297569_emb_CAA51389_ (X72875) complement factor B [Homo
                  sapiens] >gi_4261689_gb_AAD13989_S67310 1 (S67310)
                  complement factor B [Homo sapiens]
Seq. No.
                  294598
Seq. ID
                  LIB3069-015-Q1-K1-E11
Method
                  BLASTN
NCBI GI
                  g536897
BLAST score
                  324
E value
                   0.0e + 00
                   441
Match length
                   94
% identity
                  Human follistatin-related protein precursor mRNA, complete
NCBI Description
                   294599
Seq. No.
Seq. ID
                  LIB3069-015-Q1-K1-E12
Method
                   BLASTN
NCBI GI
                   g3366557
BLAST score
                   89
                   3.0e-42
E value
                   139
Match length
% identity
                   99
```

NCBI Description Homo sapiens chromosome 5, P1 clone 1307e8 (LBNL H60),

complete sequence [Homo sapiens]

Seq. No. 294600

Seq. ID LIB3069-015-Q1-K1-E9

Method BLASTX
NCBI GI g1172027
BLAST score 642
E value 1.0e-67
Match length 131
% identity 99

NCBI Description PRE-B CELL ENHANCING FACTOR PRECURSOR

>gi_1082712_pir__A55927 pre-B cell enhancing factor - human

>gi 404013 (U02020) pre-B cell enhancing factor [Homo

sapiens]



```
Seq. No.
                  294601
Seq. ID
                  LIB3069-015-Q1-K1-F11
Method
                  BLASTN
NCBI GI
                  g4589607
BLAST score
                  221
                  1.0e-121
E value
```

269 95

294602

% identity NCBI Description Homo sapiens mRNA for KIAA0982 protein, complete cds

Seq. No. Seq. ID LIB3069-015-Q1-K1-G6 Method BLASTX NCBI GI g416716 BLAST score 301 E value 2.0e-27 Match length 133

% identity 46

Match length

CELL DIVISION-ASSOCIATED PROTEIN BIMB NCBI Description

>gi_322992_pir__A42854 probable spindle pole body component

bimB - Emericella nidulans

Seq. No. 294603

Seq. ID LIB3069-015-Q1-K1-G9

Method BLASTX NCBI GI g2529707 332 BLAST score E value 6.0e-31 Match length 92

% identity

NCBI Description (AF001434) Hpast [Homo sapiens]

Seq. No. 294604

Seq. ID LIB3069-015-Q1-K1-H11

Method BLASTN NCBI GI g3171873 BLAST score 37 E value 2.0e-11 Match length 37

% identity 100

NCBI Description Homo sapiens DNA sequence from PAC 18601 on chromosome 22.

Contains an unknown gene, ESTs and a GSS, complete sequence

[Homo sapiens]

294605 Seq. No.

Seq. ID LIB3069-015-Q1-K1-H12

Method BLASTN NCBI GI g37505 BLAST score 228 E value 1.0e-125 Match length 298 % identity 98

NCBI Description H.sapiens RNA for 5' sequence of type IV collagenase

294606 Seq. No.

Seq. ID LIB3069-016-Q1-K1-E10



```
Method
                  BLASTX
                  g2129929
NCBI GI
BLAST score
                  560
                  8.0e-58
E value
Match length
                  108
% identity
                  96
                  DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB2 -
NCBI Description
                  tomato >qi 1049068 (U28403) RNA polymerase II subunit 2
                  [Solanum lycopersicum]
                  294607
Seq. No.
Seq. ID
                  LIB3069-016-Q1-K1-E9
                  BLASTX
Method
                  g2245026
NCBI GI
BLAST score
                  153
                  5.0e-10
E value
Match length
                  53
% identity
                  60
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]
                  294608
Seq. No.
Seq. ID
                  LIB3069-016-Q1-K1-F9
                  BLASTN
Method
NCBI GI
                  q902200
BLAST score
                  111
                  8.0e-56
E value
                  216
Match length
                  44
% identity
NCBI Description Z.mays complete chloroplast genome
Seq. No.
                  294609
                  LIB3069-017-Q1-K1-A12
Seq. ID
Method
                  BLASTX
                  q4567278
NCBI GI
                  294
BLAST score
                  1.0e-26
E value
                  101
Match length
% identity
                  57
                  (AC006841) putative anthracycline associated resistance ARX
NCBI Description
                  protein [Arabidopsis thaliana]
Seq. No.
                  294610
Seq. ID
                  LIB3069-017-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  q1143705
BLAST score
                  239
E value
                  2.0e-20
Match length
                  79
% identity
                   63
NCBI Description
                  (X89760) Hox2a [Zea mays]
Seq. No.
                  294611
                  LIB3069-017-Q1-K1-D3
```

Seq. ID

Method BLASTX q82696 NCBI GI BLAST score 258

2.0e-22 E value



Match length % identity 66

glycine-rich protein - maize >gi 22293_emb_CAA43431_ NCBI Description

(X61121) glycine-rich protein [Zea mays]

Seq. No.

294612 LIB3069-017-Q1-K1-D8 Seq. ID

Method BLASTX q3928093 NCBI GI BLAST score 470 4.0e-47 E value

Match length 144 % identity 65

(AC005770) IVR-like protein [Arabidopsis thaliana] NCBI Description

Seq. No.

294613

Seq. ID Method

LIB3069-017-Q1-K1-E1 BLASTX

NCBI GI g3176690 BLAST score 209 E value 1.0e-16 116 Match length % identity 49

(ACO03671) Similar to ubiquitin ligase gb D63905 from S. NCBI Description

cerevisiae. EST gb R65295 comes from this gene.

[Arabidopsis thaliana]

Seq. No.

294614 LIB3069-017-Q1-K1-E3 Seq. ID

Method BLASTX NCBI GI g3023751 BLAST score 268 E value 2.0e-23 139 Match length

49 % identity

70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS NCBI Description

ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi 1076772 pir S55383

peptidylprolyl isomerase (EC 5.2.1.8) - wheat

>gi 854626 emb CAA60505 (X86903) peptidylprolyl isomerase

[Triticum aestivum]

Seq. No. 294615

Seq. ID LIB3069-017-Q1-K1-E9

Method BLASTX NCBI GI g3915826 BLAST score 432 7.0e-43E value Match length 98 % identity 85

60S RIBOSOMAL PROTEIN L5 NCBI Description

294616 Seq. No.

Seq. ID LIB3069-017-Q1-K1-F2

Method BLASTX q4432832 NCBI GI 385 BLAST score E value 3.0e-37

```
Match length
                     55
   % identity
                     (ACO06283) similar to protein Htf9C [Arabidopsis thaliana]
  NCBI Description
                     294617
   Seq. No.
   Seq. ID
                     LIB3069-017-Q1-K1-F5
  Method
                     BLASTX
  NCBI GI
                     g3894159
                     235
  BLAST score
                     1.0e-19
   E value
                     135
  Match length
                     42
   % identity
   NCBI Description (AC005312) hypothetical protein [Arabidopsis thaliana]
                     294618
   Seq. No.
                     LIB3069-017-Q1-K1-G5
   Seq. ID
                     BLASTX
   Method
                     g1890575
   NCBI GI
                     280
   BLAST score
   E value
                     6.0e-25
   Match length
                     138
                     49
   % identity
                     (X93174) xyloglucan endotransglycosylase (XET) [Hordeum
   NCBI Description
                     vulgare]
                     294619
- Seq. No.
   Seq. ID
                     LIB3069-017-Q1-K1-G9
                     BLASTX
```

Method g3236249 NCBI GI 144 BLAST score

E value 6.0e-09 Match length 144 35 % identity

(AC004684) hypothetical protein [Arabidopsis thaliana] NCBI Description

294620 Seq. No. LIB3069-017-Q1-K1-H5 Seq. ID Method BLASTN q3294468 NCBI GI

BLAST score 34 7.0e-10 E value Match length 62 % identity 89

NCBI Description Zea mays phosphoglucomutase 2 mRNA, complete cds

294621 Seq. No.

Seq. ID LIB3069-018-Q1-K1-A3

Method BLASTX NCBI GI g2257743 BLAST score 216 E value 1.0e-17 Match length 90 % identity 57

(U62020) lysine-sensitive aspartate kinase [Arabidopsis NCBI Description

thaliana]

294622 Seq. No.



```
LIB3069-018-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1362162
BLAST score
                  394
E value
                  3.0e-38
Match length
                  139
                  52
% identity
                  beta-qlucosidase BGQ60 precursor - barley >gi 804656
NCBI Description
                   (L41869) beta-glucosidase [Hordeum vulgare]
Seq. No.
                  294623
Seq. ID
                  LIB3069-018-Q1-K1-C2
                  BLASTX
Method
NCBI GI
                  g2244865
                  179
BLAST score
E value
                  4.0e-13
Match length
                  127
% identity
                  38
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  294624
Seq. No.
Seq. ID
                  LIB3069-018-Q1-K1-C8
Method
                 BLASTX
NCBI GI
                  g2688830
BLAST score
                   307
                   8.0e-30
E value
Match length
                  122
% identity
                   64
                  (AF000952) putative sugar transporter [Prunus armeniaca]
NCBI Description
                   294625
Seq. No.
Seq. ID
                  LIB3069-019-Q1-K1-E5
Method
                   BLASTX
NCBI GI
                   q626042
BLAST score
                   165
E value
                   2.0e-11
Match length
                   127
% identity
                   39
                  beta-glucosidase, root meristem (EC 3.2.1.-) precursor -
NCBI Description
                   maize >gi 435313 emb CAA52293 (X74217) beta-glucosidase
                   [Zea mays]
Seq. No.
                   294626
Seq. ID
                   LIB3069-019-Q1-K1-H1
Method
                   BLASTX
NCBI GI
                   g66009
BLAST score
                   155
                   3.0e-10
E value
Match length
                   96
% identity
                   40
                   glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C,
NCBI Description
                   cytosolic - maize >gi 22238 emb CAA30151 (X07156) GADPH
                   (AA 1-337) [Zea mays]
```

Seq. No. 294627

Seq. ID LIB3069-019-Q1-K1-H11

Method BLASTN

% identity

86



```
g4140643
NCBI GI
                  55
BLAST score
                  2.0e-22
E value
Match length
                  83
                  93
% identity
NCBI Description
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
                  complete sequence
                  294628
Seq. No.
                  LIB3069-020-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2668742
BLAST score
                  304
                  8.0e-28
E value
Match length
                  82
                  74
% identity
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
Seq. No.
                   294629
                  LIB3069-020-Q1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4432859
BLAST score
                  193
                   4.0e-15
E value
Match length
                  73
                   59
% identity
                  (AC006300) unknown protein [Arabidopsis thaliana]
NCBI Description
                   294630
Seq. No.
Seq. ID
                   LIB3069-020-Q1-K1-E11
                   BLASTX
Method
NCBI GI
                   q4587584
BLAST score
                   172
                   6.0e-20
E value
                   99
Match length
% identity
                   54
                  (AC007232) unknown protein [Arabidopsis thaliana]
NCBI Description
                   294631
Seq. No.
Seq. ID
                   LIB3069-020-Q1-K1-E3
Method
                   BLASTX
NCBI GI
                   q4006818
BLAST score
                   356
E value
                   1.0e-36
Match length
                   109
                   73
% identity
                   (AC005970) putative translation initiation factor eIF-2B,
NCBI Description
                   alpha subunit [Arabidopsis thaliana]
Seq. No.
                   294632
                   LIB3069-020-Q1-K1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2335104
BLAST score
                   535
E value
                   8.0e-58
                   130
Match length
```



```
(AC002339) putative villin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  294633
                  LIB3069-020-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539420
BLAST score
                  154
                  4.0e-10
E value
Match length
                  54
% identity
                  57
                  (ALO49171) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                  294634
Seq. No.
                  LIB3069-020-Q1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3395436
BLAST score
                  177
                  5.0e-13
E value
                   56
Match length
% identity
                   (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                   294635
Seq. No.
                  LIB3069-020-Q1-K1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3660469
BLAST score
                   474
E value
                   1.0e-47
Match length
                   111
% identity
                   82
                   (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis
NCBI Description
                   thaliana] >gi_4512693_gb_AAD21746.1_ (AC006569)
                   succinyl-CoA ligase beta subunit [Arabidopsis thaliana]
                   294636
Seq. No.
                   LIB3069-020-Q1-K1-H10
Seq. ID
                   BLASTX
Method
                   g4521190
NCBI GI
BLAST score
                   229
                   7.0e-19
E value
                   145
Match length
% identity
                   39
                   (AB013448) Pib [Oryza sativa] >gi 4521192 dbj_BAA76282.1_
NCBI Description
                   (AB013449) Pib [Oryza sativa]
                   294637
Seq. No.
                   LIB3069-020-Q1-K1-H11
Seq. ID
                   BLASTX
Method
                   g118104
NCBI GI
BLAST score
                   502
E value
                   5.0e-51
                   118
Match length
                   83
% identity
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
```

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)

>gi 68408 pir CSZM peptidylprolyl isomerase (EC 5.2.1.8) -



maize >gi_168461 (M55021) cyclophilin [Zea mays] >qi 829148 emb CAA48638 (X68678) cyclophilin [Zea mays]

Seq. No. 294638

Seq. ID LIB3069-021-Q1-K1-A10

Method BLASTX
NCBI GI g2289003
BLAST score 258
E value 1.0e-22
Match length 99
% identity 57

NCBI Description (AC002335) membrane transporter D1 isolog [Arabidopsis

thaliana]

Seq. No. 294639

Seq. ID LIB3069-021-Q1-K1-B11

Method BLASTX
NCBI GI g66009
BLAST score 175
E value 1.0e-12
Match length 60
% identity 62

% identity 62
NCBI Description glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C,

cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH

(AA 1-337) [Zea mays]

Seq. No. 294640

Seq. ID LIB3069-021-Q1-K1-B7

Method BLASTX
NCBI GI g3152606
BLAST score 163
E value 8.0e-12
Match length 66
% identity 45

NCBI Description (AC004482) putative ring zinc finger protein [Arabidopsis

thaliana]

Seq. No. 294641

Seq. ID LIB3069-021-Q1-K1-E12

Method BLASTX
NCBI GI g2462753
BLAST score 423
E value 1.0e-41
Match length 152
% identity 56

NCBI Description (AC002292) putative polygalacturonase [Arabidopsis

thaliana]

Seq. No. 294642

Seq. ID LIB3069-021-Q1-K1-F10

Method BLASTX
NCBI GI g556409
BLAST score 186
E value 7.0e-14
Match length 60
% identity 65

NCBI Description (L34551) transcriptional activator protein [Oryza sativa]

NCBI Description

Seq. No. Seq. ID

294648

LIB3069-022-Q1-K1-E10



```
294643
Seq. No.
Seq. ID
                  LIB3069-021-Q1-K1-F12
                  BLASTX
Method
                  g484656
NCBI GI
BLAST score
                  231
E value
                  3.0e-19
                  95
Match length
                  54
% identity
                  monodehydroascorbate reductase (NADH) (EC 1.6.5.4) -
NCBI Description
                  cucumber >gi_452165_dbj_BAA05408 (D26392)
                  monodehydroascorbate reductase [Cucumis sativus]
                   294644
Seq. No.
                  LIB3069-021-Q1-K1-F3
Seq. ID
                  BLASTN
Method
                   g309567
NCBI GI
BLAST score
                   36
                   9.0e-11
E value
                   76
Match length
                   87
% identity
                  Zea mays PL transcriptional activator gene, complete cds
NCBI Description
                   294645
Seq. No.
                   LIB3069-021-Q1-K1-H6
Seq. ID
                   BLASTX
Method
                   g3004950
NCBI GI
                   172
BLAST score
                   1.0e-18
E value
                   63
Match length
                   87
% identity
NCBI Description (AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays]
                   294646
Seq. No.
Seq. ID
                   LIB3069-022-Q1-K1-A5
                   BLASTX
Method
                   q2499932
NCBI GI
                   158
BLAST score
                   2.0e-16
E value
                   78
Match length
                   60
% identity
                   ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_726305
NCBI Description
                   (U22442) adenine phosphoribosyltransferase form 1 [Triticum
                   aestivum]
                   294647
Seq. No.
Seq. ID
                   LIB3069-022-Q1-K1-D4
                   BLASTX
Method
NCBI GI
                   g3264600
BLAST score
                   516
                   1.0e-52
E value
Match length
                   101
% identity
```

41174

(AF057522) hypoxically induced transcript 2 [Zea mays]



```
BLASTX
Method
                   q2339978
NCBI GI
                   235
BLAST score
                   7.0e-20
E value
                   102
Match length
                   47
% identity
NCBI Description (Y11336) RGA1 protein [Arabidopsis thaliana]
                   294649
Seq. No.
Seq. ID
                   LIB3069-022-Q1-K1-E4
                   BLASTX
Method
                   g3927830
NCBI GI
                   241
BLAST score
                   2.0e-20
E value
                   122
Match length
                   43
_% identity
NCBI Description (AC005727) hypothetical protein [Arabidopsis thaliana]
                   294650
Seq. No.
                   LIB3069-022-Q1-K1-E7
Seq. ID
                   BLASTX
Method
                   g3402756
NCBI GI
BLAST score
                   200
                   3.0e-16
E value
                   90
Match length
                   49
% identity
                   (AL031187) receptor kinase - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   294651
 Seq. No.
                   LIB3069-022-Q1-K1-G12
 Seq. ID
                   BLASTX
Method
                   q3645899
 NCBI GI
                   532
 BLAST score
                   2.0e-54
 E value
                   112
 Match length
 % identity
                   (U68408) 5' end not determined experimentally [Zea mays]
 NCBI Description
                   294652
 Seq. No.
                   LIB3069-022-Q1-K1-H11
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q1076534
 BLAST score
                   203
                    4.0e-16
 E value
                    62
 Match length
                    58
 % identity
                   monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - garden
 NCBI Description
                   pea >gi_497120 (U06461) monodehydroascorbate reductase
                    [Pisum sativum]
                    294653
 Seq. No.
                    LIB3069-022-Q1-K1-H2
 Seq. ID
 Method
                    BLASTX
                    g123620
 NCBI GI
                    181
 BLAST score
```

2.0e-13

E value



97 Match length 43 % identity HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi 100224 pir S14950 NCBI Description heat shock cognate protein 70 - tomato >gi 19258 emb CAA37971 (X54030) heat shock protein cognate 70 [Lycopersicon esculentum] Seq. No. 294654 LIB3069-023-Q1-K1-A11 Seq. ID Method BLASTX NCBI GI g4584347 BLAST score 222 E value 2.0e-18 Match length 88 57 % identity NCBI Description (AC007127) unknown protein [Arabidopsis thaliana] Seq. No. 294655 Seq. ID LIB3069-023-Q1-K1-C11 Method BLASTX NCBI GI q3451071 BLAST score 369 2.0e-35 E value Match length 124 65 % identity. NCBI Description (AL031326) beta adaptin - like protein [Arabidopsis thaliana] Seq. No. 294656 Seq. ID LIB3069-023-Q1-K1-E5 Method BLASTX NCBI GI q1402918 BLAST score 230 E value 1.0e-20 Match length 114 % identity 54 NCBI Description (X98320) peroxidase [Arabidopsis thaliana] >gi 1429215 emb CAA67310 (X98774) peroxidase ATP6a [Arabidopsis thaliana] Seq. No. 294657 LIB3069-023-Q1-K1-H11 Seq. ID Method BLASTX NCBI GI q113456

Method BLASTX
NCBI GI g113456
BLAST score 292
E value 2.0e-26
Match length 79
% identity 75

NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)

(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)

>gi_22162_emb_CAA40781_ (X57556) adenine nucleotide

translocator [Zea mays]

Seq. No. 294658

Seq. ID LIB3069-023-Q1-K1-H9

Method BLASTN NCBI GI g2641618



```
BLAST score 102
E value 4.0e-50
Match length 172
% identity 91
NCBI Description Zea mays ubiquitin-conjugating enzyme protein E2 (ubc7)
mRNA, complete cds
```

Seq. No. 294659 Seq. ID LIB3069-024-Q1-K1-B12

Method BLASTX
NCBI GI g585202
BLAST score 152
E value 7.0e-10
Match length 127
% identity 39

NCBI Description GLUTAMINE SYNTHETASE ROOT ISOZYME 2 (GLUTAMATE--AMMONIA LIGASE) >gi 481807 pir_S39478 glutamate--ammonia ligase

(EC 6.3.1.2) 1-2, cytosolic - maize

>gi_434326_emb_CAA46720_ (X65927) glutamine synthetase [Zea

mays]

Seq. No. 294660 Seq. ID LIB3069-024-Q1-K1-F2

Method BLASTX
NCBI GI g2764802
BLAST score 301
E value 3.0e-33
Match length 114
% identity 70

NCBI Description (X77795) ras-like gene [Zea mays]

Seq. No. 294661

Seq. ID LIB3069-024-Q1-K1-F3

Method BLASTX
NCBI GI g2764802
BLAST score 164
E value 8.0e-12
Match length 67
% identity 54

NCBI Description (X77795) ras-like gene [Zea mays]

Seq. No. 294662

Seq. ID LIB3069-024-Q1-K1-G6

Method BLASTX
NCBI GI g547712
BLAST score 240
E value 1.0e-31
Match length 107
% identity 71

NCBI Description EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)

>gi 542153 pir S38358 translation initiation factor eIF-4A

- rice >gi 303844 dbj BAA02152 (D12627) eukaryotic

initiation factor 4A [Oryza sativa]

Seq. No. 294663

Seq. ID LIB3069-024-Q1-K1-H1

Method BLASTX



NCBI GI g1717957 BLAST score 140 E value 8.0e-09 Match length 75 % identity 48

NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT

PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP)

>gi_100923_pir__A41607 ubiquinol--cytochrome-c reductase
(EC 1.10.2.2) iron-sulfur protein precursor - maize
>qi 168607 (M77224) Rieske Fe-S protein [Zea mays]

Seq. No. 294664

Seq. ID LIB3069-025-Q1-K1-D2

Method BLASTN
NCBI GI g886739
BLAST score 123
E value 8.0e-63
Match length 222
% identity 91

NCBI Description Z.mays histone H4 gene

Seq. No. 294665

Seq. ID LIB3069-025-Q1-K1-E5

Method BLASTX
NCBI GI g134589
BLAST score 189
E value 3.0e-14
Match length 148
% identity 32

NCBI Description TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX

COMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY

PROTEIN GAM1) (TRANSCRIPTION FACTOR TYE3)

>gi_101629_pir__S15047 SNF2 protein - yeast (Saccharomyces cerevisiae) >gi_4500_emb_CAA40969_ (X57837) GAM1/SNF2

protein [Saccharomyces cerevisiae] >gi_172632 (M61703)

SNF2protein [Saccharomyces cerevisiae]

>gi_806532_dbj_BAA14423_ (D90459) RIC1 [Saccharomyces
cerevisiae] >gi 1279713 emb CAA61793 (X89633) regulatory

protein gam1 [Saccharomyces cerevisiae]

>gi 1420644 emb CAA99517 (Z75198) ORF YOR290c

[Saccharomyces cerevisiae]

Seq. No. 294666

Seq. ID LIB3069-025-Q1-K1-E6

Method BLASTX
NCBI GI g1076763
BLAST score 350
E value 4.0e-33
Match length 142
% identity 57

NCBI Description AWJL218 protein - wheat >gi_551212_emb_CAA57134 (X81369)

AWJL218 [Triticum aestivum]

Seq. No. 294667

Seq. ID LIB3069-025-Q1-K1-F9

Method BLASTN NCBI GI g1185553



```
BLAST score
                  7.0e-20
E value
                  75
Match length
                  46
% identity
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2)
NCBI Description
                  gene, complete cds
                  294668
Seq. No.
                  LIB3069-025-Q1-K1-H4
Seq. ID
                  BLASTX
Method
                  q3024886
NCBI GI
BLAST score
                  162
                  4.0e-11
E value
                  108
Match length
                  39
% identity
                  HYPOTHETICAL PROTEIN KIAA0310 >gi 2224561 dbj_BAA20769_
NCBI Description
                  (AB002308) KIAA0310 [Homo sapiens]
                  294669
Seq. No.
                  LIB3069-025-Q1-K1-H8
Seq. ID
Method
                  BLASTX
                  g4335754
NCBI GI
BLAST score
                  183
                  2.0e-13
E value
                  118
Match length
                  37
% identity
                  (AC006284) putative acid phophatase (contains
NCBI Description
                  metallo-phosphoesterase motif, prosite: QDOC50185)
                  [Arabidopsis thaliana]
Seq. No.
                  294670
                  LIB3069-026-Q1-K1-A9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q464707
                  177
BLAST score
                  7.0e-13
E value
Match length
                  32
% identity
                  100
                  40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal
NCBI Description
                  protein S18.A - Arabidopsis thaliana
                  >gi 405613 emb CAA80684 (Z23165) ribosomal protein S18A
                   [Arabidopsis thaliana] >gi 434343 emb CAA82273 (Z28701)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >qi 434345 emb CAA82274 (Z28702) S18 ribosomal protein
                   [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)
                  S18 ribosomal protein [Arabidopsis thaliana]
```

>gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi 3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal

protein [Arabidopsis thaliana]

Seq. No. 294671

LIB3069-026-Q1-K1-B8 Seq. ID

Method BLASTX



```
NCBI GI
                  g402753
BLAST score
                  160
                  7.0e-11
E value
                  120
Match length
% identity
NCBI Description
                  (X71439) translation elongation factor EF-G [Glycine max]
                  294672
Seq. No.
                  LIB3069-026-Q1-K1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2117937
BLAST score
                  145
                  5.0e-09
E value
                  113
Match length
                  41
% identity
NCBI Description
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  barley >qi 1212996 emb CAA62689 (X91347) UDP-glucose
                  pyrophosphorylase [Hordeum vulgare]
                  294673
Seq. No.
                  LIB3069-026-Q1-K1-C7
Seq. ID
Method
                  BLASTX
                  q3024127
NCBI GI
BLAST score
                  171
                  5.0e-12
E value
Match length
                  101
% identity
                  42
                  S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)
                  >qi 1655578 emb CAA95857 (Z71272) S-adenosyl-L-methionine
                  synthetase 2 [Catharanthus roseus]
Seq. No.
                  294674
                  LIB3069-026-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4104060
BLAST score
                  157
E value
                  2.0e-10
Match length
                  116
% identity
                  37
NCBI Description
                  (AF031231) S222 [Triticum aestivum]
Seq. No.
                  294675
                  LIB3069-026-Q1-K1-F2
Seq. ID
Method
                  BLASTX
                  q1173187
NCBI GI
BLAST score
                  167
E value
                  1.0e-11
                  111
Match length
% identity
                   41
                  40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__$56673
NCBI Description
                  ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                   strawberry >gi 643074 (U19940) putative 40S ribosomal
```

Seq. No. 294676

Seq. ID LIB3069-027-Q1-K1-D9

protein s12 [Fragaria x ananassa]

% identity

NCBI Description



fig.

```
Method
                  BLASTN
                  g602605
NCBI GI
BLAST score
                  58
                  6.0e-24
E value
                  58
Match length
                  50
% identity
NCBI Description Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin
                  294677
Seq. No.
                  LIB3069-027-Q1-K1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1346281
BLAST score
                  267
                  1.0e-23
E value
                  97
Match length
                  54
% identity
                  CHITOOLIGOSACCHARIDOLYTIC BETA-N-ACETYLGLUCOSAMINIDASE
NCBI Description
                  PRECURSOR (BETA-GLCNACASE) (BETA-HEXOSAMINIDASE)
                  (BETA-N-ACETYLHEXOSAMINIDASE) >gi_1078988_pir__JC2539
                  beta-N-acetylglucosaminidase (EC 3.2.1.-) - silkworm
                  >gi 998377 bbs 165703 (S77548) chitooligosaccharidolytic
                  beta-N-acetylglucosaminidase, beta-GlcNAcase=beta 1 enzyme
                  [Bombyx mori=silkworms, larvae, Kinshu X Shouwa, Peptide,
                  596 aa] [Bombyx mori] >gi 1094927 prf 2107188A
                  chitooligosaccharidolytic beta-N-acetylglucosaminidase
                  [Bombyx mori]
                  294678
Seq. No.
                  LIB3069-028-Q1-K1-B10
Seq. ID
                  BLASTX
Method
                  g3068809
NCBI GI
BLAST score
                  154
                  2.0e-10
E value
Match length
                  60
% identity
NCBI Description (AF059295) Skpl homolog [Arabidopsis thaliana]
                  294679
Seq. No.
Seq. ID
                  LIB3069-028-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  g1161254
BLAST score
                  198
E value
                  2.0e-15
Match length
                  90
% identity
                  (L38855) protein kinase [Glycine max]
NCBI Description
                  294680
Seq. No.
Seq. ID
                  LIB3069-028-Q1-K1-G10
                  BLASTX
Method
NCBI GI
                  g4191796
BLAST score
                  147
E value
                  2.0e-09
Match length
                  75
```

41181

[Arabidopsis thaliana]

(AC005917) putative senescence-associated protein 5

```
294681
Seq. No.
                  LIB3069-028-Q1-K1-G4
Seq. ID
                  BLASTX
Method
                  g3386600
NCBI GI
BLAST score
                  462
E value
                  3.0e-46
Match length
                  111
                  74
% identity
NCBI Description (AC004665) putative glycoprotein [Arabidopsis thaliana]
                  294682
Seq. No.
Seq. ID
                  LIB3069-029-Q1-K1-A12
                  BLASTX
Method
NCBI GI
                  g2146745
BLAST score
                  397
E value
                  1.0e-38
Match length
                  117
                  65
% identity
                  protein kinase (EC 2.7.1.-) - Arabidopsis thaliana
NCBI Description
                  >gi_642132_dbj_BAA08215_ (D45354) protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                  294683
Seq. ID
                  LIB3069-029-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g3337361
BLAST score
                  428
E value
                  3.0e-42
                  117
Match length
% identity
                  64
NCBI Description
                  (AC004481) ankyrin-like protein [Arabidopsis thaliana]
                  294684
Seq. No.
Seq. ID
                  LIB3069-029-Q1-K1-C5
                  BLASTX
Method
NCBI GI
                  g1321661
BLAST score
                  188
E value
                  1.0e-14
Match length
                  45
                  82
% identity
NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]
Seq. No.
                  294685
                  LIB3069-029-Q1-K1-D2
Seq. ID
```

Method BLASTX NCBI GI q2565275 188 BLAST score 4.0e-14 E value 39 Match length % identity 82

(AF023611) Dim1p homolog [Homo sapiens] NCBI Description

Seq. No. 294686

Seq. ID LIB3069-029-Q1-K1-E2

Method BLASTX NCBI GI g4206306

BLAST score

Match length

E value

216

89

1.0e-17



```
BLAST score
                  1.0e-67
E value
                  126
Match length
                  95
% identity
NCBI Description (AF049110) prpol [Zea mays]
Seq. No.
                  294687
                  LIB3069-029-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2506139
                  397
BLAST score
                  8.0e-39
E value
Match length
                  84
                  85
% identity
                  COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
NCBI Description
                  (ARCHAIN) >gi 1314049_emb_CAA91901_ (Z67962)
                  archain/delta-COP [Oryza sativa]
Seq. No.
                  294688
                  LIB3069-029-Q1-K1-G6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4567247
                  151
BLAST score
E value
                  2.0e-10
                  53
Match length
                  57
% identity
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]
                  294689
Seq. No.
Seq. ID
                  LIB3069-029-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  g4505823
                  300
BLAST score
                  2.0e-27
E value
                  92
Match length
                  58
% identity
                  pirin >gi 1907076 emb CAA69194 (Y07867) pirin [Homo
NCBI Description
                  sapiens] >gi 1907078 emb CAA69195 (Y07868) pirin [Homo
                  sapiens]
                  294690
Seq. No.
Seq. ID
                  LIB3069-030-Q1-K1-A1
Method
                  BLASTX
NCBI GI
                  g4581164
BLAST score
                  142
                  6.0e-09
E value
                  72
Match length
% identity
                  43
NCBI Description
                  (AC006220) putative polyprotein [Arabidopsis thaliana]
                  294691
Seq. No.
Seq. ID
                  LIB3069-030-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  q2494320
```



```
% identity
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5)
NCBI Description
                  >gi 1806575_emb_CAA67868_ (X99517) Eukaryotic initiation
                  factor-5 [Zea mays]
                  294692
Seq. No.
Seq. ID
                  LIB3069-030-Q1-K1-A8
Method
                  BLASTX
                  g3935167
NCBI GI
                  154
BLAST score
                  3.0e-10
E value
                  92
Match length
                  40
% identity
NCBI Description (AC004557) F17L21.10 [Arabidopsis thaliana]
                  294693
Seq. No.
                  LIB3069-030-Q1-K1-B10
Seq. ID
                  BLASTX
Method
                  q4262174
NCBI GI
BLAST score
                  469
E value
                  4.0e-47
Match length
                  129
% identity
                  63
NCBI Description (AC005508) 9058 [Arabidopsis thaliana]
                  294694
Seq. No.
                  LIB3069-030-Q1-K1-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g531829
                  185
BLAST score
                  8.0e-14
E value
                  79
Match length
% identity
                  51
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
                  294695
Seq. No.
Seq. ID
                  LIB3069-030-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  q3176689
BLAST score
                  169
                   5.0e-12
E value
                  96
Match length
% identity
                  (AC003671) Contains similarity to ubiquitin
NCBI Description
                   carboxyl-terminal hydrolase 14 gb Z35927 from S.
                   cerevisiae. [Arabidopsis thaliana]
Seq. No.
                   294696
                  LIB3069-031-Q1-K1-A8
Seq. ID
                  BLASTX
Method
                   q2462640
NCBI GI
```

BLAST score 153 E value 1.0e-12 Match length 71

56 % identity

(Y13370) reverse transcriptase [Oryza sativa] NCBI Description



```
294697
Seq. No.
                  LIB3069-031-Q1-K1-F8
Seq. ID
                  BLASTX
Method
                  g663070
NCBI GI
                  249
BLAST score
                  2.0e-21
E value
Match length
                  78
% identity
                  65
                  (X77806) histone H4 [Pyrenomonas salina]
NCBI Description
                  294698
Seq. No.
                  LIB3069-032-Q1-K1-B5
Seq. ID
Method
                  BLASTX
                  g4102600
NCBI GI
                  156
BLAST score
                  1.0e-10
E value
Match length
                  61
% identity
                  56
                  (AF013467) ARF6 [Arabidopsis thaliana]
NCBI Description
                  294699
Seq. No.
                  LIB3069-032-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2642159
BLAST score
                  556
                   3.0e-57
E value
Match length
                  124
% identity
                   85
                   (AC003000) putative mannose-1-phosphate guanyltransferase
NCBI Description
                   [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose
                   pyrophosphorylase [Arabidopsis thaliana] >gi_4151925
                   (AF108660) CYT1 protein [Arabidopsis thaliana]
Seq. No.
                   294700
                   LIB3069-032-Q1-K1-C11
Seq. ID
                   BLASTX
Method
                   g4585884
NCBI GI
BLAST score
                   150
                   1.0e-09
E value
                   94
Match length
                   35
% identity
                  (AC005850) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   294701
                   LIB3069-032-Q1-K1-C12
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1905943
BLAST score
                   48
E value
                   4.0e-18
                   104
Match length
                   87
% identity
                   Sorghum bicolor MADS box transcription factor SbMADS1 mRNA,
NCBI Description
```

Seq. No. 294702 Seq. ID LIB3069-

LIB3069-032-Q1-K1-C2

complete cds

```
Method
                  BLASTX
NCBI GI
                   q4033467
                   289
BLAST score
                   3.0e-26
E value
                   86
Match length
                   59
% identity
                  ARGININE/SERINE-RICH SPLICING FACTOR RSP31
NCBI Description
                   >gi_1707366_emb_CAA67798_ (X99435) splicing factor
                   [Arabidopsis thaliana]
                   294703
Seq. No.
                  LIB3069-032-Q1-K1-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4314359
BLAST score
                   469
E value
                   4.0e-47
                   142
Match length
                   58
% identity
NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]
                   294704
Seq. No.
                   LIB3069-032-Q1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3641836
BLAST score
                   220
                   7.0e-18
E value
                   123
Match length
% identity
                   41
                   (AL023094) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   294705
Seq. No.
                   LIB3069-032-Q1-K1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3024018
                   207
BLAST score
E value
                   4.0e-30
Match length
                   113
                   67
% identity
                   INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
NCBI Description
                   >gi 1546919 emb_CAA69225_ (Y07920) translation initiation
                   factor 5A [\overline{\text{Zea mays}}] >gi_2668738 (AF034943) translation
                   initiation factor 5A [Zea mays]
Seq. No.
                   294706
Seq. ID
                   LIB3069-032-Q1-K1-E8
Method
                   BLASTX
NCBI GI
                   g2909846
BLAST score
                   171
E value
                   2.0e-12
Match length
                   71
                   56
% identity
                  (AF045570) (S)-adenosyl-L-methionine:delta 24-sterol
```

294707 Seq. No.

NCBI Description

LIB3069-032-Q1-K1-F5 Seq. ID

41186

methyltransferase [Zea mays]

% identity



```
BLASTX
Method
NCBI GI
                  g122103
                  188
BLAST score
                  2.0e-14
E value
                  75
Match length
                  51
% identity
NCBI Description
                  HISTONE H4 >gi 70776 pir HSZP4 histone H4 - fission yeast
                  (Schizosaccharomyces pombe) >gi_4964 emb_CAA28853 (X05223)
                  histone H4.2 (AA 1-103) [Schizosaccharomyces pombe]
                  >gi 4967 emb CAA28855_ (X05224) histone H4.3 (AA 1 - 103)
                  [Schizosaccharomyces pombe] >gi 4969 emb CAA28850 (X05222)
                  Histone H4.1 [Schizosaccharomyces pombe]
                  >qi 2257549 dbj BAA21442 (AB004538) histone H4
                  [Schizosaccharomyces pombe] >gi_2950490_emb_CAA17818_
                  (AL022072) histone h4 [Schizosaccharomyces pombe]
                  >qi 224836 prf 1202262E histone H4.1 [Schizosaccharomyces
                  pombe]
Seq. No.
                  294708
Seq. ID
                  LIB3069-032-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  g4454477
                  153
BLAST score
E value
                  3.0e-10
Match length
                  80
% identity
                  41
NCBI Description (AC006234) hypothetical protein [Arabidopsis thaliana]
                  294709
Seq. No.
                  LIB3069-032-Q1-K1-G8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1944204
BLAST score
                  44
E value
                  1.0e-15
Match length
                  56
                  95
% identity
NCBI Description Oryza sativa mRNA for RicMT, complete cds
                  294710
Seq. No.
Seq. ID
                  LIB3069-032-Q1-K1-H9
                  BLASTX
Method
NCBI GI
                  g3386600
BLAST score
                  167
                  5.0e-12
E value
Match length
                  36
% identity
                  92
NCBI Description (AC004665) putative glycoprotein [Arabidopsis thaliana]
                  294711
Seq. No.
                  LIB3069-033-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3122638
BLAST score
                  549
E value
                  2.0e-56
Match length
                  135
```

NCBI Description PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1



>gi_1076381_pir__S49820 PRL1 protein - Arabidopsis thaliana
>gi_577733_emb_CAA58031_ (X82824) PRL1 [Arabidopsis
thaliana] >gi_577735_emb_CAA58032_ (X82825) PRL1

[Arabidopsis thaliana] >gi 2244947 emb CAB10369.1 (Z97339)

PRL1 protein - Arabidopsis thaliana

Seq. No. 294712

Seq. ID LIB3069-033-Q1-K1-B10

Method BLASTX
NCBI GI g3510262
BLAST score 241
E value 3.0e-20
Match length 53
% identity 92

NCBI Description (AC005310) NAM like protein [Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3069-033-Q1-K1-B8

294713

Method BLASTX
NCBI GI g464900
BLAST score 465
E value 1.0e-46
Match length 149
% identity 64

NCBI Description PUTATIVE KINASE-LIKE PROTEIN TMKL1 PRECURSOR

>gi_539008_pir__\$39476 kinase-like transmembrane protein

TMKL1 precursor - Arabidopsis thaliana

>gi 313190 emb CAA51385 (X72863) TMKL1 [Arabidopsis

thaliana]

Seq. No. 294714

Seq. ID LIB3069-033-Q1-K1-D9

Method BLASTX
NCBI GI g2773154
BLAST score 243
E value 1.0e-20
Match length 84
% identity 56

NCBI Description (AF039573) abscisic acid- and stress-inducible protein

[Oryza sativa]

Seq. No. 294715

Seq. ID LIB3069-033-Q1-K1-E5

Method BLASTX
NCBI GI g118104
BLAST score 715
E value 6.0e-76
Match length 136
% identity 98

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)

>gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -

 $maize > gi_168\overline{461}$ (M55021) cyclophilin [Zea mays]

>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 294716

Seq. ID LIB3069-033-Q1-K1-G3

Method

NCBI GI



```
BLASTX
Method
NCBI GI
                  g3309243
BLAST score
                  613
E value
                  6.0e-64
Match length
                  132
% identity
                  84
                  (AF073507) aconitase-iron regulated protein 1 [Citrus
NCBI Description
                  limon]
Seq. No.
                  294717
                  LIB3069-033-Q1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2735017
BLAST score
                  404
E value
                  7.0e-40
Match length
                  81
% identity
NCBI Description (U82481) KI domain interacting kinase 1 [Zea mays]
Seq. No.
                  294718
                  LIB3069-033-Q1-K1-G9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
E value
                  1.0e-10
Match length
                  48
% identity
                  67
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  294719
                  LIB3069-034-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g585203
BLAST score
                  220
E value
                  3.0e-18
Match length
                  74
                  62
% identity
                  GLUTAMINE SYNTHETASE ROOT ISOZYME 3 (GLUTAMATE--AMMONIA
NCBI Description
                  LIGASE) (GS112) >gi_481808 pir__S39479 glutamate--ammonia
                  ligase (EC 6.3.1.2) 1-3, cytosolic - maize
                  >gi_434328_emb_CAA46721_ (X65928) glutamine synthetase [Zea
                  mays]
                  294720
Seq. No.
Seq. ID
                  LIB3069-034-Q1-K1-C4
Method
                  BLASTN
NCBI GI
                  g609287
BLAST score
                  100
                  5.0e-49
E value
Match length
                  124
                  95
% identity
NCBI Description Z.diploperennis Grandel gene
                  294721
Seq. No.
Seq. ID
```

BLASTX g417745

LIB3069-034-Q1-K1-C8



```
BLAST score
                   2.0e-55
E value
                   111
Match length
                    95
 % identity
                   ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
 NCBI Description
                   HYDROLASE) (ADOHCYASE) >gi 170773 (L11872)
                   S-adenosyl-L-homocysteine \overline{h}ydrolase [Triticum aestivum]
                    294722
 Seq. No.
 Seq. ID
                   LIB3069-035-Q1-K1-A11
                   BLASTX
 Method
 NCBI GI
                    q2980891
                    168
 BLAST score
                    6.0e-12
 E value
                    44
 Match length
                    73
 % identity
 NCBI Description (D87064) histone H1 [Triticum aestivum]
                    294723
 Seq. No.
                    LIB3069-035-Q1-K1-A5
 Seq. ID
                    BLASTN
 Method
                    g444046
 NCBI GI
                    93
 BLAST score
                    7.0e-45
 E value
                    197
 Match length
% identity
                    87
 NCBI Description Z.mays OBF1 mRNA for ocs-element binding factor
                    294724
 Seq. No.
                    LIB3069-035-Q1-K1-B11
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    q531829
 BLAST score
                    147
                    1.0e-09
 E value
                    78
 Match length
                    42
 % identity
                    (U12390) beta-galactosidase alpha peptide [cloning vector
 NCBI Description
                    pSport1]
                    294725
 Seq. No.
                    LIB3069-035-Q1-K1-B2
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    q2739000
 BLAST score
                    323
                    4.0e-30
 E value
                    99
 Match length
  % identity
 NCBI Description (AF022459) CYP71D10p [Glycine max]
                    294726
 Seq. No.
                    LIB3069-035-Q1-K1-B6
  Śeq. ID
 Method
                    BLASTX
 NCBI GI
                    q4220480
                    151
 BLAST score
                    5.0e-10
 E value
                    98
 Match length
```

41190

40

% identity



```
(AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                  294727
Seq. No.
                  LIB3069-035-Q1-K1-C8
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3982617
BLAST score
                  80
E value
                  4.0e-37
Match length
                  92
                  97
% identity
                  Zea mays disease resistance gene analog PIC13 (pic13) gene,
NCBI Description
                  partial cds
                  294728
Seq. No.
                  LIB3069-035-Q1-K1-C9
Seq. ID
                  BLASTX
Method
                  g1172635
NCBI GI
                  175
BLAST score
E value
                  9.0e-13
                  46
Match length
                  83
% identity
                  26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING
NCBI Description
                  PROTEIN HOMOLOG 2) >gi 556558 dbj BAA04615_ (D17789) rice
                  homologue of Tat binding protein [Oryza sativa]
                  294729
Seq. No.
                  LIB3069-035-Q1-K1-E2
Seq. ID
Method
                  BLASTN
                  g22322
NCBI GI
BLAST score
                  218
                  1.0e-119
E value
                  286
Match length
                  94
% identity
NCBI Description Z.mays mRNA for H2B histone (clone cH2B214)
                  294730
Seq. No.
                  LIB3069-035-Q1-K1-E4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2511541
BLAST score
                  525
E value
                  1.0e-53
Match length
                  114
                  86
% identity
                  (AF020787) DNA-binding protein GBP16 [Oryza sativa]
NCBI Description
                  294731
Seq. No.
                  LIB3069-035-Q1-K1-F12
Seq. ID
                  BLASTN
Method
NCBI GI
                  g902057
BLAST score
                  42
                  2.0e-14
E value
Match length
                  54
```

Seq. No. 294732

% identity

NCBI Description

94

partial cds

Oryza sativa lipid transfer protein precursor, mRNA,



```
LIB3069-035-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2493852
BLAST score
                  237
                  7.0e-20
E value
                  46
Match length
                  93
% identity
                  CYTOCHROME C OXIDASE POLYPEPTIDE VC
NCBI Description
                  >gi 1070356 emb CAA92107 (Z68091) cytochrome c oxidase, Vc
                  subunit [Hordeum vulgare]
                  294733
Seq. No.
Seq. ID
                  LIB3069-035-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  g1522681
BLAST score
                  214
                  2.0e-17
E value
Match length
                  83
% identity
                  45
                   (U49240) symplekin [Homo sapiens] >gi_2143262_emb_CAA71861_
NCBI Description
                   (Y10931) symplekin [Homo sapiens]
                  294734
Seq. No.
Seq. ID
                  LIB3069-036-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  g3522937
BLAST score
                  177
                  8.0e-13
E value
Match length
                   66
% identity
                   50
                  (AC004411) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  294735
Seq. ID
                  LIB3069-036-Q1-K1-D10
                  BLASTN
Method
NCBI GI
                  g1045315
                   56
BLAST score
                   9.0e-23
E value
                  112
Match length
% identity
                   88
                  Arabidopsis thaliana biotin synthase (bioB) gene, complete
NCBI Description
                   cds
                   294736
Seq. No.
                  LIB3069-036-Q1-K1-E9
Seq. ID
Method
                  BLASTX
                   g2736147
NCBI GI
BLAST score
                   306
                   4.0e-28
E value
Match length
                   91
% identity
                   62
```

NCBI Description (AF021804) fatty acid hydroxylase Fahlp [Arabidopsis

thaliana] >gi 3132481 (AC003096) fatty acid hydroxylase,

FAH1 [Arabidopsis thaliana]

Seq. No. 294737

Seq. ID LIB3069-036-Q1-K1-F4

```
BLASTX
Method
                  g3176711
NCBI GI
BLAST score
                  207
                  2.0e-16
E value
Match length
                  131
% identity
                  40
NCBI Description (AC002392) bZIP-like protein [Arabidopsis thaliana]
                  294738
Seq. No.
Seq. ID
                  LIB3069-036-Q1-K1-G9
Method
                  BLASTX
                  g3912917
NCBI GI
                  228
BLAST score
                  5.0e-19
E value
                  102
Match length
                  45
% identity
NCBI Description (AF001308) putative NAK-like ser/thr protein kinase
                   [Arabidopsis thaliana]
                  294739
Seq. No.
                  LIB3069-037-Q1-K1-A12
Seq. ID
                  BLASTX
Method
                  q1899060
NCBI GI
                  408
BLAST score
                   7.0e-40
E value
                  96
Match length
% identity
NCBI Description (U79669) endosperm C-24 sterol methyltransferase [Zea mays]
                   294740
Seq. No.
                  LIB3069-037-Q1-K1-C4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3522939
BLAST score
                   142
E value
                   2.0e-09
Match length
                   35
                   71
% identity
                  (AC004411) putative squamosa-promoter binding protein
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 294741

Seq. ID LIB3069-037-Q1-K1-D8

Method BLASTX
NCBI GI g2984709
BLAST score 426
E value 2.0e-42
Match length 92
% identity 98

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 294742

Seq. ID LIB3069-037-Q1-K1-F11 Method BLASTN

NCBI GI g4454798 BLAST score 56 E value 1.0e-22 Match length 108



```
% identity
                  Zea mays translation initiation factor 4A2 (tif4A2) mRNA,
NCBI Description
                  partial cds
                  294743
Seq. No.
Seq. ID
                  LIB3069-037-Q1-K1-H1
Method
                  BLASTX
                  g2852684
NCBI GI
BLAST score
                  206
E value
                  3.0e-16
                  125
Match length
                  38
% identity
NCBI Description (AF017751) resistance protein candidate [Lactuca sativa]
                  294744
Seq. No.
Seq. ID
                  LIB3069-037-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  g1143864
BLAST score
                  147
E value
                  1.0e-09
                  86
Match length
                  42
% identity
NCBI Description (U28047) beta glucosidase [Oryza sativa]
                  294745
Seq. No.
Seq. ID
                  LIB3069-037-Q1-K1-H7
                  BLASTX
Method
NCBI GI
                  g4469025
BLAST score
                  155
                  1.0e-10
E value
Match length
                  50
                  52
% identity
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
                  294746
Seq. No.
Seq. ID
                  LIB3069-038-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  g2245057
BLAST score
                  207
                  3.0e-16
E value
                  139
Match length
% identity
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]
                  294747
Seq. No.
Seq. ID
                  LIB3069-038-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  g2522210
BLAST score
                  189
E value
                  3.0e-14
Match length
                  61
% identity
```

Seq. No. 294748

Seq. ID LIB3069-038-Q1-K1-G4

Method BLASTX

NCBI Description (AF023132) choline monooxygenase [Beta vulgaris]



```
g2129727
NCBI GI
                  143
BLAST score
                  2.0e-09
E value
                  47
Match length
                  62
% identity
                  RNA-binding protein 37 - Arabidopsis thaliana >gi_1174153
NCBI Description
                   (U44134) RNA-binding protein [Arabidopsis thaliana]
                  294749
Seq. No.
                  LIB3069-038-Q1-K1-G5
Seq. ID
                  BLASTN
Method
NCBI GI
                  q22292
BLAST score
                  42
                  1.0e-14
E value
                  165
Match length
                  82
% identity
NCBI Description Z.mays mRNA for glycine-rich protein
                  294750
Seq. No.
                  LIB3069-039-Q1-K1-B7
Seq. ID
                  BLASTN
Method
NCBI GI
                   g1256711
BLAST score
                  39
                   7.0e-13
E value
                   63
Match length
                   92
% identity
                  Zea mays O-methyltransferase (OMT) gene, complete cds
NCBI Description
Seq. No.
                   294751
Seq. ID
                   LIB3069-039-Q1-K1-C1
                   BLASTX
Method
NCBI GI
                   g3641252
BLAST score
                   256
E value
                   1.0e-26
                   131
Match length
                   48
% identity
                  (AF053127) leucine-rich receptor-like protein kinase [Malus
NCBI Description
                   domestica]
                   294752
Seq. No.
                   LIB3069-039-Q1-K1-E7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3789952
BLAST score
                   212
                   4.0e-17
E value
                   74
Match length
% identity
                   58
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                   sativa]
                   294753
Seq. No.
Seq. ID
                   LIB3069-039-Q1-K1-F12
Method
                   BLASTX
```

Method BLASTX
NCBI GI g3024552
BLAST score 412
E value 2.0e-40
Match length 81



% identity RAS-RELATED PROTEIN RGP2 (GTP-BINDING REGULATORY PROTEIN NCBI Description RGP2) >gi 419797_pir_ \$30273 GTP-binding protein rgp2 rice >gi 218204 dbj BAA02437 (D13152) GTP binding protein [Oryza sativa] >gi 446772 prf 1912297A rgp2 gene [Oryza sativa] 294754 Seq. No. Seq. ID LIB3069-039-Q1-K1-G5 Method BLASTN NCBI GI q3821780 BLAST score 36 E value 9.0e-11 Match length 36 % identity 100 NCBI Description Xenopus laevis cDNA clone 27A6-1 294755 Seq. No. LIB3069-040-Q1-K1-A12 Seq. ID Method BLASTX NCBI GI g2833378 BLAST score 221 E value 4.0e-18 Match length 110 44 % identity HEXOKINASE >gi_619928 (U18754) hexokinase [Arabidopsis NCBI Description thaliana] >qi 1582383 prf 2118367A hexokinase [Arabidopsis thaliana] 294756 Seq. No. LIB3069-040-Q1-K1-A3 Seq. ID Method BLASTX NCBI GI g4584528 BLAST score 281 E value 4.0e-25 116 Match length 57 % identity (AL049607) putative protein [Arabidopsis thaliana] NCBI Description 294757 Seq. No. LIB3069-040-Q1-K1-A5 Seq. ID BLASTX Method g282995 NCBI GI 243 BLAST score E value 1.0e-20 Match length 109 55 % identity seed protein B32E - barley (fragment) NCBI Description >gi_1345530_emb_CAA45538_ (X64254) B32E [Hordeum vulgare] 294758 Seq. No.

Seq. ID LIB3069-040-Q1-K1-D12

Method BLASTX
NCBI GI g4455338
BLAST score 313
E value 6.0e-29
Match length 83

BLAST score

Match length

% identity

E value

195

80

49

5.0e-15



```
% identity
                  (AL035525) putative protein [Arabidopsis thaliana]
NCBI Description
                  294759
Seq. No.
                  LIB3069-040-Q1-K1-E7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g951166
BLAST score
                  341
E value
                  2.0e-32
Match length
                  89
                  75
% identity
NCBI Description (U31451) invertase [Zea mays]
Seq. No.
                  294760
Seq. ID
                  LIB3069-040-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  g3157951
BLAST score
                  266
E value
                  3.0e-23
Match length
                  64
                  77
% identity
                  (AC002131) Contains similarity to vesicle trafficking
NCBI Description
                  protein gb_U91538 from Mus musculus. ESTs gb_F15494 and
                  gb F14097 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  294761
                  LIB3069-040-Q1-K1-G2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3821793
                  367
BLAST score
                  2.0e-35
E value
                  94
Match length
% identity
                  (Y11526) casein kinase II alpha subunit [Zea mays]
NCBI Description
                  294762
Seq. No.
Seq. ID
                  LIB3069-041-Q1-K1-B10
                  BLASTX
Method
NCBI GI
                  g118104
BLAST score
                  189
                  9.0e-15
E value
Match length
                  59
                  69
% identity
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi 168461 (M55021) cyclophilin [Zea mays]
                  >gi 829148 emb CAA48638 (X68678) cyclophilin [Zea mays]
                  294763
Seq. No.
                  LIB3069-041-Q1-K1-C11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2244902
```

ita.



```
NCBI Description (Z97339) allene oxide synthase [Arabidopsis thaliana]
Seq. No.
                  294764
Seq. ID
                  LIB3069-041-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  g3087737
BLAST score
                  258
E value
                  2.0e-35
Match length
                  136
% identity
                  55
NCBI Description (AJ001158) ABC1 protein [Arabidopsis thaliana]
Seq. No.
                  294765
Seq. ID
                  LIB3069-041-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  g1408473
BLAST score
                  208
E value
                  7.0e-17
Match length
                  55
% identity
                  76
                   (U48939) actin depolymerizing factor 2 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  294766
Seq. ID
                  LIB3069-041-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  q1167953
BLAST score
                  164
E value
                   2.0e-11
Match length
                  97
                   42
% identity
                   (U43496) putative 32.6 kDa jasmonate-induced protein
NCBI Description
                   [Hordeum vulgare] >gi_2465426 (AF021256) 32 kDa protein
                   [Hordeum vulgare]
                   294767
Seq. No.
Seq. ID
                  LIB3069-041-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                   g3643607
                  245
BLAST score
                   4.0e-21
E value
                  89
Match length
% identity
                   53
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
                   294768
Seq. No.
Seq. ID
                  LIB3069-041-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                   g595768
BLAST score
                  152
                   5.0e-10
E value
Match length
                   44
% identity
```

Seq. No. 294769

NCBI Description

Seq. ID LIB3069-042-Q1-K1-F12

41198

(U13866) non-functional lacZ alpha peptide [Cloning vector]



```
Method
                  BLASTX
NCBI GI
                  g3142303
BLAST score
                  468
E value
                  5.0e-47
Match length
                  106
% identity
NCBI Description
                  (AC002411) Strong similarity to MRP-like ABC transporter
                  gb U92650 from A. thaliana and canalicular multi-drug
                  resistance protein gb L49379 from Rattus norvegicus.
                  [Arabidopsis thaliana]
Seq. No.
                  294770
Seq. ID
                  LIB3069-042-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g3135274
BLAST score
                  451
E value
                  5.0e-45
Match length
                  125
% identity
                  67
                  (AC003058) putative beta-1,3-endoglucanase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  294771
Seq. ID
                  LIB3069-042-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  g3170601
BLAST score
                  495
E value
                  4.0e-50
                  117
Match length
% identity
                  81
NCBI Description (AF058757) zinc finger protein ID1 [Zea mays]
Seq. No.
                  294772
Seq. ID
                  LIB3069-042-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g1200205
BLAST score
                  148
E value
                  1.0e-09
Match length
                  77
% identity
                  40
NCBI Description (X95753) DAG [Antirrhinum majus]
Seq. No.
                  294773
                  LIB3069-042-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g663276
BLAST score
                  269
                  1.0e-23
E value
Match length
                  52
% identity
                  100
NCBI Description (X80375) maize gamma1 tubulin [Zea mays]
```

Seq. No.

294774

Seq. ID LIB3069-043-Q1-K1-A6

Method BLASTX
NCBI GI g3687240
BLAST score 164



```
3.0e-11
E value
Match length
                  61
                  51
% identity
                  (AC005169) extensin-like protein [Arabidopsis thaliana]
NCBI Description
                  294775
Seq. No.
Seq. ID
                  LIB3069-043-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g1431629
BLAST score
                  163
                  2.0e-11
E value
Match length
                  86
                  43
% identity
                  (X99348) pectinacetylesterase precursor [Vigna radiata]
NCBI Description
                  294776
Seq. No.
                  LIB3069-043-Q1-K1-G5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4586029
BLAST score
                   400
E value
                   5.0e-39
Match length
                  103
                  76
% identity
                  (AC007109) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  294777
Seq. No.
                  LIB3069-044-Q1-K1-A5
Seq. ID
                  BLASTN
Method
NCBI GI
                  g558364
BLAST score
                  33
                  5.0e-09
E value
Match length
                   45
                   93
% identity
NCBI Description Z.mays mRNA for ADP-glucose pyrophosphorylase
                  294778
Seq. No.
Seq. ID
                  LIB3069-044-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                   g4103342
BLAST score
                   439
E value
                   2.0e-43
Match length
                  108
% identity
                   79
NCBI Description
                  (AF022377) agamous-like putative transcription factor
                   [Cucumis sativus]
                   294779
Seq. No.
Seq. ID
                  LIB3069-044-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                   g1431870
BLAST score
                   319
                   2.0e-29
E value
                   144
Match length
% identity
```

.

294780

NCBI Description

Seq. No.

41200

(U43904) ent-kaurene synthase B [Cucurbita maxima]



```
LIB3069-044-Q1-K1-E6
Seq. ID
                  BLASTX
Method
                  g4538967
NCBI GI
                  345
BLAST score
                  2.0e-32
E value
Match length
                  116
% identity
NCBI Description (AL049488) major intrinsic protein (MIP)-like [Arabidopsis
                  thaliana]
                  294781
Seq. No.
Seq. ID
                  LIB3069-044-Q1-K1-F6
                  BLASTX
Method
NCBI GI
                  g4191789
BLAST score
                  183
                  2.0e-13
E value
Match length
                  41
% identity
NCBI Description (AC005917) putative transmembrane transport protein
                  [Arabidopsis thaliana]
                  294782
Seq. No.
Seq. ID
                  LIB3069-044-Q1-K1-H9
                  BLASTX
Method
                  g4204695
NCBI GI
BLAST score
                  462
                  3.0e-46
E value
                  123
Match length
% identity
                  71
NCBI Description (AF117062) putative inositol polyphosphate 5-phosphatase
                  At5P1 [Arabidopsis thaliana]
                  294783
Seq. No.
                  LIB3069-045-Q1-K1-A1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g123183
BLAST score
                  383
E value
                  5.0e-37
                  133
Match length
% identity
NCBI Description HOMEOTIC PROTEIN KNOTTED-1 >gi_100888_pir__S14283 homeotic
                  protein Kn-1 - maize >gi 22351 emb CAA43605 (X61308) Kn1
                   [Zea mays] >gi_227607_prf__1707304\overline{A} Knotted-1 gene [Zea
                  mays]
                  294784
Seq. No.
                  LIB3069-045-Q1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115815
BLAST score
                  360
E value
                  1.0e-34
Match length
                  80
% identity
                  85
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
```

41201

a/b-binding protein precursor - maize

(CAB-M9) (LHCP) >gi 100866 pir S13098 chlorophyll

>gi 22355 emb CAA39376 (X55892) light-harvesting



chlorophyll a/b binding protein [Zea mays]

```
Seq. No.
                  294785
                  LIB3069-045-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3047109
BLAST score
                  289
E value
                  6.0e-26
Match length
                  107
% identity
                  58
                  (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
                  294786
Seq. No.
Seq. ID
                  LIB3069-045-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  g1931642
BLAST score
                  143
E value
                  8.0e-09
Match length
                   68
% identity
                   50
                   (U95973) Ser/Thr protein kinase isolog [Arabidopsis
NCBI Description
                  thaliana]
                   294787
Seq. No.
Seq. ID
                  LIB3069-045-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                   q2500380
BLAST score
                   236
E value
                   6.0e-20
Match length
                   64
                   70
% identity
                   60S RIBOSOMAL PROTEIN L44 >gi 2119128 pir__JC4923 ribosomal
NCBI Description
                   protein RL44 - upland cotton >gi 1553129 (U64677) ribosomal
                   protein L44 isoform a [Gossypium hirsutum] >gi_1553131
                   (U64678) ribosomal protein L44 isoform b [Gossypium
                   hirsutum]
                   294788
Seq. No.
Seq. ID
                   LIB3069-045-Q1-K1-G8
                   BLASTX
Method
                   g3668086
NCBI GI
BLAST score
                   316
                   4.0e-29
E value
Match length
                   119
                   53
% identity
                  (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
                   294789
Seq. No.
Seq. ID
                   LIB3069-045-Q1-K1-H2
                   BLASTX
Method
                   g119958
NCBI GI
BLAST score
                   265
                   4.0e-23
E value
Match length
                   114
% identity
                   52
                   FERREDOXIN III PRECURSOR (FD III) >gi_168473 (M73831)
NCBI Description
                   ferredoxin [Zea mays] >gi_1864001_dbj_BAA19251_ (AB001387)
```





Fd III [Zea mays] >gi_444686_prf__1907324C ferredoxin:ISOTYPE=III [Zea mays]

 Seq. No.
 294790

 Seq. ID
 LIB3069-046-Q1-K1-F3

 Method
 BLASTX

 NCBI GI
 g4585993

 BLAST score
 156

 E value
 2.0e-10

Match length 35 % identity 89

NCBI Description (AC005287) Similar to serine/threonine kinases [Arabidopsis

thaliana]

Seq. No. 294791

Seq. ID LIB3069-046-Q1-K1-G12

Method BLASTX
NCBI GI g4337174
BLAST score 158
E value 1.0e-10
Match length 45
% identity 71

NCBI Description (AC006416) Similar to gi_1573829 HI0816 aminopeptidase P

homolog (pepP) from Haemophilus influenzae genome

gb U32764. [Arabidopsis thaliana]

Seq. No. 294792

Seq. ID LIB3069-047-Q1-K1-A5

Method BLASTX
NCBI GI g4585935
BLAST score 165
E value 1.0e-11
Match length 87
% identity 44

NCBI Description (AC007211) putative chlorophyll A/B binding protein

[Arabidopsis thaliana]

Seq. No. 294793

Seq. ID LIB3069-047-Q1-K1-C10

Method BLASTX
NCBI GI g1351033
BLAST score 232
E value 3.0e-19
Match length 112
% identity 46

NCBI Description STEM 31 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE

PROTEIN VSP25) >gi 170088 (M20037) vegetative storage

protein [Glycine max]

Seq. No. 294794

Seq. ID LIB3069-047-Q1-K1-D10

Method BLASTX
NCBI GI g1351033
BLAST score 240
E value 5.0e-23
Match length 98
% identity 61



NCBI Description STEM 31 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE PROTEIN VSP25) >gi_170088 (M20037) vegetative storage protein [Glycine max]

Seq. No. 294795 Seq. ID LIB3069-047-Q1-K1-D11

Method BLASTX
NCBI GI g4262147
BLAST score 155
E value 3.0e-10
Match length 69
% identity 46

NCBI Description (AC005275) putative homolog of transport inhibitor response

1 [Arabidopsis thaliana]

Seq. No. 294796

Seq. ID LIB3069-047-Q1-K1-D7

Method BLASTX
NCBI GI g3789952
BLAST score 211
E value 8.0e-17
Match length 117
% identity 46

NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza

sativa]

Seq. No. 294797

Seq. ID LIB3069-047-Q1-K1-E12

Method BLASTX
NCBI GI g2253442
BLAST score 226
E value 1.0e-18
Match length 62
% identity 56

NCBI Description (AF007784) LTCOR11 [Lavatera thuringiaca]

Seq. No. 294798

Seq. ID LIB3069-047-Q1-K1-E9

Method BLASTX
NCBI GI g498902
BLAST score 393
E value 4.0e-38
Match length 88
% identity 85

NCBI Description (U10044) ribosomal protein L27 homolog [Pisum sativum]

Seq. No. 294799

Seq. ID LIB3069-047-Q1-K1-F9

Method BLASTX
NCBI GI g1181673
BLAST score 558
E value 2.0e-57
Match length 114
% identity 94

NCBI Description (U41652) heat shock protein cognate 70 [Sorghum bicolor]

Seq. No. 294800



LIB3069-047-Q1-K1-G5 Seq. ID Method BLASTX NCBI GI g121080 346 BLAST score E value 1.0e-32 Match length 121 % identity 62 NCBI Description

GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR

>gi_1070638_pir_GCPMH glycine cleavage system protein H precursor - garden pea >gi 20737 emb CAA45978 (X64726) H protein [Pisum sativum] >gi 169093 (J05164) H-protein of glycine decarboxylase precursor (EC 2.1.2.10) [Pisum

sativum] >gi 287815 emb CAA37704 (X53656) H-protein [Pisum

sativum]

294801 Seq. No.

Seq. ID LIB3069-047-Q1-K1-H12

Method BLASTX NCBI GI g4584548 BLAST score 602 E value 1.0e-62 Match length 132 % identity 80

NCBI Description (AL049608) putative protein [Arabidopsis thaliana]

294802 Seq. No.

Seq. ID LIB3069-047-Q1-K1-H4

Method BLASTX NCBI GI g1495251 BLAST score 319 E value 2.0e-29 Match length 139 % identity 52

NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No. 294803

Seq. ID LIB3069-048-Q1-K1-A1

Method BLASTX NCBI GI g729671 BLAST score 331 8.0e-31 E value Match length 88 % identity

NCBI Description HISTONE H2A >gi 473603 (U08225) histone H2A [Zea mays]

294804 Seq. No.

Seq. ID LIB3069-048-Q1-K1-A3

Method BLASTN NCBI GI g2431768 BLAST score 99 E value 2.0e-48 Match length 225 % identity 87

NCBI Description Zea mays acidic ribosomal protein Pla (rppla) mRNA,

complete cds

294805 Seq. No.



```
Seq. ID
                  LIB3069-048-Q1-K1-F10
                  BLASTX
Method
NCBI GI
                  g2980779
BLAST score
                  199
                  8.0e-16
E value
Match length
                  53
% identity
                  75
NCBI Description (AL022198) putative protein [Arabidopsis thaliana]
                  294806
Seq. No.
Seq. ID
                  LIB3069-048-Q1-K1-F12
                  BLASTN
Method
NCBI GI
                  q444046
BLAST score
                  133
E value
                  9.0e-69
Match length
                  221
                  90
% identity
NCBI Description Z.mays OBF1 mRNA for ocs-element binding factor
Seq. No.
                  294807
Seq. ID
                  LIB3069-048-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  g4587681
BLAST score
                  214
                  9.0e-18
E value
                  62
Match length
% identity
                  63
NCBI Description (AC007197) hypothetical protein [Arabidopsis thaliana]
                  294808
Seq. No.
Seq. ID
                  LIB3069-049-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  g1916290
BLAST score
                  230
E value
                  5.0e-19
Match length
                  90
% identity
                  53
NCBI Description (U89876) ALY [Mus musculus]
                  294809
Seq. No.
Seq. ID
                  LIB3069-049-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g3913804
BLAST score
                  309
E value
                  2.0e-28
Match length
                  98
                  67
% identity
NCBI Description HISTONE H2B.3 >gi 577825 emb CAA49584 (X69960) H2B histone
                  [Zea mays]
Seq. No.
                  294810
Seq. ID
                  LIB3069-050-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  g2984709
BLAST score
```

41206

257

52

2.0e-22

E value

Match length



% identity NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays] 294811 Seq. No. Seq. ID LIB3069-050-Q1-K1-B10 BLASTX Method NCBI GI g585202 BLAST score 193 5.0e-15 E value Match length 62 65 % identity NCBI Description GLUTAMINE SYNTHETASE ROOT ISOZYME 2 (GLUTAMATE--AMMONIA LIGASE) >gi 481807 pir S39478 glutamate--ammonia ligase (EC 6.3.1.2) 1-2, cytosolic - maize >gi_434326_emb_CAA46720_ (X65927) glutamine synthetase [Zea mays] Seq. No. 294812 Seq. ID LIB3069-050-Q1-K1-B2 Method BLASTX NCBI GI g1362108 BLAST score 418 E value 4.0e-41 Match length 129 93 % identity NCBI Description histone H3 homolog - common tobacco 294813 Seq. No. Seq. ID LIB3069-050-Q1-K1-C5 BLASTX Method NCBI GI g4150965 BLAST score 183 8.0e-14 E value Match length 69 % identity NCBI Description (AJ011096) glutamate dehydrogenase [Asparagus officinalis] Seq. No. 294814 Seq. ID LIB3069-050-Q1-K1-E3 Method BLASTX NCBI GI g729882 BLAST score 311 E value 1.0e-28 Match length 95 % identity 66 NCBI Description CASEIN KINASE II BETA' CHAIN (CK II) >gi_1076300_pir__S47968 casein kinase II (EC 2.7.1.-) beta chain CKB2 - Arabidopsis thaliana >gi 467975 (U03984) casein kinase II beta subunit CKB2 [Arabidopsis thaliana]

>gi 2245122 emb CAB10544 (Z97343) unnamed protein product

[Arabidopsis thaliana]

Seq. No. 294815

Seq. ID LIB3069-051-Q1-K1-C1

Method BLASTX NCBI GI g1362162 BLAST score 321

NCBI GI

E value

BLAST score

Match length

g116333

215 3.0e-37

95



ate.

```
1.0e-29
E value
                   137
Match length
% identity
                   46
                   beta-glucosidase BGQ60 precursor - barley >gi_804656
NCBI Description
                   (L41869) beta-glucosidase [Hordeum vulgare]
Seq. No.
                   294816
Seq. ID
                   LIB3069-051-Q1-K1-C11
Method
                   BLASTX
NCBI GI
                   g3915826
BLAST score
                   231
                   3.0e-19
E value
Match length
                   75
                   65
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L5
                   294817
Seq. No.
                   LIB3069-051-Q1-K1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3913789
BLAST score
                   351
E value
                   3.0e-33
Match length
                   83
% identity
                   NONLEGUME HEMOGLOBIN >gi_1076720_pir__S46502 hemoglobin -
NCBI Description
                   barley >gi_508204 (U01228) haemoglobin apoprotein [Hordeum
                   vulgare] >gi 2071976 (U94968) hemoglobin [Hordeum vulgare]
Seq. No.
                   294818
                   LIB3069-051-Q1-K1-D8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4467152
                   154
BLAST score
                   1.0e-10
E value
Match length
                   68
% identity
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
                   294819
Seq. No.
                   LIB3069-051-Q1-K1-D9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1203832
                   595
BLAST score
                   9.0e-62
E value
Match length
                   140
 % identity
                   (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
NCBI Description
                   [Hordeum vulgare] >gi_1588407_prf_ 2208395A beta-D-glucan
                   exohydrolase [Hordeum vulgare]
                   294820
Seq. No.
                   LIB3069-051-Q1-K1-F9
 Seq. ID
                   BLASTX
Method
```



NCBI GI g3893860
BLAST score 449
E value 1.0e-44
Match length 132
% identity 68

NCBI Description (AF058708) RNA polymerase sigma factor 1 [Zea mays]

Seq. No. 294822

Seq. ID LIB3069-051-Q1-K1-G6

Method BLASTX
NCBI GI g2326947
BLAST score 177
E value 6.0e-13
Match length 100
% identity 44

NCBI Description (Z50801) Chlorophyll a/b-binding protein CP29 precursor

[Zea mays]

Seq. No. 294823

Seq. ID LIB3069-052-Q1-K1-A7

Method BLASTX
NCBI GI g3176874
BLAST score 219
E value 5.0e-22
Match length 104
% identity 60

NCBI Description (AF065639) cucumisin-like serine protease [Arabidopsis

thaliana]

Seq. No.

294824

Seq. ID LIB3069-052-Q1-K1-D7

Method BLASTN
NCBI GI g296593
BLAST score 60
E value 5.0e-25
Match length 76
% identity 95

NCBI Description H. vulgare pZE40 gene

Seq. No. 294825

Seq. ID LIB3069-052-Q1-K1-F1

Method BLASTX
NCBI GI g3860277
BLAST score 214
E value 3.0e-17
Match length 97
% identity 53

NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis

thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative

ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.

Seq. ID

294831

LIB3069-053-Q1-K1-F11

```
294826
Seq. No.
Seq. ID
                  LIB3069-052-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  g2129473
BLAST score
                  163
                  3.0e-11
E value
                  120
Match length
                  35
% identity
                  arabinogalactan-like protein - loblolly pine >gi 607774
NCBI Description
                   (U09556) arabinogalactan-like protein [Pinus taeda]
                  294827
Seq. No.
Seq. ID
                  LIB3069-053-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  g4538911
BLAST score
                  396
E value
                  1.0e-38
                  98
Match length
% identity
                  77
                  (AL049482) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  294828
Seq. ID
                  LIB3069-053-Q1-K1-B5
                  BLASTX
Method
NCBI GI
                  g4512616
BLAST score
                  518
E value
                   6.0e-53
                  117
Match length
% identity
                  77
                  (AC004793) Contains similarity to gi_1653332 extragenic
NCBI Description
                  suppressor (SuhB) from Synechocystis sp. gb D90912 and is a
                  member of the Inositol monophophatase family PF 00459. EST
                  gb AA597395 comes from this gene. [Arabidopsis tha
Seq. No.
                  294829
Seq. ID
                  LIB3069-053-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g431162
BLAST score
                  276
E value
                   2.0e-24
Match length
                  125
% identity
                   48
NCBI Description
                  (D21822) ORF [Lilium longiflorum]
Seq. No.
                  294830
                  LIB3069-053-Q1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4204265
BLAST score
                  197
E value
                  2.0e-15
Match length
                  59
% identity
                  58
NCBI Description
                  (AC005223) 45643 [Arabidopsis thaliana]
```



```
Method
                  BLASTX
NCBI GI
                  g1173187
BLAST score
                  392
E value
                  4.0e-38
Match length
                  80
% identity
                  91
                  40S RIBOSOMAL PROTEIN S23 (S12) >gi 1362041 pir __S56673
NCBI Description
                  ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                  strawberry >qi 643074 (U19940) putative 40S ribosomal
                  protein s12 [Fragaria x ananassa]
                  294832
Seq. No.
                  LIB3069-053-Q1-K1-H4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2668737
BLAST score
                  34
E value
                  1.0e-09
Match length
                  46
% identity
                  Zea mays translation initiation factor 5A (TIF5A) mRNA,
NCBI Description
                  complete cds
                  294833
Seq. No.
Seq. ID
                  LIB3069-054-Q1-K1-A1
                  BLASTX
Method
NCBI GI
                  g4204265
BLAST score
                  334
E value
                  3.0e-31
Match length
                  123
% identity
                  49
NCBI Description (AC005223) 45643 [Arabidopsis thaliana]
Seq. No.
                  294834
                  LIB3069-054-Q1-K1-B12
Seq. ID
Method
                  BLASTX
                  g4432857
NCBI GI
BLAST score
                  156
                  6.0e-11
E value
                  56
Match length
% identity
                  54
                  (AC006300) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  294835
Seq. No.
                  LIB3069-054-Q1-K1-B9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4262174
BLAST score
                  504
                  3.0e-51
E value
Match length
                  110
                  78
% identity
NCBI Description (AC005508) 9058 [Arabidopsis thaliana]
                  294836
Seq. No.
```

Seq. ID LIB3069-054-Q1-K1-C3

Method BLASTN
NCBI GI g3420038
BLAST score 61



```
E value
                  1.0e-25
Match length
                  119
                  47
% identity
                  Zea mays gypsy/Ty3-type retrotransposon Tekay, complete
NCBI Description
                  sequence
Seq. No.
                  294837
Seq. ID
                  LIB3069-054-Q1-K1-D8
                  BLASTX
Method
                  q3193293
NCBI GI
BLAST score
                  165
                  2.0e-11
E value
Match length
                  71
% identity
                  (AF069298) contains a short region of similarity to another
NCBI Description
                  Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)
                  [Arabidopsis thaliana]
                  294838
Seq. No.
                  LIB3069-054-Q1-K1-F10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3786001
BLAST score
                  167
                  1.0e-11
E value
                  38
Match length
                  79
% identity
NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]
                   294839
Seq. No.
Seq. ID
                  LIB3069-054-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                   g3892056
BLAST score
                   193
E value
                   9.0e-15
                   60
Match length
% identity
                  (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]
NCBI Description
                   294840
Seq. No.
                   LIB3069-054-Q1-K1-G7
Seq. ID
Method
                   BLASTX
                   q3892056
NCBI GI
BLAST score
                   194
E value
                   7.0e-15
Match length
                   84
                   50
% identity
NCBI Description (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]
Seq. No.
                   294841
                   LIB3069-054-Q1-K1-H4
Seq. ID
Méthod
                   BLASTX
```

Method BLASTX
NCBI GI g3337366
BLAST score 161
E value 5.0e-11
Match length 101
% identity 43

NCBI Description (AC004481) unknown protein [Arabidopsis thaliana]



Seq. No. 294842

Seq. ID LIB3069-055-Q1-K1-A1

Method BLASTN
NCBI GI g6598490
BLAST score 45
E value 3.0e-16
Match length 61
% identity 93

NCBI Description Arabidopsis thaliana chromosome II BAC F15K20 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 294843

Seq. ID LIB3069-055-Q1-K1-C9

Method BLASTX
NCBI GI g112994
BLAST score 186
E value 2.0e-14
Match length 51
% identity 76

NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN

>gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)

ABA-inducible gene protein [Zea mays]

>gi 226091 prf 1410284A abscisic acid inducible gene [Zea

mays]

Seq. No. 294844

Seq. ID LIB3069-055-Q1-K1-D11

Method BLASTX
NCBI GI g3913425
BLAST score 311
E value 1.0e-28
Match length 125
% identity 47

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE >gi 2275203 (AC002337) RNA helicase isolog

[Arabidopsis thaliana]

Seq. No. 294845

Seq. ID LIB3069-055-Q1-K1-F10

Method BLASTX
NCBI GI g2497748
BLAST score 166
E value 1.0e-11
Match length 54
% identity 56

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 4 PRECURSOR (LTP 4)

>gi_902058 (U29176) lipid transfer protein precursor [Oryza

satīva]

Seq. No. 294846

Seq. ID LIB3069-055-Q1-K1-F9

Method BLASTX
NCBI GI g2462753
BLAST score 181
E value 2.0e-13



```
Match length
                  54
                  67
% identity
                  (AC002292) putative polygalacturonase [Arabidopsis
NCBI Description
                  thaliana]
                  294847
Seq. No.
                  LIB3069-055-Q1-K1-G10
Seq. ID
                  BLASTX
Method
                  g4115925
NCBI GI
BLAST score
                  152
                  6.0e-10
E value
                  38
Match length
                  76
% identity
                  (AF118222) contains similarity to RNA recognition motifs
NCBI Description
                  (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
                  >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein
                  [Arabidopsis thaliana]
                  294848
Seq. No.
Seq. ID
                  LIB3069-055-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  g3461813
                  258
BLAST score
E value
                  2.0e-22
Match length
                  121
                  50
% identity
                  (AC004138) putative sucrose/H+ symporter [Arabidopsis
NCBI Description
                  thaliana]
                  294849
Seq. No.
                  LIB3069-056-Q1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3452091
                  313
BLAST score
                  8.0e-29
E value
Match length
                  84
% identity
NCBI Description (AJ004899) rudimentary enhancer [Glycine max]
                  294850
Seq. No.
                  LIB3069-056-Q1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2497857
BLAST score
                  155
                   2.0e-10
E value
                   49
Match length
                   67
% identity
                  MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi 2117463_pir__S57958 malate dehydrogenase (EC 1.1.1.37)
                   - rape >gi_899226_emb_CAA61621_ (X89451) malate
                   dehydrogenase [Brassica napus]
```

Seq. No. 294851

Seq. ID LIB3069-056-Q1-K1-D3

Method BLASTX NCBI GI g3776084 BLAST score 149

```
Indicated and
```

1

```
1.0e-09
E value
Match length
                  57
                  49
% identity
NCBI Description
                  (Y18251) NtN2 [Medicago truncatula]
Seq. No.
                  294852
                  LIB3069-056-Q1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1280135
BLAST score
                  153
E value
                  5.0e-10
                  125
Match length
% identity
                  31
                  (U55376) coded for by C. elegans cDNA cm21e6; coded for by
NCBI Description
                  C. elegans cDNA cm01e2; similar to melibiose carrier
                  protein (thiomethylgalactoside permease II) [Caenorhabditis
                  elegans]
                   294853
Seq. No.
Seq. ID
                  LIB3069-056-Q1-K1-F4
                  BLASTX
Method
NCBI GI
                   q2920587
                  177
BLAST score
E value
                   6.0e-13
                   65
Match length
                   49
% identity
                   (AF038362) TBP-associated factor 172 [Homo sapiens]
NCBI Description
                   >gi 2995136_emb_CAA04475_ (AJ001017) TAFII170 [Homo
                   sapiens]
                   294854
Seq. No.
                  LIB3069-056-Q1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3176671
BLAST score
                   202
                   5.0e-16
E value
Match length
                   62
% identity
                   (AC004393) Contains similarity to hypothetical gene B0495.7
NCBI Description
                   gb 687822 from C. elegans cosmid gb U21317. [Arabidopsis
                   thaliana]
Seq. No.
                   294855
Seq. ID
                   LIB3069-056-Q1-K1-H4
Method
                   BLASTX
NCBI GI
                   q3152595
BLAST score
                   224
E value
                   1.0e-18
Match length
                   101
% identity
                   (AC002986) Similar to D. melanogaster sno gene gb_U95760.
NCBI Description
                   EST gb N97148 and gb Z26221 come from this gene.
                   [Arabidopsis thaliana]
```

**

Seq. No. 294856

Seq. ID LIB3069-057-Q1-K1-B4

Method BLASTX

34.



```
g3747048
NCBI GI
                  234
BLAST score
                  7.0e-20
E value
                  86
Match length
                  56
% identity
NCBI Description (AF093539) methionine synthase [Zea mays]
                  294857
Seq. No.
                  LIB3069-057-Q1-K1-E3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3421077
BLAST score
                  151
                  3.0e-10
E value
                  59
Match length
                  54
% identity
NCBI Description (AF043521) 20S proteasome subunit PAC1 [Arabidopsis
                  thaliana]
                  294858
Seq. No.
Seq. ID
                  LIB3069-057-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  g3182915
BLAST score
                  249
E value
                  3.0e-21
                  86
Match length
                  52
% identity
NCBI Description ADP-RIBOSYLATION FACTOR >gi 1842150_dbj_BAA19225
                  (AB001051) ADP-ribosylation factor [Dugesia japonica]
                  294859
Seq. No.
Seq. ID
                  LIB3070-001-Q1-N1-A9
Method
                  BLASTX
                  g1657855
NCBI GI
BLAST score
                  396
                  1.0e-38
E value
                  102
Match length
                  72
% identity
NCBI Description (U73216) cold acclimation protein WCOR413 [Triticum
                  aestivum]
                  294860
Seq. No.
Seq. ID
                  LIB3070-001-Q1-N1-C10
Method
                  BLASTN
NCBI GI
                  g56539
BLAST score
                  56
                  5.0e-23
E value
Match length
                  84
% identity
NCBI Description R.norvegicus gene encoding prolactin, exon 5
                  >gi 206360 gb J00764 RATPRLHR5 Rat (hooded) prolactin gene
                  : exon v and flanks
                  294861
Seq. No.
Seq. ID
                  LIB3070-001-Q1-N1-C5
```

Method BLASTN NCBI GI g56539 BLAST score 103



```
E value
                  1.0e-50
Match length
                  281
% identity
                  97
                  R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                  >qi 206360 gb J00764 RATPRLHR5 Rat (hooded) prolactin gene
                  : exon v and flanks
Seq. No.
                  294862
                  LIB3070-001-Q1-N1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g206371
BLAST score
                  43
E value
                  5.0e-15
Match length
                  165
                  88
% identity
                  Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks
NCBI Description
Seq. No.
                  294863
Seq. ID
                  LIB3070-001-Q1-N1-D6
Method
                  BLASTN
NCBI GI
                  g206371
BLAST score
                  65
E value
                  2.0e-28
Match length
                  101
                  91
% identity
NCBI Description Rat(Sprague-Dawley) prolactin gene:exons IV, V and flanks
                  294864
Seq. No.
Seq. ID
                  LIB3070-001-Q1-N1-D9
Method
                  BLASTX
NCBI GI
                  q1806283
BLAST score
                  200
E value
                  1.0e-15
Match length
                  61
% identity
                  (Z79637) Histone H4 homologue [Sesbania rostrata]
NCBI Description
                  294865
Seq. No.
                  LIB3070-001-Q1-N1-E8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g206371
BLAST score
                  64
                  1.0e-27
E value
Match length
                  187
% identity
                  92
                  Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks
NCBI Description
```

294866 Seq. No.

LIB3070-001-Q1-N1-F11 Seq. ID

Method BLASTN NCBI GI g206371 BLAST score 48 E value 5.0e-18 Match length 191 % identity 88

NCBI Description Rat(Spraque-Dawley) prolactin gene: exons IV, V and flanks



294867 Seq. No.

Seq. ID LIB3070-001-Q1-N1-H11

Method BLASTX NCBI GI g1351359 BLAST score 164 E value 2.0e-11 Match length 47 % identity

NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN

(MITOCHONDRIAL HINGE PROTEIN) (CR7) >gi_1071788_pir__\$48690 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) 11K protein

- potato >gi_488712_emb_CAA55860_ (X79273) ubiquinol--cytochrome c reductase [Solanum tuberosum]

Seq. No. 294868

Seq. ID LIB3070-002-Q1-N1-A12

Method BLASTN NCBI GI g206371 BLAST score 99 2.0e-48 E value Match length 298 98 % identity

NCBI Description Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks

Seq. No. 294869

Seq. ID LIB3070-002-Q1-N1-A8

Method BLASTN NCBI GI g565391 BLAST score 52 E value 1.0e-20 Match length 96 % identity 89

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>gi 206360_gb J00764 RATPRLHR5 Rat (hooded) prolactin gene

: exon v and \overline{f} lanks

Seq. No. 294870

Seq. ID LIB3070-002-Q1-N1-E6

Method BLASTX NCBI GI g2213594 BLAST score 210 E value 9.0e-17 Match length 55 % identity

NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No. 294871

Seq. ID LIB3070-002-Q1-N1-E7

Method BLASTN NCBI GI g206371 BLAST score 67 E value 2.0e-29 Match length 187 % identity 90

NCBI Description Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks

Seq. No. 294872



```
LIB3070-002-Q1-N1-F3
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4160401
BLAST score
                   44
E value
                   1.0e-15
Match length
                   68
% identity
                   91
NCBI Description
                  Zea mays eIF-5 gene, exons 1-2
                  294873
Seq. No.
Seq. ID
                  LIB3070-002-Q1-N1-H1
                  BLASTX
Method
NCBI GI
                  g3482918
BLAST score
                  172
E value
                  1.0e-12
Match length
                  77
% identity
                   63
NCBI Description
                  (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
                  thaliana]
                  294874
Seq. No.
Seq. ID
                  LIB3070-002-Q1-N1-H10
Method
                  BLASTX
NCBI GI
                  q4090257
BLAST score
                  255
E value
                   4.0e-22
Match length
                  90
% identity
                   64
NCBI Description (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
                   294875
Seq. No.
Seq. ID
                  LIB3070-002-Q1-N1-H12
Method
                  BLASTN
NCBI GI
                   g206371
BLAST score
                   99
E value
                   2.0e-48
Match length
                  284
% identity
                   96
NCBI Description Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks
Seq. No.
                   294876
Seq. ID
                  LIB3070-003-Q1-N1-B10
Method
                  BLASTN
NCBI GI
                   g206371
BLAST score
                  78
                   9.0e-36
E value
                  288
Match length
% identity
                  89
NCBI Description Rat(Sprague-Dawley) prolactin gene:exons IV, V and flanks
Seq. No.
                  294877
                  LIB3070-003-Q1-N1-D10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g56539
BLAST score
                  38
```

5.0e-12

110

E value Match length



% identity 84 NCBI Description R.

R.norvegicus gene encoding prolactin, exon 5

>gi 206360 gb J00764 RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 294878

Seq. ID LIB3070-003-Q1-N1-E11

Method BLASTN
NCBI GI g206371
BLAST score 34
E value 1.0e-09
Match length 70
% identity 87

NCBI Description Rat(Sprague-Dawley) prolactin gene:exons IV, V and flanks

Seq. No. 294879

Seq. ID LIB3070-003-Q1-N1-E8

Method BLASTX
NCBI GI g3461828
BLAST score 154
E value 3.0e-10
Match length 63
% identity 46

NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]

Seq. No. 294880

Seq. ID LIB3070-004-Q1-N1-B1

Method BLASTN
NCBI GI g56539
BLAST score 95
E value 6.0e-46
Match length 294
% identity 96

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>qi 206360 qb J00764 RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 294881

Seq. ID LIB3070-004-Q1-N1-B3

Method BLASTX
NCBI GI g399854
BLAST score 206
E value 3.0e-16
Match length 66
% identity 68

NCBI Description HISTONE H2B.2 >gi 283042 pir S28049 histone H2B - maize

>gi_22325_emb_CAA40565_ (X57313) H2B histone [Zea mays]

Seq. No. 294882

Seq. ID LIB3070-004-Q1-N1-D1

Method BLASTN
NCBI GI g206371
BLAST score 99
E value 2.0e-48
Match length 295
% identity 99

NCBI Description Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks

Method

NCBI GI

BLAST score

BLASTN

g12434

41



```
Seq. No.
                  294883
Seq. ID
                  LIB3070-004-Q1-N1-E3
Method
                  BLASTX
NCBI GI
                  q399854
BLAST score
                  215
                  2.0e-17
E value
                  74
Match length
                  70
% identity
                  HISTONE H2B.2 >gi 283042 pir S28049 histone H2B - maize
NCBI Description
                  >gi 22325 emb CAA40565 (X57313) H2B histone [Zea mays]
                  294884
Seq. No.
Seq. ID
                  LIB3070-004-Q1-N1-E9
Method
                  BLASTN
NCBI GI
                  g206371
BLAST score
                  46
E value
                   1.0e-16
                  173
Match length
                  88
% identity
NCBI Description Rat(Sprague-Dawley) prolactin gene:exons IV, V and flanks
                   294885
Seq. No.
Seq. ID
                  LIB3070-004-Q1-N1-F11
Method
                  BLASTN
NCBI GI
                   q206371
BLAST score
                   103
E value
                   1.0e-50
Match length
                   308
% identity
                   97
NCBI Description Rat(Sprague-Dawley) prolactin gene:exons IV, V and flanks
Seq. No.
                   294886
                   LIB3070-004-Q1-N1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g729671
BLAST score
                   187
E value
                   5.0e-14
Match length
                   90
% identity
                   50
NCBI Description HISTONE H2A >gi 473603 (U08225) histone H2A [Zea mays]
Seq. No.
                   294887
                   LIB3070-004-Q1-N1-G6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g206371
BLAST score
                   44
E value
                   1.0e-15
                   104
Match length
% identity
                   87
NCBI Description Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks
Seq. No.
                   294888
                   LIB3070-004-Q1-N1-H10
Seq. ID
```



1.0e-13 E value 125 Match length % identity 83 NCBI Description Maize chloroplast psbB-psbF-petB-petD gene cluster 294889 Seq. No. LIB3070-005-Q1-N1-B1 Seq. ID BLASTX Method g2493852 NCBI GI 227 BLAST score 8.0e-19 E value 57 Match length 75 % identity CYTOCHROME C OXIDASE POLYPEPTIDE VC NCBI Description >gi_1070356_emb_CAA92107 (Z68091) cytochrome c oxidase, Vc subunit [Hordeum vulgare] 294890 Seq. No. LIB3070-005-Q1-N1-B3 Seq. ID BLASTX Method g729671 NCBI GI 190 BLAST score 3.0e-15 E value 106 Match length 51 % identity NCBI Description HISTONE H2A >gi 473603 (U08225) histone H2A [Zea mays] 294891 Seq. No. LIB3070-005-Q1-N1-C4 Seq. ID BLASTN Method NCBI GI g56539 71 BLAST score 1.0e-31 E value Match length 204 90 % identity R.norvegicus gene encoding prolactin, exon 5 NCBI Description >qi 206360 gb J00764_RATPRLHR5 Rat (hooded) prolactin gene : exon v and flanks 294892 Seq. No. LIB3070-005-Q1-N1-C6 Seq. ID Method BLASTN NCBI GI g206371 BLAST score 83 9.0e-39 E value 309 Match length 91 % identity NCBI Description Rat(Sprague-Dawley) prolactin gene:exons IV, V and flanks

Seq. No. 294893

Seq. ID LIB3070-005-Q1-N1-C9

97

Method BLASTN
NCBI GI g206371
BLAST score 91
E value 1.0e-43
Match length 206

% identity



```
NCBI Description Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks
                  294894
Seq. No.
                  LIB3070-005-Q1-N1-D4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g206371
                  87
BLAST score
                   3.0e-41
E value
                   306
Match length
                   92
% identity
NCBI Description Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks
                   294895
Seq. No.
                   LIB3070-005-Q1-N1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g399854
BLAST score
                   265
                   3.0e-23
E value
                   106
Match length
                   58
% identity
NCBI Description HISTONE H2B.2 >gi 283042 pir_S28049 histone H2B - maize
                   >gi 22325_emb_CAA40565_ (X57313) H2B histone [Zea mays]
                   294896
Seq. No.
                   LIB3070-005-Q1-N1-H12
Seq. ID
                   BLASTN
Method
NCBI GI
                   g717080
BLAST score
                   62
                   3.0e-26
E value
                   185
Match length
% identity
                   84
                   Zea mays glyceraldehyde-3-phosphate dehydrogenase (GapC4)
NCBI Description
                   gene, promoter region
                   294897
Seq. No.
Seq. ID
                   LIB3070-006-Q1-N1-B9
                   BLASTX
Method
NCBI GI
                   q2344886
BLAST score
                   448
                   1.0e-44
E value
Match length
                   137
% identity
                   60
                   (AC002388) hypothetical protein, 5' partial [Arabidopsis
NCBI Description
                   thaliana]
                   294898
Seq. No.
                   LIB3070-006-Q1-N1-C6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g206371
BLAST score
                   87
                   3.0e-41
E value
                   142
Match length
% identity
                   96
                   Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks
NCBI Description
```

294899

LIB3070-006-Q1-N1-D11

Seq. No.

Seq. ID

E value

Match length

3.0e-71

149



```
Method
                  BLASTX
                  g4406764
NCBI GI
BLAST score
                  158
                  9.0e-11
E value
                  74
Match length
                  50
% identity
NCBI Description (AC006836) putative uridylyl transferase [Arabidopsis
                  thaliana]
                  294900
Seq. No.
Seq. ID
                  LIB3070-006-Q1-N1-F3
                  BLASTN
Method
NCBI GI
                  g206371
                  39
BLAST score
                  1.0e-12
E value
                  103
Match length
                  84
% identity
NCBI Description Rat(Sprague-Dawley) prolactin gene:exons IV, V and flanks
Seq. No.
                  294901
                  LIB3070-006-Q1-N1-F4
Seq. ID
                  BLASTN
Method
NCBI GI
                  g206371
BLAST score
                  47
                  2.0e-17
E value
Match length
                  103
                  86
% identity
NCBI Description Rat(Sprague-Dawley) prolactin gene:exons IV,V and flanks
                  294902
Seq. No.
Seq. ID
                  LIB3070-006-Q1-N1-H10
Method
                  BLASTN
NCBI GI
                   q206371
                   73
BLAST score
                   7.0e-33
E value
Match length
                  188
                   93
% identity
NCBI Description Rat(Sprague-Dawley) prolactin gene:exons IV, V and flanks
                   294903
Seq. No.
                  LIB3070-006-Q1-N1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3122753
BLAST score
                   178
                   4.0e-13
E value
                   68
Match length
% identity
                   54
                  60S RIBOSOMAL PROTEIN L44 >gi 2244789 emb CAB10211.1
NCBI Description
                   (Z97336) ribosomal protein [Arabidopsis thaliana]
                   294904
Seq. No.
Seq. ID
                   LIB3070-007-Q1-N1-A2
Method
                   BLASTN
NCBI GI
                   g440233
BLAST score
                   137
```

BLAST score

Match length

E value

83 8.0e-39

285



```
% identity
                  Zea mays ribosomal DNA internal transcribed spacer
NCBI Description
                  294905
Seq. No.
Seq. ID
                  LIB3070-007-Q1-N1-A8
Method
                  BLASTX
                  g4206196
NCBI GI
                  245
BLAST score
                  8.0e-21
E value
                  118
Match length
% identity
                  (AF071527) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  294906
Seq. No.
                  LIB3070-007-Q1-N1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1085650
BLAST score
                   170
                   2.0e-12
E value
Match length
                   58
                   66
% identity
                  aspartate transcarbomoylase - wheat >gi_688218_bbs_156442
NCBI Description
                   aspartate carbamoyltransferase {C-terminal} {EC 2.1.3.2}
                   [Triticum aestivum=wheat, avalon, seedlings, Peptide
                   Partial, 233 aa]
Seq. No.
                   294907
Seq. ID
                   LIB3070-007-Q1-N1-C2
                   BLASTN
Method
NCBI GI
                   q56539
BLAST score
                   95
                   6.0e - 46
E value
Match length
                   310
                   93
% identity
                   R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                   >gi 206360 gb J00764 RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and flanks
                   294908
Seq. No.
                   LIB3070-007-Q1-N1-D10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g56539
BLAST score
                   103
                   1.0e-50
E value
                   301
Match length
                   98
% identity
                   R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                   >gi 206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and flanks
                   294909
Seq. No.
                   LIB3070-007-Q1-N1-E10
Seq. ID
Method
                   BLASTN
                   g56539
NCBI GI
```



% identity 92

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>gi 206360 gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 294910

Seq. ID LIB3070-007-Q1-N1-E8

Method BLASTN
NCBI GI g56539
BLAST score 103
E value 1.0e-50
Match length 309
% identity 98

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>gi 206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 294911

Seq. ID LIB3070-007-Q1-N1-F2

Method BLASTX
NCBI GI g4115933
BLAST score 163
E value 3.0e-11
Match length 58
% identity 72

NCBI Description (AF118223) contains similarity to human RNA polymerase II

complex component SRB7 (GB:U52960) [Arabidopsis thaliana]

Seq. No. 294912

Seq. ID LIB3070-007-Q1-N1-G12

Method BLASTN
NCBI GI g4185305
BLAST score 154
E value 3.0e-81
Match length 198
% identity 95

NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21

(sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No. 294913

Seq. ID LIB3070-007-Q1-N1-H3

Method BLASTN
NCBI GI g56539
BLAST score 39
E value 1.0e-12
Match length 103
% identity 84

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>gi 206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 294914

Seq. ID LIB3070-008-Q1-N1-A8

Method BLASTX NCBI GI q2213632



```
BLAST score
                  6.0e-28
E value
Match length
                  106
                  58
% identity
NCBI Description (AC000103) F21J9.24 [Arabidopsis thaliana]
                  294915
Seq. No.
                  LIB3070-008-Q1-N1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4185311
BLAST score
                  540
                  2.0e-55
E value
                  134
Match length
% identity
                  80
NCBI Description (AF090446) polyprotein [Zea mays]
Seq. No.
                  294916
Seq. ID
                  LIB3070-008-Q1-N1-E1
                  BLASTX
Method
```

q3935148 NCBI GI 224 BLAST score E value 2.0e-18

294917

Match length 61 72 % identity

NCBI Description (AC005106) T25N20.12 [Arabidopsis thaliana]

Seq. No. LIB3070-008-Q1-N1-G9 Seq. ID BLASTX Method NCBI GI q3122703 BLAST score 262 7.0e-23 E value

Match length 81 69 % identity

60S RIBOSOMAL PROTEIN L23A >gi_2641201 (AF031542) ribosomal NCBI Description

protein L23a [Fritillaria agrestis]

Seq. No. 294918

Seq. ID LIB3070-009-Q1-N1-E1

Method BLASTN NCBI GI g206371 BLAST score 45 E value 4.0e-16 Match length 69 % identity 91

NCBI Description Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks

Seq. No. 294919

LIB3070-009-Q1-N1-E12 Seq. ID

Method BLASTN g433038 NCBI GI BLAST score 61 E value 1.0e-25 Match length 81 94 % identity

Zea mays W-22 clone cDNA7 retroelement PREM-1-containing NCBI Description

mRNA

NCBI Description



```
294920
Seq. No.
Seq. ID
                 LIB3070-009-Q1-N1-E5
                 BLASTX
Method
                 g2706450
NCBI GI
                 144
BLAST score
                 4.0e-09
E value
Match length
                 48
% identity
                 60
                 (AJ225172) magnesium dependent soluble inorganic
NCBI Description
                 pyrophosphatase [Solanum tuberosum]
                 294921
Seq. No.
                 LIB3070-009-Q1-N1-E7
Seq. ID
                 BLASTX
Method
NCBI GI
                 g2499497
                 153
BLAST score
                  1.0e-10
E value
Match length
                  36
% identity
                 83
NCBI Description: PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR
          [Nicotiana tabacum]
Seq. No.
                  294922
                 LIB3070-010-Q1-N1-B9
Seq. ID
                  BLASTN
Method
                  g4416300
NCBI GI
                  72
BLAST score
                  3.0e-32
E value
                  226
Match length
                  88
% identity
                  Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                  region, complete sequence
                  294923
Seq. No.
Seq. ID
                  LIB3070-010-Q1-N1-C10
                  BLASTN
Method
NCBI GI
                  g4140643
BLAST score
                  61
                  9.0e-26
E value
                  81
Match length
                  94
% identity
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                  complete sequence
                  294924
Seq. No.
Seq. ID
                  LIB3070-010-Q1-N1-D7
Method
                  BLASTX
                  q4263517
NCBI GI
                  185
BLAST score
                  6.0e-14
E value
                  111
Match length
% identity
```

41228

2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis

phenazine-1-carboxylic acid to

(AC004044) similar to PHZF, catalyzing the hydroxylation of



thaliana]

```
294925
Seq. No.
                  LIB3070-010-Q1-N1-E3
Seq. ID
                  BLASTN
Method
                  g168436
NCBI GI
                  48
BLAST score
                  6.0e-18
E value
Match length
                  56
                  96
% identity
                  Zea mays catalase (Cat3) gene, complete cds
NCBI Description
                  294926
Seq. No.
                  LIB3070-010-Q1-N1-G7
Seq. ID
                  BLASTX
Method
                   g4585900
NCBI GI
                   253
BLAST score
                   6.0e-22
E value
Match length
                   77
                   71
% identity
NCBI Description (AC007133) putative histone H2A [Arabidopsis thaliana]
Seq. No.
                   294927
                   LIB3070-010-Q1-N1-H2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q122007
                   156
BLAST score
                   1.0e-10
E value
Match length
                   69
                   58
% identity
                   HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley
NCBI Description
                   >gi 20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1
                   - 149) [Petroselinum crispum]
Seq. No.
                   294928
                   LIB3070-011-Q1-N1-B9
Seq. ID
                   BLASTX
Method
                   g2245394
NCBI GI
                   199
BLAST score
                   1.0e-15
E value
                   68
Match length
                   59
 % identity
                  (U89771) ARF1-binding protein [Arabidopsis thaliana]
NCBI Description
                   294929
 Seq. No.
                   LIB3070-011-Q1-N1-C11
 Seq. ID
                   BLASTX
 Method
                   g2668742
 NCBI GI
                   176
 BLAST score
                   2.0e-14
 E value
                   74
 Match length
 % identity
                   (AF034945) glycine-rich RNA binding protein [Zea mays]
 NCBI Description
 Seq. No.
                   294930
                   LIB3070-011-Q1-N1-C9
 Seq. ID
```

BLASTX

Method

Seq. ID Method



```
g100226
NCBI GI
                  151
BLAST score
                  3.0e-10
E value
                  40
Match length
% identity
                  hypothetical protein - tomato >gi_19275_emb_CAA78112
NCBI Description
                  (Z12127) protein of unknown function [Lycopersicon
                  esculentum] >gi_445619_prf__1909366A Leu zipper protein
                  [Lycopersicon esculentum]
Seq. No.
                  294931
                  LIB3070-011-Q1-N1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q309558
BLAST score
                  41
                  1.0e-13
E value
Match length
                  128
                  84
% identity
                  Corn nuclear-encoded mitochondrial chaperonin 60 (cpn60II)
NCBI Description
                  gene, complete cds
                   294932
Seq. No.
                  LIB3070-011-Q1-N1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4507125
                   220
BLAST score
                   5.0e-18
E value
                   101
Match length
                   47
% identity
                   small nuclear ribonucleoprotein polypeptides B and B1
NCBI Description
                   >gi_88613_pir__S10594 snRNP protein B - human
                   >gi 29410 emb CAA33902 (X15893) B/B' protein (AA 1-231)
                   [Homo sapiens]
                   294933
Seq. No.
                   LIB3070-011-Q1-N1-G5
Seq. ID
                   BLASTN
Method
                   g206371
NCBI GI
BLAST score
                   62
                   2.0e-26
E value
                   98
Match length
                   92
% identity
NCBI Description Rat(Sprague-Dawley) prolactin gene:exons IV, V and flanks
Seq. No.
                   294934
                   LIB3070-011-Q1-N1-H10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4586031
BLAST score
                   254
                   5.0e-22
E value
                   62
Match length
 % identity
                  (AC007109) unknown protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                   294935
```

41230

LIB3070-012-Q1-N1-C9

BLASTX



```
NCBI GI
                  q82466
                  300
BLAST score
                  3.0e-27
E value
                  58
Match length
                  95
% identity
                  probable ferredoxin--NADP+ reductase (EC 1.18.1.2) - rice
NCBI Description
                  >gi 218163_dbj BAA02248_ (D12815) ferredoxin-NADP+
                 reductase enzyme [Oryza sativa]
                  294936
Seq. No.
                  LIB3070-013-Q1-N1-A12
Seq. ID
                  BLASTN
Method
                  g206371
NCBI GI
                  75
BLAST score
                  5.0e-34
E value
                  260
Match length
                  93
% identity
NCBI Description Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks
                  294937
Seq. No.
                  LIB3070-013-Q1-N1-B11
Seq. ID
                  BLASTN
Method
                  g206371
NCBI GI
                   99
BLAST score
                   2.0e-48
E value
                   309
Match length
                   98
% identity
NCBI Description Rat(Sprague-Dawley) prolactin gene:exons IV, V and flanks
                   294938
Seq. No.
Seq. ID
                   LIB3070-013-Q1-N1-B3
                   BLASTN
Method
NCBI GI
                   q206371
                   99
BLAST score
                   2.0e-48
E value
                   309
Match length
                   98
% identity
                  Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks
NCBI Description
                   294939
Seq. No.
                   LIB3070-013-Q1-N1-C2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4416300
BLAST score
                   64
                   2.0e-27
E value
Match length
                   124
% identity
                   88
                   Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                   region, complete sequence
                   294940
Seq. No.
                   LIB3070-013-Q1-N1-F4
Seq. ID
Method
                   BLASTN
                   g206371
NCBI GI
                   79
BLAST score
```

41231

2.0e-36

170

E value

Match length



```
% identity
NCBI Description Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks
                  294941
Seq. No.
Seq. ID
                  LIB3070-014-Q1-N1-A5
                  BLASTX
Method
NCBI GI
                  g1706403
                  142
BLAST score
                   8.0e-16
E value
                   62
Match length
                   73
% identity
                  GLUTAMATE DEHYDROGENASE (GDH) >gi_1085815_pir__S54797
NCBI Description
                   glutamate dehydrogenase (EC 1.4.1.2) - Vitis vinifera
                   >gi_806595_emb_CAA60507_ (X86924) glutamate dehydrogenase
                   [Vitis vinifera]
                   294942
Seq. No.
                   LIB3070-014-Q1-N1-B5
Seq. ID
                   BLASTN
Method
                   g1935910
NCBI GI
BLAST score
                   66
                   1.0e-28
E value
                   182
Match length
                   85
% identity
NCBI Description Zea mays lethal leaf-spot 1 (lls1) gene, partial cds
                   294943
Seq. No.
                   LIB3070-014-Q1-N1-C2
Seq. ID
                   BLASTN
Method
                   g22211
NCBI GI
                   49
BLAST score
                   2.0e-18
E value
                   81
Match length
                   90
% identity
                   Maize bronze bz1 gene 5' region with DS1 element Bz-wm
NCBI Description
                   inserted
                   294944
Seq. No.
                   LIB3070-014-Q1-N1-C4
 Seq. ID
                   BLASTX
Method
                   q3913804
NCBI GI
BLAST score
                   377
E value
                   2.0e-36
Match length
                   115
                   69
 % identity
                   HISTONE H2B.3 >gi_577825_emb_CAA49584_ (X69960) H2B histone
 NCBI Description
                   [Zea mays]
                   294945
 Seq. No.
                   LIB3070-014-Q1-N1-C6
 Seq. ID
                   BLASTX
 Method
                   g2500497
 NCBI GI
 BLAST score
                   227
                   3.0e-19
 E value
                    46
 Match length
```

NCBI Description 40S RIBOSOMAL PROTEIN S21 >gi_1419372_emb_CAA67225_

93

% identity

NCBI Description





(X98656) ribosomal protein S21 [Zea mays]

```
294946
Seq. No.
Seq. ID
                  LIB3070-014-Q1-N1-D10
                  BLASTN
Method
NCBI GI
                  g507770
                  36
BLAST score
                  8.0e-11
E value
                  72
Match length
                  89
% identity
                  Zea mays D3L H(+)-transporting ATPase (Mha1) gene, complete
NCBI Description
                  294947
Seq. No.
                  LIB3070-014-Q1-N1-D5
Seq. ID
                  BLASTX
Method
                  g1076670
NCBI GI
                  166
BLAST score
                   1.0e-11
E value
                   45
Match length
                   73
% identity
                  NADH dehydrogenase (EC 1.6.99.3) - potato
NCBI Description
                   >gi 668985_emb_CAA59062_ (X84319) NADH dehydrogenase
                   [Solanum tuberosum]
                   294948
Seq. No.
                  LIB3070-014-Q1-N1-F10
Seq. ID
                  BLASTX
Method
                   g2290989
NCBI GI
                   173
BLAST score
                   2.0e-12
E value
                   90
Match length
                   39
% identity
                   (AF006000) D-3-phosphoglycerate dehydrogenase homolog
NCBI Description
                   [Bordetella pertussis]
                   294949
Seq. No.
Seq. ID
                   LIB3070-014-Q1-N1-F12
                   BLASTX
Method
                   g1346251
NCBI GI
BLAST score
                   189
E value
                   2.0e-14
Match length
                   79
% identity
                   53
                   HISTONE H2B.4 >gi_577819_emb_CAA49585_ (X69961) H2B histone
NCBI Description
                   [Zea mays]
                   294950
Seq. No.
                   LIB3070-014-Q1-N1-F3
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1870198
BLAST score
                   53
E value
                   3.0e-21
Match length
                   61
                   98
 % identity
```

Z.mays mRNA for acyl carrier protein



```
294951
Seq. No.
                  LIB3070-014-Q1-N1-H3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g56539
BLAST score
                  88
                  9.0e-42
E value
Match length
                  201
                  97
% identity
                  R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                  >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                  : exon v and flanks
                  294952
Seq. No.
Seq. ID
                  LIB3070-015-Q1-N1-B11
                  BLASTN
Method
NCBI GI
                  g206371
                  95
BLAST score
                  5.0e-46
E value
                  276
Match length
                  95
% identity
NCBI Description Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks
                  294953
Seq. No.
Seq. ID
                  LIB3070-015-Q1-N1-D3
                  BLASTN
Method
NCBI GI
                  g498774
                  128
BLAST score
                   6.0e-66
E value
                  152
Match length
                   96
% identity
NCBI Description Z.mays (cv DH5xDH7) hsp70-5 mRNA for heat shock protein
                   294954
Seq. No.
Seq. ID
                  LIB3070-015-Q1-N1-E5
                  BLASTN
Method
NCBI GI
                   q206371
BLAST score
                   37
E value
                   2.0e-11
                   65
Match length
% identity
                   89
NCBI Description Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks
Seq. No.
                   294955
Seq. ID
                   LIB3070-015-Q1-N1-F5
Method
                   BLASTX
NCBI GI
                   q3894187
BLAST score
                   300
E value
                   3.0e-27
Match length
                   69
% identity
                  (AC005662) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 294956

Seq. ID LIB3070-016-Q1-N1-A6

Method BLASTX NCBI GI g4455192 BLAST score 154



```
3.0e-10
E value
Match length
                  102
% identity
                 (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                  294957
Seq. No.
Seq. ID
                  LIB3070-016-Q1-N1-E1
                  BLASTN
Method
                  g206371
NCBI GI
                  99
BLAST score
                  2.0e-48
E value
                  103
Match length
                  99
% identity
NCBI Description Rat(Sprague-Dawley) prolactin gene:exons IV, V and flanks
                  294958
Seq. No.
                  LIB3070-016-Q1-N1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g537604
                  209
BLAST score
                  1.0e-16
E value
                  111
Match length
                  45
% identity
NCBI Description (D30652) peroxidase [Populus kitakamiensis]
                  294959
Seq. No.
                  LIB3070-016-Q1-N1-G3
Seq. ID
                  BLASTX
Method
                  g4646221
NCBI GI
BLAST score
                  174
                  1.0e-12
E value
Match length
                  110
                  35
% identity
                  (AC007290) putative membrane-associated protein, 3' partial
NCBI Description
                   [Arabidopsis thaliana]
                  294960
Seq. No.
Seq. ID
                  LIB3070-016-Q1-N1-G8
                  BLASTN
Method
                   q206371
NCBI GI
BLAST score
                   103
E value
                   9.0e-51
Match length
                   302
% identity
                   97
NCBI Description Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks
                   294961
Seq. No.
Seq. ID
                   LIB3070-016-Q1-N1-H10
Method
                   BLASTX
                   g4454307
NCBI GI
BLAST score
                   329
```

Method BLASTX
NCBI GI g4454307
BLAST score 329
E value 3.0e-31
Match length 72
% identity 83

NCBI Description (AJ132763) cyclophilin [Pseudotsuga menziesii]

Seq. No. 294962

NCBI GI BLAST score

E value

229 2.0e-19



```
LIB3075-001-Q1-K1-B9
Seq. ID
                  BLASTX
Method
                  g2160690
NCBI GI
                  244
BLAST score
                  7.0e-21
E value
Match length
                  74
% identity
                  (U73526) B' regulatory subunit of PP2A [Arabidopsis
NCBI Description
                  thaliana]
                  294963
Seq. No.
Seq. ID
                  LIB3075-001-Q1-K1-C12
                  BLASTN
Method
                  g288611
NCBI GI
                  62
BLAST score
                  3.0e-26
E value
                  117
Match length
                  88
% identity
NCBI Description Z.mays PG gene for polygalacturonase
                  294964
Seq. No.
                  LIB3075-001-Q1-K1-H5
Seq. ID
                  BLASTX
Method
                  q3702336
NCBI GI
                  256
BLAST score
                   2.0e-22
E value
                   83
Match length
                   65
% identity
NCBI Description (AC005397) putative 3-methyl-2-oxobutanoate
                   hydroxy-methyl-transferase [Arabidopsis thaliana]
                   294965
Seq. No.
Seq. ID
                   LIB3075-002-Q1-K1-F10
                   BLASTX
Method
                   q3080390
NCBI GI
                   294
BLAST score
                   1.0e-26
E value
Match length
                   131
% identity
NCBI Description (AL022603) putative protein [Arabidopsis thaliana]
Seq. No.
                   294966
Seq. ID
                   LIB3075-002-Q1-K1-H10
Method
                   BLASTX
                   q2982277
NCBI GI
BLAST score
                   419
                   3.0e-41
E value
                   88
Match length
% identity
NCBI Description (AF051223) Rac-like GTP binding protein [Picea mariana]
Seq. No.
                   294967
                   LIB3075-003-Q1-K1-A9
Seq. ID
Method
                   BLASTX
                   q4262242
```

% identity

94



```
Match length
                  68
                  68
% identity
                  (AC006200) NADC homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  294968
                  LIB3075-003-Q1-K1-B11
Seq. ID
Method
                  BLASTX
                  g2244830
NCBI GI
BLAST score
                  155
E value
                  4.0e-10
Match length
                  49
% identity
                  61
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  294969
Seq. ID
                  LIB3075-003-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  q4584957
BLAST score
                  314
E value
                  2.0e-29
Match length
                  78
% identity
                  92
NCBf Description (AF077337) heat shock protein 101; 101 kDa heat shock
                  protein [Zea mays]
Seq. No.
                  294970
Seq. ID
                  LIB3075-003-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  q3599966
BLAST score
                  181
E value
                  3.0e-13
Match length
                  72
                  47
% identity
                  (AF026852) h-scol [Homo sapiens]
NCBI Description
                  294971
Seq. No.
                  LIB3075-003-Q1-K1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3851002
BLAST score
                  168
                   9.0e-90
E value
Match length
                   192
                   97
% identity
                  Zea mays pyruvate dehydrogenase E1 beta subunit isoform 3
NCBI Description
                  mRNA, nuclear gene encoding mitochondrial protein, complete
                  cds
                   294972
Seq. No.
                  LIB3075-003-Q1-K1-G9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22458
BLAST score
                   107
E value
                   4.0e-53
Match length
                   139
```

NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)



```
294973
  Seq. No.
                     LIB3075-003-Q1-K1-H5
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g2708532
  BLAST score
                     286
  E value
                     5.0e-26
  Match length
                     86
  % identity
  NCBI Description
                     (AF029351) putative RNA binding protein [Nicotiana tabacum]
  Seq. No.
                     294974
  Seq. ID
                     LIB3075-004-Q1-K1-A9
  Method
                     BLASTX
  NCBI GI
                     g2384758
  BLAST score
                     167
  E value
                     3.0e-12
  Match length
                     47
  % identity
                     72
                     (AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza
  NCBI Description
                     sativa]
 .Seq. No.
                     294975
୍ଦ୍ର ID
                     LIB3075-004-Q1-K1-B3
  Method
                     BLASTX
  NCBI GI
                     g2982268
  BLAST score
                     290
  E value
                     2.0e-26
  Match length
                     92
  % identity
                     62
  NCBI Description
                     (AF051217) probable 40S ribosomal protein S15 [Picea
                     mariana]
  Seq. No.
                     294976
                     LIB3075-004-Q1-K1-D4
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g283049
  BLAST score
                     226
                     8.0e-19
  E value
  Match length
                     70
  % identity
                     73
  NCBI Description
                     polygalacturonase (EC 3.2.1.15) precursor (clone W2247) -
                     maize (fragment) >gi_481079_pir__S37718 polygalacturonase -
                     maize >gi 22426 emb \overline{CAA44248} (\overline{X6}2384) polygalacturonase
                     [Zea mays] >gi 287830 emb CAA47234 (X66692)
                     polygalacturonase [Zea mays]
  Seq. No.
                     294977
  Seq. ID
                     LIB3075-004-Q1-K1-D8
  Method
                     BLASTN
```

` "≈

NCBI GI g288611 BLAST score 44 E value 9.0e-16 56 Match length % identity 95

NCBI Description Z.mays PG gene for polygalacturonase

Seq. No. 294978



```
LIB3075-004-Q1-K1-E9
Seq. ID
                  BLASTX
Method
                  g1171005
NCBI GI
                  429
BLAST score
                  2.0e-42
E value
Match length
                  119
% identity
                   68
                  MAJOR POLLEN ALLERGEN HOL L 1 PRECURSOR (HOL L I)
NCBI Description
                  >gi_1085628_pir__S38581 allergen Hol-II - Holcus lanatus
                  >gi_414703_emb_CAA81610_ (Z27084) allergen Hol-II [Holcus
                  lanatus]
                  294979
Seq. No.
Seq. ID
                  LIB3075-004-Q1-K1-G11
                  BLASTX
Method
NCBI GI
                   g3152588
BLAST score
                   234
                   2.0e-19
E value
                   78
Match length
% identity
                  (AC002986) Contains similarity to Cf-2.2 gene gb_U42445
NCBI Description
                   from Solanum pimpinellifolium. [Arabidopsis thal\overline{i}ana]
                   294980
Seq. No.
                   LIB3075-005-Q1-K1-C10
Seq. ID
                   BLASTN
Method
                   g3328211
NCBI GI
BLAST score
                   33
                   3.0e-09
E value
                   65
Match length
                   88
% identity
NCBI Description Cloning vector pCMVTAG4c, complete sequence
                   294981
Seq. No.
                   LIB3075-005-Q1-K1-C11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2347190
BLAST score
                   218
                   1.0e-17
E value
                   138
Match length
% identity
                   (AC002338) Na/H antiporter isolog [Arabidopsis thaliana]
NCBI Description
                   >gi_3150398 (AC004165) putative Na/H antiporter
                   [Arabidopsis thaliana]
                   294982
Seq. No.
Seq. ID
                   LIB3075-005-Q1-K1-C12
                   BLASTX
Method
NCBI GI
                   g4467146
BLAST score
                   241
```

2.0e-20 E value Match length 91 47 % identity

(AL035540) galactosidase like protein [Arabidopsis NCBI Description

thaliana]

294983 Seq. No.



```
LIB3075-005-Q1-K1-C8
Seq. ID
                  BLASTX
Method
                  g4335731
NCBI GI
                  294
BLAST score
                  1.0e-26
E value
Match length
                  142
% identity
NCBI Description (AC006248) putative polyprotein [Arabidopsis thaliana]
                  294984
Seq. No.
Seq. ID
                  LIB3075-005-Q1-K1-G1
Method
                  BLASTX
                  g3915847
NCBI GI
BLAST score
                  211
                  5.0e-22
E value
                  104
Match length
                  64
% identity
                  40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
NCBI Description
                   40S ribosomal protein S2 [Arabidopsis thaliana]
                  294985
Seq. No.
Seq. ID
                  LIB3075-005-Q1-K1-G8
                  BLASTN
Method
                  g2911359
NCBI GI
                  261
BLAST score
                   1.0e-145
E value
                   438
Match length
                   90
% identity
                  Zea mays NADPH HC toxin reductase (hml) gene, hml-Pr
NCBI Description
                   allele, complete cds
                   294986
Seq. No.
Seq. ID
                   LIB3075-005-Q1-K1-H9
                   BLASTN
Method
                   g433041
NCBI GI
BLAST score
                   67
                   3.0e-29
E value
Match length
                   201
                   84
% identity
                   Zea mays W-22 clone PREM-1B retroelement PREM-1, partial
NCBI Description
                   sequence
Seq. No.
                   294987
                   LIB3075-006-Q1-K1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4154352
BLAST score
                   163
E value
                   2.0e-11
                   99
Match length
% identity
                   41
                  (AF110333) PrMC3 [Pinus radiata]
NCBI Description
                   294988
Seq. No.
                   LIB3075-006-Q1-K1-C5
Seq. ID
```

41240

BLASTX

155

g4455203

Method

NCBI GI BLAST score



```
1.0e-10
E value
Match length
% identity
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                  294989
Seq. No.
Seq. ID
                  LIB3075-006-Q1-K1-D12
                  BLASTX
Method
                  g729944
NCBI GI
BLAST score
                  165
                  2.0e-11
E value
                  48
Match length
% identity
                  60
                  POLLEN ALLERGEN ZEA M 1 (ZEA M I) >gi_478272_pir__JC1524
NCBI Description
                  major allergen mI protein - maize >gi_293902 (L14271) Zea
                  mI [Zea mays]
                  294990
Seq. No.
Seq. ID
                  LIB3075-006-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g1353516
                  210
BLAST score
                   4.0e-17
E value
                  82
Match length
% identity
                 (U38651) sugar transporter [Medicago truncatula]
NCBI Description
                   294991
Seq. No.
                  LIB3075-006-Q1-K1-H11
Seq. ID
                  BLASTN
Method
                   g168652
NCBI GI
BLAST score
                   54
                   1.0e-21
E value
Match length
                   106
                   88
% identity
                  Maize amyloplast-specific transit protein (waxy; wx+
NCBI Description
                   locus), complete cds
                   294992
Seq. No.
                   LIB3075-007-Q1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q466053
BLAST score
                   197
E value
                   4.0e-15
                   42
Match length
% identity
                   64
                   HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III
NCBI Description
                   >gi_482217_pir__S41011 hypothetical protein ZK757.1 -
                   Caenorhabditis elegans >gi 3881771 emb CAA82387 (Z29121)
                   ZK757.1 [Caenorhabditis elegans]
```

Seq. No. 294993

Seq. ID LIB3075-007-Q1-K1-B11

Method BLASTX
NCBI GI g2853081
BLAST score 385
E value 5.0e-40



```
Match length
% identity
                  (AL021768) ATP binding protein-like [Arabidopsis thaliana]
NCBI Description
                  294994
Seq. No.
Seq. ID
                  LIB3075-007-Q1-K1-F3
                  BLASTX
Method
                  g1928981
NCBI GI
                  167
BLAST score
                  1.0e-20
E value
                  98
Match length
                  60
% identity
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                  oleracea var. botrytis]
                  294995
Seq. No.
Seq. ID
                  LIB3075-007-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  q548493
BLAST score
                  286
                  1.0e-25
E value
                   54
Match length
                   98
% identity
                  EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                   (GALACTURAN 1, 4-ALPHA-GALACTURONIDASE)
                   >gi 629854 pir__S30067 polygalacturonase - maize
                   >gi 288612 emb CAA47052 (X66422) polygalacturonase [Zea
                   mays]
                   294996
Seq. No.
                   LIB3075-007-Q1-K1-H9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3107905
BLAST score
                   151
                   9.0e-10
E value
                   118
Match length
% identity
                  (D85101) leaf protein [Ipomoea nil]
NCBI Description
                   294997
Seq. No.
Seq. ID
                   LIB3075-008-Q1-K1-A1
Method
                   BLASTX
NCBI GI
                   g1171008
BLAST score
                   197
E value
                   2.0e-15
Match length
                   58
% identity
                   59
                   POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I)
NCBI Description
```

>gi 629812_pir__S44182 allergen Phl p I - common timothy >gi 473360 emb CAA55390 (X78813) Phl p I allergen [Phleum

pratense]

Seq. No.

294998

Seq. ID

LIB3075-008-Q1-K1-A6

BLASTN Method g3420038 NCBI GI BLAST score 167

Match length

% identity

83 90



```
7.0e-89
E value
                  395
Match length
                  43
% identity
                  Zea mays gypsy/Ty3-type retrotransposon Tekay, complete
NCBI Description
                  sequence
                  294999
Seq. No.
                  LIB3075-008-Q1-K1-A7
Seq. ID
                  BLASTN
Method
                  g3420038
NCBI GI
                  66
BLAST score
                  1.0e-28
E value
                  288
Match length
                  43
% identity
NCBI Description Zea mays gypsy/Ty3-type retrotransposon Tekay, complete
                  sequence
                  295000
Seq. No.
                  LIB3075-008-Q1-K1-B12
Seq. ID
                  BLASTX
Method
                  g1362010
NCBI GI
                   226
BLAST score
                   1.0e-18
E value
                   47
Match length
                   23
% identity
NCBI Description ubiquitin-like protein 9 - Arabidopsis thaliana
                   295001
Seq. No.
                   LIB3075-008-Q1-K1-D10
Seq. ID
                   BLASTN
Method
                   q22458
NCBI GI
                   123
BLAST score
                   8.0e-63
E value
                   262
Match length
                   87
% identity
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)
                   295002
Seq. No.
                   LIB3075-008-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   q2369714
NCBI GI
BLAST score
                   605
E value
                   4.0e-63
Match length
                   122
 % identity
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]
                   295003
 Seq. No.
                   LIB3075-008-Q1-K1-F6
 Seq. ID
                   BLASTN
Method
                   g3184049
 NCBI GI
 BLAST score
                   51
 E value
                   8.0e-20
```

NCBI Description Sorghum bicolor F1-ATP synthase, cultivar 2077A, partial

Seq. No.

Seq. ID Method



```
295004
Seq. No.
Seq. ID
                  LIB3075-009-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  q2558666
BLAST score
                  250
E value
                  2.0e-21
                  89
Match length
% identity
                  (U49971) GTP binding protein RoplAt [Arabidopsis thaliana]
NCBI Description
                  >gi 3603426 (AF085480) rac-like GTP binding protein Aracl1
                   [Arabidopsis thaliana]
                  295005
Seq. No.
Seq. ID
                  LIB3075-009-Q1-K1-B7
                  BLASTX
Method
NCBI GI
                  g4580389
BLAST score
                  406
                  1.0e-39
E value
Match length
                  131
                   61
% identity
                  (AC007171) unknown protein [Arabidopsis thaliana]
NCBI Description
                   295006
Seq. No.
                  LIB3075-009-Q1-K1-C3
Seq. ID
Method
                  BLASTN
                   q433041
NCBI GI
BLAST score
                   96
                   2.0e-46
E value
Match length
                   156
                   91
% identity
                   Zea mays W-22 clone PREM-1B retroelement PREM-1, partial
NCBI Description
                   sequence
Seq. No.
                   295007
Seq. ID
                   LIB3075-009-Q1-K1-D3
Method
                   BLASTN
NCBI GI
                   g4140643
BLAST score
                   98
E value
                   1.0e-47
Match length
                   363
% identity
                   66
                   Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                   complete sequence
Seq. No.
                   295008
                   LIB3075-009-Q1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2760084
BLAST score
                   261
E value
                   1.0e-22
Match length
                   110
% identity
                   46
                  (Y16045) leucine-rich repeat protein [Arabidopsis thaliana]
NCBI Description
                   295009
```

LIB3075-010-Q1-K1-A1

BLASTX

E value

Match length



```
g2464901
NCBI GI
                  398
BLAST score
                  7.0e-39
E value
                  122
Match length
% identity
                  (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
                  295010
Seq. No.
                  LIB3075-010-Q1-K1-A9
Seq. ID
                  BLASTX
Method
                  q629849
NCBI GI
BLAST score
                  357
                  7.0e-34
E value
                  137
Match length
                   55
% identity
                  pectate lyase (EC 4.2.2.2) - maize >gi_405535 (L20140)
NCBI Description
                  homology with pectate lyase [Zea mays]
                   295011
Seq. No.
Seq. ID
                  LIB3075-010-Q1-K1-C11
                   BLASTN
Method
                   g22458
NCBI GI
BLAST score
                   44
                   5.0e-16
E value
                   140
Match length
                   83
% identity
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)
                   295012
Seq. No.
                   LIB3075-010-Q1-K1-E6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4336747
                   238
BLAST score
                   6.0e-20
E value
                   134
Match length
% identity
                   39
NCBI Description (AF104924) unconventional myosin heavy chain [Zea mays]
                   295013
Seq. No.
Seq. ID
                   LIB3075-010-Q1-K1-H6
                   BLASTX
Method
NCBI GI
                   q3687301
BLAST score
                   169
E value
                   5.0e-12
                   66
Match length
% identity
                   (AJ006376) subtilisin-like protease [Lycopersicon
NCBI Description
                   esculentum] >gi 3687309_emb_CAA07001_ (AJ006380)
                   subtilisin-like protease [Lycopersicon esculentum]
                   295014
Seq. No.
                   LIB3075-011-Q1-K1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2511531
BLAST score
                   603
                   9.0e-63
```



```
% identity
                  (AF008120) alpha tubulin 1 [Eleusine indica]
NCBI Description
                  >gi 3163944 emb CAA06618 (AJ005598) alpha-tubulin 1
                  [Eleusine indica]
Seq. No.
                  295015
                  LIB3075-011-Q1-K1-C1
Seq. ID
Method
                  BLASTX
                  g2766450
NCBI GI
                  685
BLAST score
E value
                  2.0e-72
                  152
Match length
% identity
NCBI Description (AF029857) cytochrome P450 CYP99A1 [Sorghum bicolor]
```

295016 Seq. No. Seq. ID LIB3075-011-Q1-K1-E12 Method BLASTX NCBI GI g1019946 BLAST score 167 1.0e-11 E value Match length 47

% identity NCBI Description (U37060) ascorbate peroxidase [Gossypium hirsutum]

295017 Seq. No. Seq. ID LIB3075-011-Q1-K1-F10 BLASTX Method g2781363 NCBI GI BLAST score 178 6.0e-13 E value

Match length 55 % identity

NCBI Description (AC003113) F2401.19 [Arabidopsis thaliana]

Seq. No. 295018

Seq. ID LIB3075-011-Q1-K1-F5

Method BLASTX NCBI GI g1362010 BLAST score 310 2.0e-28 E value Match length 66 % identity 23

NCBI Description ubiquitin-like protein 9 - Arabidopsis thaliana

295019 Seq. No.

LIB3075-012-Q1-K1-B6 Seq. ID

Method BLASTX g3183991 NCBI GI 224 BLAST score 2.0e-18 E value Match length 118 % identity 42

(AJ005173) P69F protein [Lycopersicon esculentum] NCBI Description

295020 Seq. No.

Seq. ID LIB3075-012-Q1-K1-H5

BLAST score

E value

422

2.0e-41



```
Method
                  BLASTX
NCBI GI
                  g2618691
BLAST score
                  399
                  4.0e-39
E value
Match length
                  93
                  84
% identity
                  (AC002510) putative chloroplast envelope Ca2+-ATPase
NCBI Description
                   [Arabidopsis thaliana]
                  295021
Seq. No.
Seq. ID
                  LIB3075-013-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  g567893
BLAST score
                  157
E value
                  2.0e-10
Match length
                  63
% identity
                  44
                  (L37382) beta-galactosidase-complementation protein
NCBI Description
                  [Cloning vector]
Seq. No.
                  295022
                  LIB3075-013-Q1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3043428
BLAST score
                  383
E value
                  4.0e-37
Match length
                  93
% identity
                  76
NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
                  295023
Seq. No.
                  LIB3075-013-Q1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4580389
BLAST score
                  142
                  2.0e-18
E value
Match length
                  81
                  65
% identity
NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]
Seq. No.
                  295024
Seq. ID
                  LIB3075-013-Q1-K1-D9
Method
                  BLASTN
                  g405532
NCBI GI
BLAST score
                  66
E value
                  9.0e-29
Match length
                  86
% identity
                  94
NCBI Description
                  Zea mays pollen specific pectate lyase homologue mRNA, 3'
                  end of cds
Seq. No.
                  295025
Seq. ID
                  LIB3075-013-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  q4204284
```

```
Match length
                   147
% identity
                   56
NCBI Description
                   (AC003027) 1cl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                  295026
Seq. ID
                  LIB3075-013-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g4539660
BLAST score
                  239
E value
                  2.0e-27
Match length
                  127
% identity
                  47
NCBI Description
                  (AF061282) polyprotein [Sorghum bicolor]
Seq. No.
                  295027
Seq. ID
                  LIB3075-014-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g1575130
BLAST score
                  560
E value
                  8.0e-58
Match length
                  110
% identity
NCBI Description (U58209) lumenal binding protein cBiPe3 [Zea mays]
Seq. No.
                  295028
Seq. ID
                  LIB3075-014-Q1-K1-A12
                  BLASTN
                  g433038
                  60
                  3.0e-25
                  96
```

Method NCBI GI BLAST score E value Match length 92 % identity

Zea mays W-22 clone cDNA7 retroelement PREM-1-containing NCBI Description

mRNA

Seq. No. 295029

Seq. ID LIB3075-014-Q1-K1-B9

Method BLASTX NCBI GI g4538897 BLAST score 227 E value 1.0e-18 Match length 77 % identity 61

NCBI Description (AL049482) AX110P-like protein [Arabidopsis thaliana]

Seq. No. 295030

Seq. ID LIB3075-014-Q1-K1-D7

Method BLASTX NCBI GI g4559380 BLAST score 261 E value 9.0e-23 Match length 103 % identity 53

NCBI Description (AC006526) putative auxin-responsive GH3 protein

[Arabidopsis thaliana]

BLAST score

Match length

E value

82

158

2.0e-38



```
Seq. No.
                   295031
Seq. ID
                   LIB3075-014-Q1-K1-F12
Method
                   BLASTX
NCBI GI
                   q3163946
BLAST score
                   596
E value
                   4.0e-62
Match length
                   114
% identity
                   97
NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]
Seq. No.
                   295032
Seq. ID
                   LIB3075-015-Q1-K1-A9
Method
                   BLASTX
NCBI GI
                   g3062907
BLAST score
                   286
E value
                   1.0e-25
Match length
                   59
% identity
                   90
NCBI Description (AB012107) myo-inositol phosphate synthase [Oryza sativa]
Seq. No.
                   295033
Seq. ID
                   LIB3075-015-Q1-K1-B12
Method
                   BLASTX
NCBI GI
                   g4191785
BLAST score
                   328
E value
                   1.0e-30
Match length
                   135
% identity
                   55
NCBI Description (AC005917) putative hydrolase [Arabidopsis thaliana]
Seq. No.
                   295034
Seq. ID
                  LIB3075-015-01-K1-D6
Method
                  BLASTX
NCBI GI
                   q4105800
BLAST score
                   156
E value
                   8.0e-11
Match length
                   63
% identity
                   49
NCBI Description
                  (AF049931) PGP301 [Petunia x hybrida]
Seq. No.
                  295035
Seq. ID
                  LIB3075-015-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  q2832695
BLAST score
                  264
E value
                  4.0e-23
Match length
                  77
% identity
                  58
NCBI Description
                  (AL021713) putative protein [Arabidopsis thaliana]
Seq. No.
                  295036
Seq. ID
                  LIB3075-015-Q1-K1-F7
Method
                  BLASTN
NCBI GI
                  g288611
```



```
% identity
   NCBI Description Z.mays PG gene for polygalacturonase
   Seq. No.
                     295037
   Seq. ID
                     LIB3075-015-Q1-K1-G11
   Method
                     BLASTX
   NCBI GI
                     q4490740
   BLAST score
                     185
   E value
                     2.0e-14
   Match length
                     59
   % identity
                     64
   NCBI Description
                     (AL035708) small GTP-binding protein-like [Arabidopsis
                     thaliana]
                     295038
   Seq. No.
   Seq. ID
                     LIB3075-015-Q1-K1-G8
   Method
                     BLASTX
   NCBI GI
                     g1086989
   BLAST score
                     316
   E value
                     3.0e-29
   Match length
                     99
   % identity
                     67
                    (S79323) plasma membrane H(+)-ATPase [Vicia faba, Otafuku,
   NCBI Description
                     abaxial epidermis, guard cell protoplasts, Peptide, 963 aa]
                     [Vicia faba]
  Seq. No.
                     295039
   Seq. ID
                     LIB3075-016-Q1-K1-H12
  Method
                     BLASTX
  NCBI GI
                     g2501555
  BLAST score
                     385
  E value
                     4.0e-37
  Match length
                     101
   % identity
                     76
  NCBI Description POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi 549984 (U13148)
                     possible apospory-associated protein [Pennisetum ciliare]
  Seq. No.
                     295040
  Seq. ID
                     LIB3075-017-Q1-K1-A8
  Method
                     BLASTX
  NCBI GI
                     g3281870
  BLAST score
                     194
  E value
                     8.0e-15
  Match length
                    104
  % identity
                     43
  NCBI Description (AL031004) putative protein [Arabidopsis thaliana]
  Seq. No.
                    295041
  Seq. ID
                    LIB3075-017-Q1-K1-B2
  Method
                    BLASTX
  NCBI GI
                    g113621
  BLAST score
                    232
  E value
                    1.0e-19
  Match length
                    95
  % identity
                    58
  NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
```

>gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC





4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A cytoplasmic aldolase [Zea mays]

Seq. No. 295042

Seg. ID LIB3075-017-Q1-K1-C6

Method BLASTX
NCBI GI g548493
BLAST score 277
E value 7.0e-25
Match length 94
% identity 67

NCBI Description EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)

(GALACTURAN 1,4-ALPHA-GALACTURONIDASE)

>gi 629854 pir S30067 polygalacturonase - maize

>gi 288612 emb CAA47052 (X66422) polygalacturonase [Zea

mays]

Seq. No. 295043

Seq. ID LIB3075-017-Q1-K1-C9

Method BLASTX
NCBI GI g729944
BLAST score 204
E value 1.0e-17
Match length 68
% identity 72

NCBI Description POLLEN ALLERGEN ZEA M 1 (ZEA M I) >gi_478272_pir__JC1524

major allergen mI protein - maize >gi_293902 (L14271) Zea

mI [Zea mays]

Seq. No. 295044

Seq. ID LIB3075-017-Q1-K1-F1

Method BLASTX
NCBI GI g4467124
BLAST score 255
E value 5.0e-22
Match length 139
% identity 34

NCBI Description (AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No. 295045

Seq. ID LIB3075-017-Q1-K1-F2

Method BLASTX
NCBI GI g3420057
BLAST score 286
E value 1.0e-25
Match length 124
% identity 70

NCBI Description (AC004680) putative ABC transporter [Arabidopsis thaliana]

Seq. No. 295046

Seq. ID LIB3075-017-Q1-K1-H9

Method BLASTX
NCBI GI g129940
BLAST score 362
E value 1.0e-34



```
105
Match length
                  70
% identity
                  EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                  (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi_100911_pir__S18570 polygalacturonase (EC 3.2.1.15)
                  precursor - maize >gi_22417_emb_CAA40850_ (X57627)
                  polygalacturonase [Zea mays] >gi_22419_emb_CAA44249_
                  (X62385) polygalacturonase [Zea mays]
                  >gi_288374_emb_CAA46679_ (X65844) polygalacturonase [Zea
                  mays]
                  295047
Seq. No.
                  LIB3075-018-Q1-K1-C11
Seq. ID
                  BLASTX
Method
                  g4150963
NCBI GI
                  165
BLAST score
                  2.0e-11
E value
                  60
Match length
% identity
NCBI Description (Y18620) DsPTP1 protein [Arabidopsis thaliana]
                  295048
Seq. No.
                  LIB3075-018-Q1-K1-D2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2911058
                  154
BLAST score
                  3.0e-10
E value
                  79
Match length
% identity
                  (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
                  295049
Seq. No.
                  LIB3075-018-Q1-K1-G6
Seq. ID
                  BLASTX
Method
                   g2244990
NCBI GI
BLAST score
                   195
                   5.0e-15
E value
Match length
                   88
                   48
% identity
                  (Z97340) similarity to LIM homeobox protein -
NCBI Description
                   Caenorhabditis [Arabidopsis thaliana]
Seq. No.
                   295050
                   LIB3075-019-Q1-K1-B8
Seq. ID
                   BLASTN
Method
                   g22258
NCBI GI
                   147
BLAST score
                   5.0e-77
E value
                   155
Match length
                   99
 % identity
NCBI Description Maize DNA for Ds103 controlling element (Ds1-related)
```

295051

Seq. No. LIB3075-019-Q1-K1-C5 Seq. ID

BLASTN Method g433043 NCBI GI 37 BLAST score



```
2.0e-11
E value
Match length
                   49
% identity
                  94
                  Zea mays W-22 clone PREM-1E retroelement PREM-1, partial
NCBI Description
                  sequence
Seq. No.
                  295052
Seq. ID
                  LIB3075-019-Q1-K1-E9
                  BLASTX
Method
NCBI GI
                  g2244876
BLAST score
                  249
                  2.0e-21
E value
                  86
Match length
                  58
% identity
NCBI Description (Z97338) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  295053
Seq. ID
                  LIB3075-019-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g2827631
BLAST score
                  174
E value
                  9.0e-13
Match length
                  69
                  51
% identity
NCBI Description (AL021636) putative protein [Arabidopsis thaliana]
Seq. No.
                  295054
                  LIB3075-019-Q1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2982459
BLAST score
                  162
                  3.0e-11
E value
                  89
Match length
                  38
% identity
NCBI Description (AL022223) putative protein [Arabidopsis thaliana]
Seq. No.
                   295055
Seq. ID
                  LIB3075-019-Q1-K1-G4
Method
                   BLASTX
NCBI GI
                   q3281853
BLAST score
                   186
E value
                   6.0e-14
Match length
                   62
% identity
                   58
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]
Seq. No.
                   295056
Seq. ID
                  LIB3075-019-Q1-K1-G7
Method
                  BLASTX
                  g3281853
NCBI GI
BLAST score
                  265
```

E value 3.0e-23 Match length 70 69 % identity

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 295057



```
LIB3075-019-Q1-K1-G8
Seq. ID
                  BLASTX
Method
                  g3660471
NCBI GI
                  158
BLAST score
                  4.0e-11
E value
                  55
Match length
% identity
                   (AJ001809) succinate dehydrogenase flavoprotein alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
                   295058
Seq. No.
                  LIB3075-020-Q1-K1-A5
Seq. ID
                   BLASTX
Method
                   g1169421
NCBI GI
                   300
BLAST score
                   2.0e-27
E value
                   105
Match length
                   59
% identity
                   DEVELOPMENTALLY REGULATED GTP-BINDING PROTEIN DRG (XDRG)
NCBI Description
                   >gi 2120159 pir__I51426 GTP-binding protein DRG - African
                   clawed frog >gi 433422 dbj BAA02978 (D13865) GTP-binding
                   protein DRG [Xenopus laevis]
                   295059
Seq. No.
                   LIB3075-020-Q1-K1-B4
Seq. ID
                   BLASTN
Method
                   g4140643
NCBI GI
BLAST score
                   45
                   5.0e-16
E value
                   81
Match length
% identity
                   Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                   complete sequence
                   295060
Seq. No.
                   LIB3075-020-Q1-K1-B8
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4140643
                   131
BLAST score
                   2.0e-67
 E value
                   410
Match length
 % identity
                   88
                   Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
 NCBI Description
                   complete sequence
 Seq. No.
                   295061
                   LIB3075-020-Q1-K1-C10
 Seq. ID
                   BLASTX
 Method
                   q626029
 NCBI GI
                   257
 BLAST score
```

Method BLASTX
NCBI GI g626029
BLAST score 257
E value 3.0e-22
Match length 63
% identity 73

NCBI Description pollen allergen Lol p XI - perennial ryegrass

>gi_1582249_prf__2118270A allergen Lol p XI [Lolium

perenne]



```
Seq. No.
                  LIB3075-020-Q1-K1-E10
Seq. ID
                  BLASTX
Method
                  q1171005
NCBI GI
                  212
BLAST score
                  6.0e-17
E value
Match length
                  121
                  38
% identity
                  MAJOR POLLEN ALLERGEN HOL L 1 PRECURSOR (HOL L I)
NCBI Description
                  >gi 1085628 pir__S38581 allergen Hol-II - Holcus lanatus
                   >gi 414703 emb CAA81610 (Z27084) allergen Hol-II [Holcus
                   lanatus]
                   295063
Seq. No.
                  LIB3075-020-Q1-K1-E5
Seq. ID
                   BLASTN
Method
                   g3452297
NCBI GI
                   56
BLAST score
                   1.0e-22
E value
                   274
Match length
                   86
% identity
NCBI Description Zea mays retrotransposon Ji-4 5' LTR, partial sequence
                   295064
Seq. No.
                   LIB3075-020-Q1-K1-G4
Seq. ID
                   BLASTX
Method
                   g4490330
NCBI GI
                   638
BLAST score
                   8.0e-67
E value
                   149
Match length
% identity
                   (AL035656) splicing factor-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   295065
Seq. No.
Seq. ID
                   LIB3075-020-Q1-K1-H4
                   BLASTX
Method
NCBI GI
                   g4218991
                   166
BLAST score
                   2.0e-11
E value
                   59
Match length
 % identity
NCBI Description (AF098632) subtilisin-like protease [Arabidopsis thaliana]
                   295066
 Seq. No.
                   LIB3075-021-Q1-K1-A11
 Seq. ID
                   BLASTX
 Method
                   g4539351
 NCBI GI
 BLAST score
                   334
                   3.0e-31
 E value
 Match length
                   138
```

% identity NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. ID

295067 Seq. No. LIB3075-021-Q1-K1-A8

50

BLASTN Method

E value

2.0e-17



```
g4140643
NCBI GI
BLAST score
                  70
                  5.0e-31
E value
                  94
Match length
                  94
% identity
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                  complete sequence
                  295068
Seq. No.
                  LIB3075-021-Q1-K1-B6
Seq. ID
Method
                  BLASTX
                  g3378527
NCBI GI
                  335
BLAST score
                  2.0e-31
E value
                  101
Match length
% identity
NCBI Description (AJ224355) anther specific protein [Zea mays]
                  295069
Seq. No.
                  LIB3075-021-Q1-K1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1184776
                  586
BLAST score
                  8.0e-61
E value
                  116
Match length
                   97
% identity
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
                  GAPC4 [Zea mays]
Seq. No.
                   295070
                  LIB3075-021-Q1-K1-E8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3758826
BLAST score
                   41
                   1.0e-13
E value
Match length
                   89
                   87
% identity
                  Hordeum vulgare mRNA for putative amino acid selective
NCBI Description
                   channel protein
Seq. No.
                   295071
                   LIB3075-021-Q1-K1-F8
Seq. ID
Method
                   BLASTX
                   g629852
NCBI GI
                   451
BLAST score
                   6.0e-45
E value
                   133
Match length
% identity
                   74
                  polygalacturonase - maize >gi_288367_emb_CAA46680_ (X65845)
NCBI Description
                   polygalacturonase [Zea mays]
                   295072
Seq. No.
                   LIB3075-021-Q1-K1-F9
Seq. ID
                   BLASTX
Method
                   g99808
NCBI GI
BLAST score
                   212
```

1.142



```
Match length
% identity
                  gene Bp10 protein - rape >gi_17797_emb_CAA47178 (X66609)
NCBI Description
                  Bplo [Brassica napus]
                  295073
Seq. No.
                  LIB3075-021-Q1-K1-H5
Seq. ID
                  BLASTX
Method
                  q1076511
NCBI GI
                  515
BLAST score
                  2.0e-52
E value
                  146
Match length
                   68
% identity
                  H+-transporting ATPase (EC 3.6.1.35) - kidney bean
NCBI Description
                   >gi_758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase
                   [Phaseolus vulgaris]
                   295074
Seq. No.
                   LIB3075-022-Q1-K1-B11
Seq. ID
                   BLASTN
Method
                   g22458
NCBI GI
                   46
BLAST score
                   6.0e-17
E value
                   74
Match length
                   91
% identity
                  Z.mays pollen specific mRNA C-terminal (clone 4H7)
NCBI Description
                   295075
Seq. No.
                   LIB3075-022-Q1-K1-E4
Seq. ID
                   BLASTX
Method
                   q4581150
NCBI GI
                   142
BLAST score
                   4.0e-09
E value
Match length
                   61
% identity
                   (AC006919) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   295076
Seq. No.
Seq. ID
                   LIB3075-022-Q1-K1-F1
                   BLASTX
Method
                   q3492806
NCBI GI
BLAST score
                   148
                   8.0e-10
E value
Match length
                   60
 % identity
                   (AJ225045) adventitious rooting related oxygenase [Malus
 NCBI Description
                   domestica]
                   295077
 Seq. No.
                   LIB3075-022-Q1-K1-F6
 Seq. ID
                   BLASTX
 Method
                   g3212854
 NCBI GI
 BLAST score
                   152
 E value
                   3.0e-10
                   50
 Match length
                   58
 % identity
                   (AC004005) unknown protein [Arabidopsis thaliana]
 NCBI Description
```

Seq. No.

Seq. ID

Method

295083

BLASTX

LIB3075-023-Q1-K1-E9



```
Seq. No.
                  295078
Seq. ID
                  LIB3075-022-Q1-K1-F8
Method
                  BLASTN
NCBI GI
                  g4140643
BLAST score
                  59
E value
                  2.0e-24
Match length
                  107
% identity
                  89
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
                  complete sequence
Seq. No.
                  295079
Seq. ID
                  LIB3075-022-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g4586242
BLAST score
                  261
E value
                  1.0e-25
Match length
                  96
                  67
% identity
NCBI Description (AL049640) putative protein (fragment) [Arabidopsis
                  thaliana]
Seq. No.
                  295080
Seq. ID
                  LIB3075-023-Q1-K1-B10
Method
                  BLASTN
NCBI GI
                  g4206305
BLAST score
                  45
                  3.0e-16
E value
Match length
                  174
% identity
                  80
NCBI Description Zea mays retrotransposon Cinful-1, complete sequence
                  295081
Seq. No.
                  LIB3075-023-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4512667
BLAST score
                  201
E value
                  2.0e-23
Match length
                  101
% identity
                  58
NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]
                  295082
Seq. No.
Seq. ID
                  LIB3075-023-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g3249105
BLAST score
                  438
E value
                  2.0e-43
                  134
Match length
                  59
% identity
NCBI Description (AC003114) Contains similarity to protein phosphatase 2C
                  (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]
```



```
g3548810
NCBI GI
BLAST score
                  182
E value
                  2.0e-13
Match length
                  119
                   40
% identity
                  (AC005313) putative chloroplast nucleoid DNA binding
NCBI Description
                  protein [Arabidopsis thaliana]
                  295084
Seq. No.
Seq. ID
                  LIB3075-023-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  q3935150
BLAST score
                  157
                  4.0e-11
E value
Match length
                  49
% identity
                   61
NCBI Description (AC005106) T25N20.14 [Arabidopsis thaliana]
                  295085
Seq. No.
Seq. ID
                  LIB3075-023-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  q3093294
BLAST score
                  194
E value
                   6.0e-15
Match length
                  95
% identity
                   48
                  (Y12782) putative villin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  295086
                  LIB3075-023-Q1-K1-G5
Seq. ID
                  BLASTX
Method
                  g422032
NCBI GI
BLAST score
                  152
E value
                   2.0e-12
                  79
Match length
% identity
                  56
NCBI Description
                  profilin 2 - maize >gi_313140_emb_CAA51719_ (X73280)
                  profilin 2 [Zea mays]
Seq. No.
                   295087
Seq. ID
                  LIB3075-024-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                   g3193316
BLAST score
                   233
                   3.0e - 30
E value
Match length
                  117
% identity
                   61
                  (AF069299) contains similarity to nucleotide sugar
NCBI Description
                  epimerases [Arabidopsis thaliana]
Seq. No.
                   295088
Seq. ID
                  LIB3075-025-Q1-K1-A10
```

BLASTX Method

NCBI GI g1763711 BLAST score 149 E value 2.0e-09 Match length 101



% identity (Z83337) similar to B. subtilis YcsE hypothetical protein NCBI Description [Bacillus subtilis] >gi_2636154_emb_CAB15646.1_ (Z99122) similar to hypothetical proteins [Bacillus subtilis] 295089 Seq. No. Seq. ID LIB3075-025-Q1-K1-C1 BLASTX Method q112994 NCBI GI 330 BLAST score 5.0e-31 E value 74 Match length % identity GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN NCBI Description >gi 82685 pir__S04536 embryonic abundant protein, glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564) ABA-inducible gene protein [Zea mays] >gi_226091_prf__1410284A abscisic acid inducible gene [Zea mays] 295090 Seq. No. LIB3075-025-Q1-K1-E11 Seq. ID BLASTX Method q4325045 NCBI GI 243 BLAST score 1.0e-20 E value 126 Match length 46 % identity (AF117660) S-adenosylmethionine decarboxylase precursor NCBI Description [Triticum aestivum] 295091 Seq. No. Seq. ID LIB3075-025-Q1-K1-E2 BLASTX Method g2983448 NCBI GI 175 BLAST score 5.0e-28 E value Match length 127 % identity (AE000714) cell division protein FtsH [Aquifex aeolicus] NCBI Description 295092 Seq. No. Seq. ID LIB3075-025-Q1-K1-G1 Method BLASTX q3891593 NCBI GI BLAST score 585 1.0e-60 E value 112 Match length % identity 100 NCBI Description Structure Of Glutathione S-Transferase Iii In Apo Form 295093 Seq. No. LIB3075-025-Q1-K1-H6 Seq. ID Method BLASTX

· .

Method BLASTX
NCBI GI g2245021
BLAST score 327
E value 2.0e-30



```
135
Match length
                  54
% identity
                  (Z97341) heat shock protein 110 homolog [Arabidopsis
NCBI Description
                  thaliana]
                  295094
Seq. No.
                  LIB3075-026-Q1-K1-B1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22458
BLAST score
                  118
                  6.0e-60
E value
                  214
Match length
                  89
% identity
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)
                  295095
Seq. No.
                  LIB3075-026-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1171005
BLAST score
                  143
E value
                   2.0e-14
Match length
                  106
% identity
                   41
                  MAJOR POLLEN ALLERGEN HOL L 1 PRECURSOR (HOL L I)
NCBI Description
                   >gi_1085628_pir__S38581 allergen Hol-II - Holcus lanatus
                   >gi 414703 emb CAA81610 (Z27084) allergen Hol-II [Holcus
                   lanatus]
                   295096
Seq. No.
                   LIB3075-026-Q1-K1-E12
Seq. ID
                   BLASTX
Method
                   g464470
NCBI GI
                   362
BLAST score
                   1.0e-34
E value
Match length
                   85
                   80
% identity
                  PROFILIN 3 >gi 422033 pir S35798 profilin 3 - maize
NCBI Description
                   >gi_313142_emb_CAA51720_ (X73281) profilin 3 [Zea mays]
                   295097
Seq. No.
                   LIB3075-026-Q1-K1-E2
Seq. ID
                   BLASTX
Method
                   g3551838
NCBI GI
BLAST score
                   174
                   9.0e-13
E value
                   83
Match length
                   43
% identity
NCBI Description (AF070967) SKP1-like protein [Nicotiana clevelandii]
                   295098
Seq. No.
                   LIB3075-026-Q1-K1-E6
Seq. ID
                   BLASTX
Method
                   q4490704
NCBI GI
BLAST score
                   437
E value
                   3.0e-43
```

41261

102

82

Match length

% identity



```
NCBI Description
                  (AL035680) putative protein [Arabidopsis thaliana]
                  295099
Seq. No.
Seq. ID
                  LIB3075-026-Q1-K1-E9
Method
                  BLASTN
NCBI GI
                  g313141
BLAST score
                  40
E value
                  2.0e-13
Match length
                  64
% identity
                  91
NCBI Description Z.mays ZmPRO3 mRNA for profilin
                  295100
Seq. No.
Seq. ID
                  LIB3075-026-Q1-K1-F9
                  BLASTX
Method
NCBI GI
                  g3935167
BLAST score
                  165
                  9.0e-12
E value
Match length
                  63
                  52
% identity
NCBI Description (AC004557) F17L21.10 [Arabidopsis thaliana]
Seq. No.
                  295101
                  LIB3075-026-Q1-K1-G11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g603189
BLAST score
                  60
E value
                  3.0e-25
Match length
                  180
% identity
                  84
                  Zea mays translation initiation factor eIF-4A mRNA,
NCBI Description
                  complete cds
                  295102
Seq. No.
                  LIB3075-026-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112994
                  303
BLAST score
                  7.0e-28
E value
Match length
                  72
% identity
                  83
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi 22313 emb CAA31077 (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi 226091 prf _1410284A abscisic acid inducible gene [Zea
                  mays]
Seq. No.
                  295103
Seq. ID
                  LIB3075-026-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g2980770
                  230
BLAST score
E value
                  4.0e-19
Match length
                  77
% identity
                  57
```

NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]



```
295104
Seq. No.
                   LIB3075-027-Q1-K1-C11
Seq. ID
Method
                  BLASTX
                   q2500195
NCBI GI
                   292
BLAST score
                   3.0e-26
E value
```

116

57

% identity NCBI Description RAC-LIKE GTP BINDING PROTEIN RHO1 >gi 974780 emb CAA89050

(Z49191) small G protein [Beta vulgaris]

295105 Seq. No.

Match length

LIB3075-027-Q1-K1-D5 Seq. ID

Method BLASTX NCBI GI g4587554 BLAST score 289 E value 6.0e-26 Match length 84 % identity 61

(AC006577) Similar to gb AJ005701 Na/Ca, K-exchanger from NCBI Description

Caenorhabditis elegans. ESTs gb T04173 and gb AA585918

come from this gene. [Arabidopsis thaliana]

295106 Seq. No.

Seq. ID LIB3075-027-Q1-K1-E11

Method BLASTX NCBI GI q1781115 BLAST score 152 E value 6.0e-10 49 Match length

55 % identity

NCBI Description (Z83864) glpQ1 [Mycobacterium tuberculosis]

Seq. No. 295107

Seq. ID LIB3075-027-Q1-K1-G6

Method BLASTX NCBI GI q3258569 BLAST score 218 9.0e-18 E value 79 Match length % identity 61

(U89959) Similar to yeast general negative regulator of NCBI Description

transcription subunit 1 [Arabidopsis thaliana]

295108 Seq. No.

Seq. ID LIB3075-027-Q1-K1-G7

Method BLASTX q2129575 NCBI GI BLAST score 160 E value 5.0e-11 77 Match length % identity 47

NCBI Description DNA repair protein homolog XPBara - Arabidopsis thaliana

295109 Seq. No.

LIB3075-028-Q1-K1-A10 Seq. ID



```
Method
                  BLASTX
NCBI GI
                  g2127768
BLAST score
                  158
E value
                  1.0e-10
Match length
                  66
% identity
                  48
                  arsenical pump-driving ATPase homolog - Methanococcus
NCBI Description
                  jannaschii >gi 1591774 (U67556) arsenical pump-driving
                  ATPase (arsA) [Methanococcus jannaschii]
                  295110
Seq. No.
Seq. ID
                  LIB3075-028-Q1-K1-B5
                  BLASTX
```

Method NCBI GI q629852 BLAST score 396 1.0e-38 E value 87 Match length % identity 89

NCBI Description polygalacturonase - maize >gi 288367 emb_CAA46680_ (X65845)

polygalacturonase [Zea mays]

Seq. No. 295111 LIB3075-028-Q1-K1-C2 Seq. ID Method BLASTX q4505291 NCBI GI

BLAST score 142 E value 8.0e-09 Match length 103 % identity

NCBI Description myxovirus (influenza) resistance 1, homolog of murine

(interferon-inducible protein p78)

>gi 127566 sp P20591 MX1 HUMAN INTERFERON-REGULATED RESISTANCE GTP-BINDING PROTEIN MXA (INTERFERON-INDUCED PROTEIN P78) (IFI-78K) >gi 190136 (M33882) p78 protein

[Homo sapiens]

295112 Seq. No.

LIB3075-028-Q1-K1-C7 Seq. ID

Method BLASTX NCBI GI a399334 BLAST score 173 E value 4.0e-21 Match length 64 % identity 66

CYSTATIN I PRECURSOR (CORN KERNEL CYSTEINE PROTEINASE NCBI Description

INHIBITOR) >gi_322868 pir_S27239 cysteine proteinase
inhibitor - maize >gi_217962 dbj_BAA01472 (D10622) corn
cystatin I [Zea mays]

Seq. No. 295113

Seq. ID LIB3075-028-Q1-K1-D2

Method BLASTX NCBI GI q3451074 BLAST score 252 E value 5.0e-22 Match length 83 % identity 63

% identity

NCBI Description

51





```
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]
Seq. No.
                  295114
                  LIB3075-028-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3236250
BLAST score
                  158
E value
                  9.0e-11
                  47
Match length
% identity
                  60
NCBI Description (AC004684) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  295115
Seq. ID
                  LIB3075-028-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  q548492
BLAST score
                  270
E value
                  8.0e-24
Match length
                  128
% identity
                  45
NCBI Description EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
                  (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi_629853 pir__S30066 polygalacturonase - maize
                  >gi 288379_emb_CAA45751_ (X64408) polygalacturonase [Zea
                  mays]
                  295116
Seq. No.
                  LIB3075-029-Q1-K1-A12
Seq. ID
Method
                  BLASTX
                  q4138262
NCBI GI
BLAST score
                  236
E value
                  3.0e-20
Match length
                  80
% identity
                  62
NCBI Description (Y08161) aquaporin 1 [Nicotiana tabacum]
                  295117
Seq. No.
Seq. ID
                  LIB3075-029-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g2832695
BLAST score
                  217
                  1.0e-17
E value
Match length
                  105
% identity
                  46
NCBI Description (AL021713) putative protein [Arabidopsis thaliana]
                  295118
Seq. No.
                  LIB3075-029-Q1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3860256
BLAST score
                  202
                  6.0e-16
E value
Match length
                  85
```

transferase [Arabidopsis thaliana]

(AC005824) putative tRNA isopentenylpyrophosphate



```
Seq. No.
Seq. ID
                  LIB3075-029-Q1-K1-E1
                  BLASTN
Method
                  g5091496
NCBI GI
                  44
BLAST score
                  1.0e-15
E value
Match length
                  64
                  92
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
                  complete sequence
                  295120
Seq. No.
                  LIB3075-029-Q1-K1-E4
Seq. ID
                  BLASTN
Method
                  g22458
NCBI GI
                  201
BLAST score
                  1.0e-109
E value
                  293
Match length
                   92
% identity
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)
                   295121
Seq. No.
                  LIB3075-029-Q1-K1-E6
Seq. ID
                  BLASTX
Method
                   g2623299
NCBI GI
                   170
BLAST score
                   3.0e-12
E value
                   65
Match length
% identity
NCBI Description (AC002409) hypothetical protein [Arabidopsis thaliana]
                   295122
Seq. No.
                   LIB3075-029-Q1-K1-E9
Seq. ID
                   BLASTX
Method
                   q1084457
NCBI GI
                   322
BLAST score
                   9.0e-30
E value
                   139
Match length
                   51
% identity
                   elongation factor 1-beta - Rice >gi_432368_dbj_BAA04903_
NCBI Description
                   (D23674) elongation factor 1 beta [Oryza sativa]
                   295123
Seq. No.
                   LIB3075-030-Q1-K1-A10
Seq. ID
                   BLASTX
Method
                   q4510345
NCBI GI
                   149
BLAST score
                   1.0e-09
E value
Match length
                   43
 % identity
                   (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                   295124
 Seq. No.
                   LIB3075-030-Q1-K1-D3
 Seq. ID
 Method
                   BLASTX
```

41266

g1170373

321

NCBI GI BLAST score



E value 4.0e-30 Match length 83 % identity 78

NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70

. 4

cognate [Arabidopsis thaliana]

Seq. No. 295125

Seq. ID LIB3075-030-Q1-K1-E10

Method BLASTN
NCBI GI g2062705
BLAST score 36
E value 9.0e-11
Match length 40
% identity 97

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.

Seq. ID LIB3075-030-Q1-K1-E7

295126

Method BLASTX
NCBI GI g3107931
BLAST score 227
E value 5.0e-19
Match length 81
% identity 64

NCBI Description (AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]

Seq. No. 295127

Seq. ID LIB3075-030-Q1-K1-F1

Method BLASTX
NCBI GI g1134882
BLAST score 300
E value 3.0e-27
Match length 86
% identity 64

NCBI Description (Z68291) cysteine protease [Pisum sativum]

Seq. No. 295128

Seq. ID LIB3075-031-Q1-K1-B5

Method BLASTX
NCBI GI g2462745
BLAST score 174
E value 2.0e-12
Match length 73
% identity 44

NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 295129

Seq. ID LIB3075-031-Q1-K1-C1

Method BLASTX
NCBI GI g2245131
BLAST score 154
E value 3.0e-10
Match length 62
% identity 53

NCBI Description (297344) hypothetical protein [Arabidopsis thaliana]



Seq. No. 295130

Seq. ID LIB3075-032-Q1-K1-B3

Method BLASTX
NCBI GI g113621
BLAST score 162
E value 6.0e-20
Match length 85
% identity 69

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A

cytoplasmic aldolase [Zea mays]

Seq. No. 295131

Seq. ID LIB3075-032-Q1-K1-C11

Method BLASTX
NCBI GI g1706261
BLAST score 428
E value 3.0e-42
Match length 121
% identity 74

NCBI Description CYSTEINE PROTEINASE 2 PRECURSOR >gi 2118129 pir S59598

cysteine proteinase 2 precursor - maize

>gi 644490 dbj BAA08245 (D45403) cysteine proteinase [Zea

mays]

Seq. No. 295132

Seq. ID LIB3075-032-Q1-K1-C12

Method BLASTX
NCBI GI g1076791
BLAST score 438
E value 1.0e-43
Match length 110
% identity 74

NCBI Description calcium-binding protein - maize >gi_2119370_pir__\$58170

Calreticulin precursor - maize >gi 577612_emb CAA86728

(Z46772) calcium-binding protein [Zea mays]

>gi_927572_emb_CAA61939_ (X89813) Calreticulin precursor
[Zea mays] >gi_1587033 prf 2205314A calreticulin [Zea

mays]

Seq. No. 295133

Seq. ID LIB3075-032-Q1-K1-G6

Method BLASTX
NCBI GI 93355486
BLAST score 208
E value 1.0e-16
Match length 93
% identity 54

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 295134

Seq. ID LIB3075-033-Q1-K1-A12

Method BLASTX



```
NCBI GI
                  g4263787
BLAST score
                  179
E value
                  2.0e-13
Match length
                  80
% identity
                  46
NCBI Description (AC006068) unknown protein [Arabidopsis thaliana]
                  295135
Seq. No.
Seq. ID
                  LIB3075-033-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g90626
BLAST score
                  143
E value
                  1.0e-10
                  77
Match length
                  53
% identity
NCBI Description histone H4 (clone 53) - mouse >gi_51311_emb_CAA31622_
                  (X13236) histone H4 (AA 1 - 103) [Mus musculus]
Seq. No.
                  295136
Seq. ID
                  LIB3075-033-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  q3093294
BLAST score
                  322
E value
                  8.0e-30
Match length
                  147
% identity
                  53
NCBI Description (Y12782) putative villin [Arabidopsis thaliana]
Seq. No.
                  295137
                  LIB3075-033-Q1-K1-E9
Seq. ID
Method
                  BLASTN
                  g288611
NCBI GI
BLAST score
                  169
E value
                  4.0e-90
                  365
Match length
% identity
                  87
NCBI Description Z.mays PG gene for polygalacturonase
Seq. No.
                  295138
Seq. ID
                  LIB3075-033-Q1-K1-F1
                  BLASTX
Method
NCBI GI
                  g2443755
BLAST score
                  188
E value
                  3.0e-14
Match length
                  73
% identity
                  60
NCBI Description (AF020433) cyclophilin [Arabidopsis thaliana]
Seq. No.
                  295139
                  LIB3075-033-Q1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g464863
BLAST score
                  216
E value
                  6.0e-18
Match length
                  65
% identity
                  71
```

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 8 (TAT-BINDING PROTEIN



HOMOLOG 10) >gi_422297_pir__JN0610 probable transcription factor DdTBP10 - slime mold (Dictyostelium discoideum) (fragment) >gi 290057 (L16579) HIV1 TAT-binding protein [Dictyostelium discoideum]

Seq. No. 295140 Seq. ID LIB3075-034-Q1-K1-A10 Method BLASTX NCBI GI g2832691 BLAST score 204 7.0e-19

E value Match length 102 % identity 47

(AL021713) polygalacturonase-like protein [Arabidopsis NCBI Description

thalianal

Seq. No. 295141

LIB3075-034-Q1-K1-A8 Seq. ID

Method BLASTX NCBI GI g4432860 BLAST score 164 E value 3.0e-11Match length 107 % identity 16

NCBI Description (AC006300) putative glucose-induced repressor protein

[Arabidopsis thaliana]

Seq. No. 295142

Seq. ID LIB3075-034-Q1-K1-B3

Method BLASTX NCBI GI g1076820 BLAST score 148 E value 1.0e-09 105 Match length

43 % identity

NCBI Description phosphoglycerate mutase (EC 5.4.2.1) - maize

Seq. No. 295143

LIB3075-034-Q1-K1-B4 Seq. ID

Method BLASTX NCBI GI q548492 BLAST score 232 E value 2.0e-19 Match length 102 % identity 45

EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE) NCBI Description

(GALACTURAN 1,4-ALPHA-GALACTURONIDASE)

>gi 629853 pir S30066 polygalacturonase - maize

>gi 288379 emb_CAA45751 (X64408) polygalacturonase [Zea

mays]

Seq. No. 295144

Seq. ID LIB3075-034-Q1-K1-E9

Method BLASTX NCBI GI g4539320 BLAST score 491 1.0e-49 E value

Method

NCBI GI

BLAST score

BLASTN

49

q829147



```
Match length
                  131
% identity
                  (AL035679) putative endo-1, 4-beta-glucanase [Arabidopsis
NCBI Description
                  thaliana]
                  295145
Seq. No.
                  LIB3075-035-Q1-K1-B10
Seq. ID
Method
                  BLASTN
                  g22418
NCBI GI
BLAST score
                  53
                  4.0e-21
E value
Match length
                  193
% identity
                  82
NCBI Description Z.mays gene for polygalacturonase (clone 17)
                  295146
Seq. No.
Seq. ID
                  LIB3075-035-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g112994
BLAST score
                  324
E value
                  2.0e-30
Match length
                  70
                  93
% identity
NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
                  >gi 82685 pir S04536 embryonic abundant protein,
                  glycine-rich - maize >gi 22313 emb CAA31077 (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi_226091_prf__1410284A abscisic acid inducible gene [Zea
                  mays]
Seq. No.
                  295147
Seq. ID
                  LIB3075-040-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  g3096927
                  287
BLAST score
E value
                  2.0e-32
                  119
Match length
% identity
                  66
NCBI Description (AL023094) putative protein [Arabidopsis thaliana]
                  295148
Seq. No.
Seq. ID
                  LIB3075-040-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g283050
                  170
BLAST score
E value
                  9.0e-21
Match length
                  83
                  73
% identity
NCBI Description polygalacturonase (EC 3.2.1.15) precursor (clone W2265) -
                  maize (fragment) >gi 22428 emb CAA44247 (X62383)
                  polygalacturonase [Zea mays]
Seq. No.
                  295149
Seq. ID
                  LIB3075-040-Q1-K1-B6
```



E value 5.0e-19 Match length 128 % identity 85

NCBI Description Z.mays gene for cyclophilin

Seq. No.

295150

Seq. ID

LIB3075-040-Q1-K1-D9

Method BLASTX
NCBI GI g2137216
BLAST score 189
E value 2.0e-14
Match length 98
% identity 39

NCBI Description cellular nucleic acid binding protein clone 6 - mouse

>gi_50471_emb_CAA45345_ (X63866) cellular nucleic acid

binding protein clone 6 [Mus musculus]

>gi_50473_emb_CAA77896_ (Z11870) cellular nucleic acid

binding protein clone 6 [Mus musculus]

Seq. No. 295151

Seq. ID LIB3075-041-Q1-K1-B4

Method BLASTX
NCBI GI g2190419
BLAST score 253
E value 7.0e-22
Match length 116
% identity 44

NCBI Description (Y13632) dem [Lycopersicon esculentum]

Seq. No. 295152

Seq. ID LIB3075-041-Q1-K1-C5

Method BLASTX
NCBI GI g1946356
BLAST score 317
E value 3.0e-29
Match length 114
% identity 47

NCBI Description (U93215) hypothetical protein H1.2flk [Arabidopsis

thaliana] >gi 2880041 (AC002340) hypothetical protein

H1.2flk [Arabidopsis thaliana]

Seq. No. 295153

Seq. ID LIB3075-041-Q1-K1-D4

Method BLASTX
NCBI GI g129940
BLAST score 193
E value 1.0e-21
Match length 83

% identity 67

NCBI Description EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)

(GALACTURAN 1,4-ALPHA-GALACTURONIDASE)

>gi_100911_pir__S18570 polygalacturonase (EC 3.2.1.15)
precursor - maize >gi_22417_emb_CAA40850_ (X57627)
polygalacturonase [Zea mays] >gi_22419_emb_CAA44249_

(X62385) polygalacturonase [Zea mays]

>gi 288374 emb CAA46679 (X65844) polygalacturonase [Zea

mays]



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```
295154
Seq. No.
                  LIB3075-041-Q1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q283050
BLAST score
                  234
E value
                  8.0e-20
Match length
                  56
% identity
                  86
NCBI Description
                  polygalacturonase (EC 3.2.1.15) precursor (clone W2265) -
                  maize (fragment) >gi_22428_emb_CAA44247_ (X62383)
                  polygalacturonase [Zea mays]
Seq. No.
                  295155
                  LIB3075-041-Q1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3421378
BLAST score
                  143
E value
                  5.0e-09
Match length
                  58
% identity
                  47
NCBI Description (AF080249) kinesin-like heavy chain [Arabidopsis thaliana]
Seq. No.
                  295156
Seq. ID
                  LIB3075-041-Q1-K1-F5
Method
                  BLASTN
NCBI GI
                  g829147
BLAST score
                  110
E value
                  4.0e-55
Match length
                  233
                  87
% identity
NCBI Description Z.mays gene for cyclophilin
                  295157
Seq. No.
                  LIB3075-041-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4335731
BLAST score
                  215
                  2.0e-17
E value
Match length
                  100
% identity
                   45
                  (AC006248) putative polyprotein [Arabidopsis thaliana]
NCBI Description
                   295158
Seq. No.
Seq. ID
                  LIB3075-042-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  q1702988
BLAST score
                  161
                   4.0e-11
E value
Match length
                  73
                   42
% identity
```

Seq. No. 295159

NCBI Description

upsilon chain [Arabidopsis thaliana]

GF14 upsilon [Arabidopsis thaliana]

14-3-3-LIKE PROTEIN GF14 UPSILON >gi 1508785 (L09109) GF14

>gi_2232148_gb_AAB62225_ (AF001415) 14-3-3-like protein

Seq. No.

295164



```
LIB3075-042-Q1-K1-D11
Seq. ID
Method
                    BLASTX
NCBI GI
                    g4006978
BLAST score
                    180
E value
                    3.0e-13
Match length
                    107
% identity
                    37
NCBI Description (AJ131335) pollen allergen (group II) [Cynodon dactylon]
Seq. No.
                   295160
                   LIB3075-042-Q1-K1-D4
Seq. ID
Method
                   BLASTX
                   q283049
NCBI GI
BLAST score
                   173
E value
                    7.0e-13
Match length
                    55
% identity
                    67
                   polygalacturonase (EC 3.2.1.15) precursor (clone W2247) -
NCBI Description
                   maize (fragment) >gi_481079_pir__S37718 polygalacturonase -maize >gi_22426_emb_CAA44248 (X62384) polygalacturonase [Zea mays] >gi_287830_emb_CAA47234 (X66692)
                   polygalacturonase [Zea mays]
Seq. No.
                   295161
Seq. ID
                   LIB3075-042-Q1-K1-D5
Method
                   BLASTX
NCBI GI
                   q4191797
BLAST score
                   189
E value
                    2.0e-14
Match length
                   103
% identity
NCBI Description
                   (AC005917) putative receptor protein kinase, 3' partial
                    [Arabidopsis thaliana]
Seq. No.
                    295162
Seq. ID
                   LIB3075-042-Q1-K1-G7
Method
                    BLASTX
NCBI GI
                    g1575705
BLAST score
                    142
                    5.0e-09
E value
                    39
Match length
% identity
                    62
NCBI Description
                   (U70480) abscission polygalacturonase [Lycopersicon
                    esculentum] >gi_2459813 (AF001001) polygalacturonase 2
                    [Lycopersicon esculentum]
Seq. No.
                    295163
Seq. ID
                   LIB3075-043-Q1-K1-C3
Method
                   BLASTX
NCBI GI
                   g3372671
BLAST score
                    327
E value
                    2.0e-30
Match length
                   89
% identity
                    66
NCBI Description (AF061286) gamma-adaptin 1 [Arabidopsis thaliana]
```

NCBI GI

BLAST score

q4027901

152



```
LIB3075-043-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454484
BLAST score
                   355
                   1.0e-42
E value
Match length
                  115
% identity
NCBI Description
                  (AC006234) putative diacylglycerol kinase [Arabidopsis
                  thaliana]
Seq. No.
                   295165
                  LIB3075-043-Q1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g542036
BLAST score
                  239
                   4.0e-20
E value
                  72
Match length
                  65
% identity
NCBI Description TDR8 protein ~ tomato >gi_19388_emb_CAA43172_ (X60760) TDR8
                   [Lycopersicon esculentum]
                  295166
Seq. No.
                  LIB3075-043-Q1-K1-G2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q248336
BLAST score
                  180
E value
                  9.0e-97
Match length
                  245
% identity
                  80
NCBI Description polyubiquitin [maize, Genomic, 3841 nt]
                  295167
Seq. No.
                  LIB3075-043-Q1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g320553
BLAST score
                  221
E value
                  4.0e-18
Match length
                  63
                   67
% identity
NCBI Description
                  anthranilate synthase (EC 4.1.3.27) alpha-2 chain -
                  Arabidopsis thaliana
                   295168
Seq. No.
Seq. ID
                   LIB3075-044-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  g2130133
BLAST score
                   342
E value
                  2.0e-37
Match length
                  78
                  91
% identity
NCBI Description heat shock factor (clone hsfa) - maize (fragment)
Seq. No.
                   295169
Seq. ID
                  LIB3075-044-Q1-K1-E11
Method
                  BLASTX
```



```
4.0e-10
E value
                  51
Match length
                  51
% identity
                  (AF049355) alpha-expansin precursor [Nicotiana tabacum]
NCBI Description
                  295170
Seq. No.
                  LIB3075-045-Q1-K1-B7
Seq. ID
                  BLASTX
Method
                  q3493019
NCBI GI
                  231
BLAST score
                   2.0e-19
E value
                   91
Match length
                   57
% identity
                   (AF079247) granule-bound starch synthase [Cymbopogon
NCBI Description
                   commutatus]
                   295171
Seq. No.
Seq. ID
                   LIB3075-045-Q1-K1-D1
                   BLASTX
Method
                   g2444180
NCBI GI
                   392
BLAST score
                   5.0e-38
E value
                   136
Match length
                   55
% identity
NCBI Description (U94785) unconventional myosin [Helianthus annuus]
                   295172
Seq. No.
Seq. ID
                   LIB3075-045-Q1-K1-D10
                   BLASTX
Method
                   g442691
NCBI GI
                   191
BLAST score
                   8.0e-15
E value
                   90
Match length
% identity
                   47
                   Beta-Amylase (E.C.3.2.1.2) Complex With Alpha-Cyclodextrin
NCBI Description
                   (Alpha-14-Maltohydrolase)
                   295173
Seq. No.
                   LIB3075-045-Q1-K1-D3
Seq. ID
                   BLASTX
Method
                   g2498576
NCBI GI
BLAST score
                   321
E value
                   5.0e-30
Match length
                   90
                   62
 % identity
                   MAJOR POLLEN ALLERGEN PHA A 1 PRECURSOR (PHA A I)
NCBI Description
                   >gi 1246116_bbs_174854 (S80654) major allergen Pha a 1
                   [Phalaris aquatica=canary grass, pollen, Peptide, 269 aa]
                   [Phalaris aquatica]
                   295174
 Seq. No.
                   LIB3075-045-Q1-K1-D5
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q3088646
                   198
 BLAST score
                   1.0e-15
 E value
```

88

Match length

NCBI GI

E value

BLAST score

Match length



```
% identity
                  (AF056493) pectin methylesterase [Pisum sativum]
NCBI Description
                  >gi 3426335 (AF081457) pectin methylesterase [Pisum
                  sativum]
                  295175
Seq. No.
                  LIB3075-045-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4417267
BLAST score
                  208
E value
                  2.0e-16
Match length
                  117
                  37
% identity
NCBI Description (AC007019) hypothetical protein [Arabidopsis thaliana]
                  295176
Seq. No.
Seq. ID
                  LIB3075-045-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g544421
BLAST score
                  251
                  5.0e-22
E value
                  58
Match length
% identity
                  90
NCBI Description
                  GLYCINE-RICH RNA-BINDING PROTEIN 1 >gi 485420 pir S12311
                  glycine-rich RNA-binding protein (clone S1) - sorghum
                  (fragment) >gi 21623 emb CAA40863 (X57663) glycine-rich
                  RNA-binding protein [Sorghum bicolor]
Seq. No.
                  295177
                  LIB3075-045-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q541849
BLAST score
                  190
E value
                  2.0e-14
Match length
                  38
                  89
% identity
NCBI Description
                  anthranilate synthase (EC 4.1.3.27) beta chain -
                  Arabidopsis thaliana >gi_403434 (L22585) anthranilate
                  synthase beta subunit [Arabidopsis thaliana]
Seq. No.
                  295178
Seq. ID
                  LIB3075-045-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g100912
BLAST score
                  373
E value
                  7.0e-36
Match length
                  115
                  69
% identity
NCBI Description polygalacturonase (EC 3.2.1.15) - maize
                  295179
Seq. No.
Seq. ID
                  LIB3075-045-Q1-K1-G11
Method
                  BLASTX
```

41277

q4567282

3.0e-17

214



GAPC4 [Zea mays]

% identity

NCBI Description

```
% identity
NCBI Description (AC006841) putative DNAJ protein [Arabidopsis thaliana]
                  295180
Seq. No.
Seq. ID
                  LIB3075-046-Q1-K1-B1
Method
                  BLASTN
                  q22458
NCBI GI
                  186
BLAST score
                  1.0e-100
E value
                  261
Match length
% identity
                  98
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)
                  295181
Seq. No.
                  LIB3075-046-Q1-K1-B3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4558666
BLAST score
                  293
                  2.0e-26
E value
                  116
Match length
% identity
                  (AC007063) putative Na/H antiporter isolog [Arabidopsis
NCBI Description
                  thaliana]
                  295182
Seq. No.
                  LIB3075-046-Q1-K1-C10
Seq. ID
                  BLASTX
Method
                   q2625088
NCBI GI
                   184
BLAST score
                   1.0e-13
E value
                   44
Match length
                   80
% identity
                  (AF030384) ADP-glucose pyrophosphorylase large subunit
NCBI Description
                   [Cucumis melo var. markuwa Markino]
                   295183
Seq. No.
                   LIB3075-046-Q1-K1-C11
Seq. ID
Method
                   BLASTN
                   g415249
NCBI GI
BLAST score
                   235
E value
                   1.0e-129
                   250
Match length
% identity
                   99
                   Zea mays mitochondrial Mn-superoxidase dismutase (Sod3.4)
NCBI Description
                   mRNA, complete cds
                   295184
Seq. No.
                   LIB3075-046-Q1-K1-C9
Seq. ID
                   BLASTX
Method
                   g1184776
NCBI GI
                   536
BLAST score
                   5.0e-55
E value
Match length
                   106
```

(U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase

Match length

NCBI Description

% identity

49



```
Seq. No.
                  LIB3075-046-Q1-K1-D9
Seq. ID
                  BLASTX
Method
                  q1864024
NCBI GI
                  188
BLAST score
                  6.0e-18
E value
Match length
                  80
                  70
% identity
                   (U35683) calcium-binding pollen allergen [Cynodon dactylon]
NCBI Description
                  >gi_1871507_emb_CAA62634_ (X91256) calcium-binding pollen
                  allergen [Cynodon dactylon]
                   295186
Seq. No.
                  LIB3075-046-Q1-K1-E9
Seq. ID
                  BLASTX
Method
                   g3096918
NCBI GI
BLAST score
                   258
                   2.0e-22
E value
Match length
                   101
                   55
% identity
                   (AL023094) putative cyclase associated protein CAP
NCBI Description
                   [Arabidopsis thaliana] >gi_3169136_dbj_BAA28621_ (AB014759)
                   Atcap1 [Arabidopsis thaliana]
                   295187
Seq. No.
                   LIB3075-047-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                   g3004547
NCBI GI
                   377
BLAST score
                   3.0e-36
E value
                   82
Match length
% identity
                   (AC003673) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4185150 (AC005724) unknown protein [Arabidopsis
                   thaliana]
                   295188
Seq. No.
                   LIB3075-047-Q1-K1-C5
Seq. ID
                   BLASTX
Method
                   g1203832
NCBI GI
                   370
BLAST score
E value
                   2.0e-35
Match length
                   127
% identity
                   59
                   (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
NCBI Description
                   [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan
                   exohydrolase [Hordeum vulgare]
Seq. No.
                   295189
                   LIB3075-047-Q1-K1-C8
 Seq. ID
Method
                   BLASTX
                   q4455371
NCBI GI
 BLAST score
                   144
                   4.0e-09
E value
                   73
```

41279

(AL035524) putative protein [Arabidopsis thaliana]

BLAST score

Match length

% identity

E value

191

83

46

2.0e-14



```
295190
Seq. No.
Seq. ID
                  LIB3075-047-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  q676884
BLAST score
                  182
                  2.0e-13
E value
                  60
Match length
                  58
% identity
NCBI Description
                  (D29681) The expression is induced by Pi starvation.
                   [Nicotiana tabacum] >gi_1094819_prf__2106387C Al-induced
                  protein [Nicotiana tabacum]
                  295191
Seq. No.
Seq. ID
                  LIB3075-048-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  g4587518
BLAST score
                  185
E value
                  6.0e-14
                  59
Match length
% identity
                  (AC007060) Strong similarity to F19I3.8 gi_3033381 putative
NCBI Description
                  UDP-galactose-4-epimerase from Arabidopsis thaliana BAC
                  gb AC004238 and is a member of PF 01370 the NAD dependent
                  epimerase/dehydratase family. ES\overline{T} gb AA59
Seq. No.
                  295192
Seq. ID
                  LIB3075-048-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  g283050
BLAST score
                  266
                  1.0e-23
E value
                  93
Match length
                  63
% identity
NCBI Description
                  polygalacturonase (EC 3.2.1.15) precursor (clone W2265) -
                  maize (fragment) >gi_22428_emb_CAA44247_ (X62383)
                  polygalacturonase [Zea mays]
Seq. No.
                  295193
Seq. ID
                  LIB3075-048-Q1-K1-D11
Method
                  BLASTX
                  g3386614
NCBI GI
                  191
BLAST score
E value
                  2.0e-14
Match length
                  76
                  51
% identity
NCBI Description
                  (AC004665) putative transcription factor SF3 [Arabidopsis
                  thaliana]
Seq. No.
                  295194
Seq. ID
                  LIB3075-049-Q1-K1-D8
Method
                  BLASTX
                  g4467137
NCBI GI
```

41280



```
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
                  295195
Seq. No.
                  LIB3075-049-Q1-K1-E1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q288373
BLAST score
                  194
                  1.0e-105
E value
                  260
Match length
                  100
% identity
NCBI Description Z.mays PGg6 gene for polygalacturonase
                   295196
Seq. No.
                  LIB3075-049-Q1-K1-H5
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3548818
BLAST score
                   504
                   4.0e-51
E value
Match length
                   135
                   71
% identity
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]
                   295197
Seq. No.
                   LIB3075-050-Q1-K1-B8
Seq. ID
                   BLASTX
Method
                   g530088
NCBI GI
BLAST score
                   189
                   2.0e-14
E value
                   49
Match length
% identity
NCBI Description (U12735) aminoalcoholphosphotransferase [Glycine max]
Seq. No.
                   295198
                   LIB3075-050-Q1-K1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3122060
BLAST score
                   288
E value
                   3.0e-26
                   74
Match length
                   77
% identity
                   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                   >gi 2598657_emb_CAA10847_ (AJ222579) elongation factor
                   1-alpha (EF1-a) [Vicia faba]
                   295199
Seq. No.
                   LIB3075-050-Q1-K1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2723471
BLAST score
                   167
                   9.0e-12
E value
                   55
Match length
                   64
% identity
                   (D87819) sucrose transporter [Oryza sativa]
NCBI Description
                   295200
 Seq. No.
                   LIB3075-050-Q1-K1-F2
 Seq. ID
```

BLASTX

Method



```
g541951
NCBI GI
                  250
BLAST score
                  1.0e-21
E value
                  61
Match length
                  72
% identity
                  SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26
NCBI Description
                  [Glycine max]
                  295201
Seq. No.
                  LIB3075-050-Q1-K1-H2
Seq. ID
                  BLASTX
Method
                  g1168748
NCBI GI
                  236
BLAST score
                  5.0e-20
E value
                  87
Match length
                  54
% identity
NCBI Description CALMODULIN-4 >gi_479693_pir__S35185 calmodulin 4 -
                  Arabidopsis thaliana >gi_16223_emb_CAA78057_ (Z12022)
                  calmodulin [Arabidopsis thaliana]
                   295202
Seq. No.
                   LIB3075-051-Q1-K1-B6
Seq. ID
                  BLASTN
Method
                   g1546918
NCBI GI
                   75
BLAST score
                   2.0e-34
E value
                   143
Match length
                   89
% identity
NCBI Description Z.mays mRNA for translation initiation factor 5A
                   295203
Seq. No.
                   LIB3075-051-Q1-K1-H3
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4140643
BLAST score
                   73
                   5.0e-33
E value
                   157
Match length
% identity
                   48
                   Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                   complete sequence
                   295204
 Seq. No.
 Seq. ID
                   LIB3075-052-Q1-K1-D1
Method
                   BLASTN
                   q293886
NCBI GI
                   82
 BLAST score
                   2.0e-38
E value
                   86
 Match length
 % identity
                   99
                   Zea mays glyceraldehyde-3-phosphate dehydrogenase mRNA, 3'
 NCBI Description
                   end, (clone GAPC3)
                   295205
 Seq. No.
                   LIB3075-052-Q1-K1-E9
 Seq. ID
                   BLASTX
 Method
```

g3236250

164

NCBI GI

BLAST score



```
E value
                   2.0e-11
Match length
                  64
% identity
                  52
NCBI Description (AC004684) hypothetical protein [Arabidopsis thaliana]
                  295206
Seq. No.
Seq. ID
                  LIB3075-052-Q1-K1-F11
Method
                  BLASTX
                  g283049
NCBI GI
BLAST score
                  399
E value
                  3.0e-39
Match length
                  78
                  99
% identity
NCBI Description polygalacturonase (EC 3.2.1.15) precursor (clone W2247) -
                  maize (fragment) >gi 481079 pir S37718 polygalacturonase -
                  maize >gi 22426 emb CAA44248 (X62384) polygalacturonase
                  [Zea mays] >gi 287830 emb CAA47234 (X66692)
                  polygalacturonase [Zea mays]
Seq. No.
                  295207
Seq. ID
                  LIB3075-053-Q1-K1-B12
Method
                  BLASTX
                  g3250687
NCBI GI
                  158
BLAST score
E value
                  1.0e-10
Match length
                  67
% identity
                  43
NCBI Description
                  (AL024486) putative LTR retrotransposon (fragment)
                   [Arabidopsis thaliana]
                  295208
Seq. No.
Seq. ID
                  LIB3075-053-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  g2317901
BLAST score
                  284
                  1.0e-25
E value
                  83
Match length
% identity
                  63
                  (U89959) Similar to vesicle transport protein, PIR
NCBI Description
                  Accession Number A55931 [Arabidopsis thaliana]
                  295209
Seq. No.
Seq. ID
                  LIB3075-053-Q1-K1-D11
                  BLASTX
Method
NCBI GI
                  q2833374
BLAST score
                  208
                  1.0e-16
E value
Match length
                  46
                  91
% identity
```

Tar Sec

NCBI Description TRANSCRIPTION INITIATION FACTOR IIA GAMMA CHAIN

(TFIIA-GAMMA) >gi_1429228_emb_CAA67369_ (X98862) putative

small subunit [Arabidopsis thaliana]

Seq. No. 295210

Seq. ID LIB3075-053-Q1-K1-F5

Method BLASTX NCBI GI g3294469

% identity

79



```
BLAST score
E value
                  2.0e-36
Match length
                  85
% identity
                  84
                 (U89342) phosphoglucomutase 2 [Zea mays]
NCBI Description
Seq. No.
                  295211
Seq. ID
                  LIB3075-053-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  g3913191
BLAST score
                  191
E value
                  4.0e-15
Match length
                  41
                  88
% identity
NCBI Description CALMODULIN >gi_1296524_emb_CAA66215_ (X97612) CaMF-1 [Fagus
                  sylvatica]
Seq. No.
                  295212
Seq. ID
                  LIB3075-054-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  q4538931
BLAST score
                  277
E value
                  2.0e-24
Match length
                  119
% identity
NCBI Description
                  (AL049483) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  295213
                  LIB3075-054-Q1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1709798
BLAST score
                  403
                  2.0e-39
E value
Match length
                  98
% identity
                  84
NCBI Description
                  26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG >gi 1155334
                  (U43398) POTATP1 [Solanum tuberosum]
Seq. No.
                  295214
Seq. ID
                  LIB3075-054-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  g1519253
BLAST score
                  330
E value
                  4.0e-31
Match length
                  73
                  92
% identity
NCBI Description (U65958) GF14-d protein [Oryza sativa]
                  295215
Seq. No.
Seq. ID
                  LIB3075-054-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g3043428
BLAST score
                  556
E value
                  3.0e-57
Match length
                  131
```

NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

Method

BLASTX



```
295216
Seq. No.
                  LIB3075-054-Q1-K1-G8
Seq. ID
                  BLASTX
Method
                  g3043428
NCBI GI
                  277
BLAST score
                  7.0e-25
E value
                  90
Match length
% identity
NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
                  295217
Seq. No.
                  LIB3075-054-Q1-K1-G9
Seq. ID
                  BLASTX
Method
                   g1498229
NCBI GI
                   375
BLAST score
                   5.0e-36
E value
                   133
Match length
                   56
% identity
NCBI Description (X98743) RNA helicase [Homo sapiens]
                   295218
Seq. No.
                   LIB3075-055-Q1-K1-A10
Seq. ID
                   {\tt BLASTX}
Method
                   g398963
NCBI GI
                   151
BLAST score
                   5.0e-10
E value
                   89
Match length
                   37
% identity
                   4-COUMARATE--COA LIGASE 1 (4CL) >gi_100413_pir__A39827
NCBI Description
                   4-coumarate--CoA ligase (EC 6.2.1.12) 1 - potato >gi_169574
                   (M62755) 4-coumarate--CoA ligase [Solanum tuberosum]
                   295219
Seq. No.
                   LIB3075-055-Q1-K1-B4
Seq. ID
                   BLASTX
Method
                   g3821795
NCBI GI
                   277
BLAST score
                   1.0e-24
E value
                   71
Match length
 % identity
                   (Y11649) protein kinase CK2, alpha subunit [Zea mays]
 NCBI Description
                   295220
 Seq. No.
                   LIB3075-055-Q1-K1-E10
 Seq. ID
                   BLASTN
 Method
 NCBI GI
                   q433043
                   74
 BLAST score
                    2.0e-33
 E value
                    153
 Match length
 % identity
                    93
                    Zea mays W-22 clone PREM-1E retroelement PREM-1, partial
 NCBI Description
                    sequence
 Seq. No.
                    295221
                    LIB3075-055-Q1-K1-E3
 Seq. ID
```

41285

Method

NCBI GI



```
g3851001
NCBI GI
                  201
BLAST score
                  9.0e-16
E value
                  67
Match length
% identity
                  (AF069909) pyruvate dehydrogenase E1 beta subunit isoform 2
NCBI Description
                  [Zea mays]
                  295222
Seq. No.
                  LIB3075-055-Q1-K1-E8
Seq. ID
                  BLASTX
Method
                  g4105123
NCBI GI
                  271
BLAST score
                  2.0e-24
E value
                  63
Match length
                  89
% identity
                  (AF043346) cell wall invertase; Incw3;
NCBI Description
                  beta-fructofuranosidase [Zea mays]
                   295223
Seq. No.
                  LIB3075-055-Q1-K1-F10
Seq. ID
                  BLASTN
Method
                   g22458
NCBI GI
BLAST score
                   103
                   4.0e-51
E value
                   127
Match length
                   95
% identity
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)
                   295224
Seq. No.
                   LIB3075-055-Q1-K1-G1
Seq. ID
                   BLASTX
Method
                   q3687301
NCBI GI
                   190
BLAST score
                   6.0e-15
E value
                   68
Match length
                   60
% identity
                   (AJ006376) subtilisin-like protease [Lycopersicon
NCBI Description
                   esculentum] >gi_3687309_emb_CAA07001_ (AJ006380)
                   subtilisin-like protease [Lycopersicon esculentum]
                   295225
Seq. No.
Seq. ID
                   LIB3075-055-Q1-K1-G11
Method
                   BLASTX
                   q1173257
NCBI GI
                   170
BLAST score
                   1.0e-12
E value
                   37
Match length
 % identity
                   89
                   40S RIBOSOMAL PROTEIN S4 >gi_1076674_pir__S47642 ribosomal
NCBI Description
                   protein S4 - potato >gi_457803_emb_CAA54095_ (X76651)
                   ribosomal protein S4 [Solanum tuberosum]
 Seq. No.
                   295226
                   LIB3075-055-Q1-K1-G12
 Seq. ID
                   BLASTN
```

41286

g473602

NCBI Description



```
BLAST score
                   5.0e-16
E value
                  68
Match length
                   91
% identity
NCBI Description Zea mays W-22 histone H2A mRNA, complete cds
                  295227
Seq. No.
                  LIB3075-056-Q1-K1-C10
Seq. ID
                  BLASTX
Method
                   g22424
NCBI GI
                   336
BLAST score
                   1.0e-31
E value
                   74
Match length
                   89
% identity
NCBI Description (X57575) polygalacturonase [Zea mays]
                   295228
Seq. No.
                   LIB3075-056-Q1-K1-C9
Seq. ID
                   BLASTX
Method
                   g3337361
NCBI GI
                   371
BLAST score
                   6.0e-36
E value
                   90
Match length
                   76
% identity
NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]
                   295229
Seq. No.
                   LIB3075-056-Q1-K1-D1
Seq. ID
                   BLASTX
Method
                   g4580389
NCBI GI
BLAST score
                   143
                   3.0e-09
E value
                   66
Match length
                   45
% identity
NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]
                   295230
Seq. No.
                   LIB3075-056-Q1-K1-D10
Seq. ID
                   BLASTX
Method
                   q3080371
NCBI GI
                   219
BLAST score
E value
                   3.0e-18
Match length
                   66
 % identity
                   64
                    (AL022580) putative pectinacetylesterase protein
NCBI Description
                    [Arabidopsis thaliana]
                   295231
 Seq. No.
                   LIB3075-056-Q1-K1-D4
 Seq. ID
                   BLASTX
 Method
                   g4204859
 NCBI GI
                   278
 BLAST score
 E value
                   3.0e-25
 Match length
                   67
                   85
 % identity
                   (U55859) heat shock protein 80 [Triticum aestivum]
```

Seq. ID

Method



```
Seq. No.
                  LIB3075-056-Q1-K1-F3
Seq. ID
                  BLASTX
Method
                  q2582381
NCBI GI
BLAST score
                  443
E value
                  5.0e-44
                  144
Match length
                  59
% identity
NCBI Description (AF021220) cation-chloride co-transporter [Nicotiana
                  tabacum]
                  295233
Seq. No.
                  LIB3075-056-Q1-K1-H5
Seq. ID
                  BLASTX
Method
                  g417745
NCBI GI
                  268
BLAST score
                   1.0e-26
E value
                  119
Match length
                   57
% identity
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                   HYDROLASE) (ADOHCYASE) >gi_170773 (L11872)
                   S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]
                   295234
Seq. No.
                   LIB3076-001-Q1-K1-A4
Seq. ID
                   BLASTX
Method
                   q3913804
NCBI GI
BLAST score
                   144
                   4.0e-09
E value
                   90
Match length
                   44
% identity
NCBI Description HISTONE H2B.3 >gi_577825_emb_CAA49584_ (X69960) H2B histone
                   [Zea mays]
                   295235
Seq. No.
                   LIB3076-001-Q1-K1-F7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g445612
BLAST score
                   169
                   5.0e-14
E value
                   59
Match length
                   69
 % identity
 NCBI Description ribosomal protein S19 [Solanum tuberosum]
                   295236
 Seq. No.
                   LIB3076-001-Q1-K1-G6
 Seq. ID
                   BLASTN
 Method
                   g902585
 NCBI GI
                   35
 BLAST score
                   4.0e-10
 E value
                   51
 Match length
                   92
 % identity
 NCBI Description Zea mays clone MubG9 ubiquitin gene, complete cds
                   295237
 Seq. No.
```

41288

LIB3076-001-Q1-K1-G7

BLASTX

Seq. ID Method



```
g1709970
NCBI GI
                  293
BLAST score
                  1.0e-26
E value
                  89
Match length
                  66
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L10A
                  295238
Seq. No.
                  LIB3076-003-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                  q3776015
NCBI GI
                  331
BLAST score
                  5.0e-31
E value
                  88
Match length
                  73
% identity
                  (AJ010471) RNA helicase [Arabidopsis thaliana]
NCBI Description
                  >gi 4249378_gb_AAD14475_ (AC005966) Identical to
                  gb AJ010471 mRNA for DEAD box RNA helicase (RH22) from
                  Arabidopsis thaliana. EST gb_Y11191 comes from this gene.
                   [Arabidopsis thaliana]
                   295239
Seq. No.
                  LIB3076-003-Q1-K1-B12
Seq. ID
                  BLASTX
Method
                   g4190974
NCBI GI
                   188
BLAST score
                   2.0e-14
E value
                   62
Match length
% identity
NCBI Description (AB018442) phytochrome C [Oryza sativa]
                   295240
Seq. No.
Seq. ID
                   LIB3076-003-Q1-K1-D6
                   BLASTX
Method
                   q1143511
NCBI GI
                   319
BLAST score
                   1.0e-29
E value
                   91
Match length
                   73
 % identity
                   (Z47076) Ser/Thr protein phosphatase homologous to PPX
NCBI Description
                   [Malus domestica] >gi 1586034_prf__2202340A Ser/Thr protein
                   phosphatase [Malus domestica]
                   295241
 Seq. No.
                   LIB3076-003-Q1-K1-F6
 Seq. ID
                   BLASTX
Method
                   q3850821
 NCBI GI
                   357
 BLAST score
                   6.0e-34
 E value
                   106
 Match length
                   66
 % identity
                   (Y18350) U2 snRNP auxiliary factor, large subunit
 NCBI Description
                   [Nicotiana plumbaginifolia]
                   295242
 Seq. No.
```

41289

LIB3076-003-Q1-K1-F7

BLASTX

Match length

48



```
g3935148
NCBI GI
                  374
BLAST score
                  4.0e-36
E value
                  98
Match length
% identity
NCBI Description (AC005106) T25N20.12 [Arabidopsis thaliana]
                  295243
Seq. No.
                  LIB3076-003-Q1-K1-F9
Seq. ID
                  BLASTX
Method
                  q1519249
NCBI GI
BLAST score
                  300
                  2.0e-27
E value
                  68
Match length
% identity
NCBI Description (U65956) GF14-b protein [Oryza sativa]
                  295244
Seq. No.
                  LIB3076-003-Q1-K1-G9
Seq. ID
                  BLASTX
Method
                  g1086587
NCBI GI
                  150
BLAST score
                   9.0e-10
E value
                   104
Match length
                   37
% identity
NCBI Description (U41007) similar to G beta repeats (PROSITE: PS00670)
                   [Caenorhabditis elegans]
                   295245
Seq. No.
Seq. ID
                   LIB3076-004-Q1-K1-A11
                   BLASTX
Method
                   q1076777
NCBI GI
BLAST score
                   153
                   4.0e-10
E value
                   43
Match length
                   74
% identity
NCBI Description protein H2A - wheat >gi_536890_dbj_BAA07277_ (D38088)
                   protein H2A [Triticum aestivum]
                   295246
Seq. No.
                   LIB3076-004-Q1-K1-D1
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g1346251
BLAST score
                   270
                   9.0e-24
E value
                   76
Match length
 % identity
                   HISTONE H2B.4 >gi_577819_emb_CAA49585_ (X69961) H2B histone
 NCBI Description
                   [Zea mays]
                   295247
 Seq. No.
 Seq. ID
                   LIB3076-004-Q1-K1-D10
                   BLASTX
 Method
 NCBI GI
                   q3319341
                   194
 BLAST score
                   5.0e-15
 E value
```

41290

NCBI Description



```
% identity
                 (AF077407) similar to Medicago sativa nucleic acid binding
NCBI Description
                  protein Alfin-1 (GB:L07291) [Arabidopsis thaliana]
                  295248
Seq. No.
Seq. ID
                  LIB3076-005-Q1-K1-B6
Method
                  BLASTX
                  q1657619
NCBI GI
                  337
BLAST score
                  1.0e-31
E value
                  123
Match length
                  51
% identity
NCBI Description (U72504) G5p [Arabidopsis thaliana] >gi_3068710 (AF049236)
                  putative transmembrane protein G5p [Arabidopsis thaliana]
                  295249
Seq. No.
                  LIB3076-005-Q1-K1-D5
Seq. ID
                  BLASTX
Method
                  q1346251
NCBI GI
                  391
BLAST score
                  7.0e-38
E value
                  115
Match length
                   71
% identity
NCBI Description HISTONE H2B.4 >gi 577819 emb CAA49585 (X69961) H2B histone
                   [Zea mays]
                   295250
Seq. No.
                  LIB3076-005-Q1-K1-H1
Seq. ID
                  BLASTX
Method
                   g2262159
NCBI GI
BLAST score
                   242
                   1.0e-20
E value
                   92
Match length
% identity
NCBI Description (AC002329) predicted protein similar to S.pombe protein
                   C5H10.03 [Arabidopsis thaliana]
Seq. No.
                   295251
                   LIB3076-005-Q1-K1-H6
Seq. ID
                   BLASTX
Method
                   q4559339
NCBI GI
BLAST score
                   160
E value
                   5.0e-11
Match length
                   80
 % identity
                   (AC007087) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                   thaliana]
                   295252
 Seq. No.
                   LIB3076-005-Q1-K1-H8
 Seq. ID
                   BLASTX
Method
                   g2668742
 NCBI GI
 BLAST score
                   161
                   3.0e-11
 E value
                   56
 Match length
                   62
 % identity
```

41291

(AF034945) glycine-rich RNA binding protein [Zea mays]



```
295253
Seq. No.
                  LIB3076-006-Q1-K1-G9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2459420
BLAST score
                  569
                  6.0e-59
E value
                  112
Match length
% identity
                  (AC002332) putative ribosomal protein L17 [Arabidopsis
NCBI Description
                  thaliana]
                  295254
Seq. No.
                  LIB3076-006-Q1-K1-H5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1345588
BLAST score
                   433
                   2.0e-45
E value
                   126
Match length
% identity
                  14-3-3-LIKE PROTEIN GF14-12 >gi 998432 bbs 164524
NCBI Description
                   GF14-12=GRF2 product/14-3-3 protein homolog [Zea mays,
                   XL80, Peptide, 261 aa]
                   295255
Seq. No.
                   LIB3076-007-Q1-K1-H11
Seq. ID
Method
                   BLASTX
                   q397396
NCBI GI
BLAST score
                   225
                   9.0e-19
E value
Match length
                   105
% identity
NCBI Description (X66077) DNA-binding protein [Zea mays]
                   295256
Seq. No.
                   LIB3076-007-Q1-K1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3582436
BLAST score
                   162
                   2.0e-11
E value
Match length
                   57
 % identity
                   58
                   (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]
NCBI Description
                   295257
Seq. No.
                   LIB3076-008-Q1-K1-B11
 Seq. ID
                   BLASTX
Method
                   g584706
NCBI GI
                   368
BLAST score
                   2.0e-35
E value
                   88
Match length
                   82
 % identity
                   ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
 NCBI Description
                   >gi_2130066_pir__JC5124 aspartate transaminase (EC
```

2.6.1.1), cytoplasmic - rice >gi_287298_dbj_BAA03504_(D14673) aspartate aminotransferase [Oryza sativa]

NCBI Description

L16 partial



```
Seq. No.
                  LIB3076-008-Q1-K1-C7
Seq. ID
                  BLASTX
Method
                  q3548802
NCBI GI
BLAST score
                  316
E value
                  4.0e-29
                  86
Match length
% identity
                  (AC005313) axi 1-like protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein
                  [Nicotiana tabacum] [Arabidopsis thaliana]
                  295259
Seq. No.
Seq. ID
                  LIB3076-008-Q1-K1-H2
                  BLASTX
Method
                  g3395440
NCBI GI
BLAST score
                  173
                   7.0e-19
E value
Match length
                  86
% identity
NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]
                   295260
Seq. No.
                  LIB3076-008-Q1-K1-H8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g122022
                   264
BLAST score
                   4.0e-23
E value
                   78
Match length
% identity
                   HISTONE H2B >gi 283025_pir S22323 histone H2B - wheat
NCBI Description
                   >gi_21801_emb_CAA42530_ (X59873) histone H2B [Triticum
                   aestivum]
                   295261
Seq. No.
                   LIB3076-009-Q1-K1-E5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q730449
                   149
BLAST score
                   5.0e-10
E value
                   49
Match length
% identity
                   59
                   60S RIBOSOMAL PROTEIN L13-1 (COLD INDUCED PROTEIN C24A)
NCBI Description
                   >gi_480647_pir__S37132 ribosomal protein L13.A - rape
                   >gi 398918 emb CAA80341 (Z22618) cold induced protein
                   (BnC24A) [Brassica napus]
                   295262
 Seq. No.
                   LIB3076-009-Q1-K1-E9
 Seq. ID
                   BLASTN
Method
                   q12451
NCBI GI
BLAST score
                   77
E value
                   2.0e-35
Match length
                   149
 % identity
                   89
```

Maize chloroplast genes for ribosomal proteins L14, S8 and



```
295263
Seq. No.
Seq. ID
                  LIB3076-009-Q1-K1-H2
                  BLASTX
Method
                  q738308
NCBI GI
BLAST score
                  211
                  7.0e-17
E value
                  62
Match length
                  65
% identity
NCBI Description blue light photoreceptor [Arabidopsis thaliana]
                  295264
Seq. No.
                  LIB3076-010-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                  g4091080
NCBI GI
                  245
BLAST score
                   5.0e-21
E value
                  63
Match length
% identity
NCBI Description (AF045571) nucleic acid binding protein [Oryza sativa]
                   295265
Seq. No.
                  LIB3076-010-Q1-K1-B1
Seq. ID
                   BLASTN
Method
                   g2062705
NCBI GI
                   37
BLAST score
                   3.0e-11
E value
                   37
Match length
                   100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                   295266
Seq. No.
                   LIB3076-010-Q1-K1-B11
Seq. ID
                   BLASTN
Method
                   g22312
NCBI GI
                   39
BLAST score
                   1.0e-12
E value
                   179
Match length
                   81
 % identity
                   Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                   abscisic acid)
                   295267
 Seq. No.
                   LIB3076-010-Q1-K1-B8
 Seq. ID
                   BLASTX
 Method
                   g2274859
 NCBI GI
 BLAST score
                   272
                   4.0e-24
 E value
 Match length
                   73
                   67
 % identity
                   (AJ000016) Cks1 protein [Arabidopsis thaliana]
 NCBI Description
                   >gi_4510420_gb_AAD21506.1_ (AC006929) putative
                   cyclin-dependent kinase regulatory subunit [Arabidopsis
                   thaliana]
```

295268

LIB3076-010-Q1-K1-D6

Seq. No.

Seq. ID



```
Method
                  BLASTX
NCBI GI
                  q3860277
BLAST score
                  276
                  5.0e-26
E value
Match length
                  84
                  77
% identity
                  (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                  thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
                  295269
Seq. No.
Seq. ID
                  LIB3076-010-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g2708532
BLAST score
                  187
E value
                  5.0e-14
Match length
                  51
% identity
                  61
NCBI Description
                  (AF029351) putative RNA binding protein [Nicotiana tabacum]
                  295270
Seq. No.
Seq. ID
                  LIB3076-010-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  g3176686
BLAST score
                  174
E value
                  4.0e-17
Match length
                  138
% identity
NCBI Description
                  (AC003671) Similar to high affinity potassium transporter,
                  HAK1 protein gb U22945 from Schwanniomyces occidentalis.
                  [Arabidopsis thaliana]
                  295271
Seq. No.
                  LIB3076-010-Q1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4096786
BLAST score
                  273
                  4.0e-24
E value
                  121
Match length
% identity
                  54
                  (U39958) NADP-malic enzyme [Zea mays]
NCBI Description
Seq. No.
                  295272
Seq. ID
                  LIB3076-010-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  g558367
BLAST score
                  347
E value
                  6.0e-33
Match length
                  105
                  70
% identity
                  (X81830) cytochrome P450 [Zea mays]
NCBI Description
```

295273 Seq. No.

LIB3076-011-Q1-K1-A9 Seq. ID

Method BLASTX NCBI GI g1171978 BLAST score 153



```
3.0e-10
E value
Match length
                  86
                  42
% identity
                  POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
NCBI Description
                   (PABP 2) >gi_304109 (L19418) poly(A)-binding protein
                   [Arabidopsis thaliana] >gi 2911051 emb CAA17561 (AL021961)
                  poly(A) -binding protein [Arabidopsis thaliana]
                  295274
Seq. No.
                  LIB3076-011-Q1-K1-B12
Seq. ID
Method
                  BLASTX
                  g136739
NCBI GI
BLAST score
                  174
                  2.0e-18
E value
                  85
Match length
% identity
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
NCBI Description
                   PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU
                  UTP--glucose-1-phosphate uridy ltransferase (EC 2.7.7.9) -
                  potato >gi_218001 dbj_BAA00570 (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
                   295275
Seq. No.
                  LIB3076-011-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   g4572671
NCBI GI
BLAST score
                   336
                   2.0e-31
E value
                   124
Match length
% identity
                   (AC006954) putative cyclic nucleotide regulated ion channel
NCBI Description
                   [Arabidopsis thaliana]
                   295276
Seq. No.
                   LIB3076-014-Q1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1497987
BLAST score
                   152
E value
                   4.0e-13
Match length
                   109
% identity
                   44
                   (U62798) SCARECROW [Arabidopsis thaliana]
NCBI Description
                   295277
Seq. No.
                   LIB3076-015-Q1-K1-A1
Seq. ID
                   BLASTX
Method
                   g3128228
NCBI GI
BLAST score
                   143
                   3.0e-09
E value
                   78
Match length
```

37 % identity

(AC004077) putative ribosomal protein L18A [Arabidopsis NCBI Description thaliana] >gi_3337376 (AC004481) putative ribosomal protein

L18A [Arabidopsis thaliana]

295278 Seq. No.

Seq. ID LIB3076-015-Q1-K1-B6



```
BLASTX
Method
                  g2191136
NCBI GI
                  162
BLAST score
                  3.0e-11
E value
                  106
Match length
                  33
% identity
NCBI Description (AF007269) Similar to UTP-Glucose Glucosyltransferase;
                  coded for by A. thaliana cDNA T46230; coded for by A.
                  thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                  [Arabidopsis thaliana]
                  295279
Seq. No.
                  LIB3076-015-Q1-K1-B7
Seq. ID
Method
                  BLASTX
                  g3738297
NCBI GI
                  249
BLAST score
                  3.0e-21
E value
                  72
Match length
                  20
% identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
                  295280
Seq. No.
                  LIB3076-015-Q1-K1-D10
Seq. ID
                  BLASTX
Method
                  g2920666
NCBI GI
                  317
BLAST score
                   3.0e-29
E value
                   97
Match length
% identity
                   (AF048978) 2,4-D inducible glutathione S-transferase
NCBI Description
                   [Glycine max]
                   295281
Seq. No.
                   LIB3076-015-Q1-K1-D11
Seq. ID
                   BLASTX
Method
                   q2920666
NCBI GI
                   383
BLAST score
E value
                   6.0e-37
                   132
Match length
% identity
                   (AF048978) 2,4-D inducible glutathione S-transferase
NCBI Description
                   [Glycine max]
Seq. No.
                   295282
                   LIB3076-015-Q1-K1-E9
Seq. ID
                   BLASTX
Method
                   q417745
NCBI GI
BLAST score
                   505
E value
                   3.0e-51
                   144
Match length
                   72
 % identity
                   ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                   HYDROLASE) (ADOHCYASE) >gi 170773 (L11872)
                   S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]
```

LIB3076-015-Q1-K1-G1

Seq. No.

Seq. ID

Seq. ID



```
BLASTN
Method
                  q2707976
NCBI GI
BLAST score
                  52
                  2.0e-20
E value
Match length
                  244
% identity
                  80
NCBI Description Zea mays phytoene desaturase mRNA, complete cds
                  295284
Seq. No.
Seq. ID
                  LIB3076-015-Q1-K1-H10
Method
                  BLASTX
                  q132849
NCBI GI
                  208
BLAST score
                  1.0e-16
E value
                  92
Match length
                  46
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L2 >gi_20001_emb_CAA44362.1_ (X62500)
                  60S ribosomal protein L2 [Nicotiana tabacum]
                  295285
Seq. No.
Seq. ID
                  LIB3076-017-Q1-K1-B11
                  BLASTX
Method
NCBI GI
                  q3036805
                  278
BLAST score
                   8.0e-25
E value
                   73
Match length
% identity
NCBI Description (AL022373) thaumatin-like protein [Arabidopsis thaliana]
                   295286
Seq. No.
Seq. ID
                   LIB3076-017-Q1-K1-B8
                   BLASTX
Method
NCBI GI
                   q82728
                   145
BLAST score
                   1.0e-15
E value
                   57
Match length
% identity
                   superoxide dismutase (EC 1.15.1.1) (Mn) precursor - maize
NCBI Description
                   >gi 168624 (M33119) manganese superoxide dismutase (SOD-3)
                   (EC 1.15.1.1) [Zea mays]
Seq. No.
                   295287
Seq. ID
                   LIB3076-017-Q1-K1-H12
Method
                   BLASTX
                   q312179
NCBI GI
BLAST score
                   303
                   8.0e-28
E value
Match length
                   103
% identity
                   (X73151) glyceraldehyde 3-phosphate dehydrogenase
NCBI Description
                   (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic
                   glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]
                   >gi_1185554 (U45858) glyceraldehyde-3-phosphate
                   dehydrogenase [Zea mays]
                   295288
Seq. No.
```

LIB3076-018-Q1-K1-A4



```
BLASTX
Method
                  g2529340
NCBI GI
                  166
BLAST score
                  2.0e-11
E value
                  54
Match length
                  59
% identity
NCBI Description (L81162) homologue; putative [Zea mays]
                   295289
Seq. No.
                  LIB3076-018-Q1-K1-C8
Seq. ID
                  BLASTX
Method
                   g3176711
NCBI GI
                   300
BLAST score
                   3.0e-27
E value
                   129
Match length
                   48
% identity
NCBI Description (AC002392) bZIP-like protein [Arabidopsis thaliana]
                   295290
Seq. No.
                   LIB3076-018-Q1-K1-D4
Seq. ID
                   BLASTN
Method
                   g758352
NCBI GI
BLAST score
                   34
                   1.0e-09
E value
                   168
Match length
                   86
% identity
NCBI Description Z.mays mRNA for cysteine synthase
                   295291
Seq. No.
Seq. ID
                   LIB3076-018-Q1-K1-E11
                   BLASTX
Method
NCBI GI
                   q1296955
                   199
BLAST score
                   2.0e-15
E value
                   67
Match length
% identity
NCBI Description (X95402) duplicated domain structure protein [Oryza sativa]
                   295292
Seq. No.
                   LIB3076-018-Q1-K1-E6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q729671
BLAST score
                   228
E value
                   3.0e-19
                   71
Match length
 % identity
NCBI Description HISTONE H2A >gi_473603 (U08225) histone H2A [Zea mays]
                   295293
 Seq. No.
                   LIB3076-018-Q1-K1-E7
 Seq. ID
                   BLASTN
Method
                   g1060934
 NCBI GI
 BLAST score
                   160
 E value
                   8.0e-85
 Match length
                   294
                   96
 % identity
 NCBI Description Maize mRNA for mLIP15 (DNA-binding factor), complete cds
```

Seq. ID

Method



```
Seq. No.
                  295294
Seq. ID
                  LIB3076-018-Q1-K1-F9
Method
                  BLASTN
NCBI GI
                  g22292
BLAST score
                  116
E value
                  1.0e-58
Match length
                  256
                  87
% identity
NCBI Description Z.mays mRNA for glycine-rich protein
                  295295
Seq. No.
Seq. ID
                  LIB3076-019-Q1-K1-A12
                  BLASTX
Method
NCBI GI
                  g82694
BLAST score
                  298
E value
                  4.0e-27
Match length
                  115
% identity
                  57
                  glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) 2 -
NCBI Description
                  maize (fragment) >gi_293889 (L13432)
                  glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
                  295296
Seq. No.
Seq. ID
                  LIB3076-019-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  g729671
BLAST score
                  257
E value
                  3.0e-22
Match length
                  82
% identity
                  70
NCBI Description
                 HISTONE H2A >gi 473603 (U08225) histone H2A [Zea mays]
                  295297
Seq. No.
                  LIB3076-019-Q1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g729671
                  178
BLAST score
                  3.0e-13
E value
Match length
                  64
                  59
% identity
NCBI Description HISTONE H2A >gi 473603 (U08225) histone H2A [Zea mays]
Seq. No.
                  295298
Seq. ID
                  LIB3076-019-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g531829
BLAST score
                  168
E value
                  7.0e-12
                  79
Match length
                  47
% identity
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
Seq. No.
                  295299
```

41300

LIB3076-019-Q1-K1-C2

BLASTX



```
q112994
NCBI GI
                  181
BLAST score
                  1.0e-28
E value
                  81
Match length
% identity
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi_226091_prf__1410284A abscisic acid inducible gene [Zea
                  mays]
                   295300
Seq. No.
                  LIB3076-019-Q1-K1-C4
Seq. ID
                  BLASTX
Method
                   g2702284
NCBI GI
                   515
BLAST score
                   2.0e-52
E value
                   134
Match length
                   74
% identity
                   (AC003033) Argonaute (AGO1)-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   295301
Seq. No.
                   LIB3076-019-Q1-K1-C5
Seq. ID
                   BLASTX
Method
                   q531829
NCBI GI
                   163
BLAST score
                   2.0e-11
E value
                   52
Match length
                   63
% identity
                   (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                   pSport1]
                   295302
Seq. No.
                   LIB3076-019-Q1-K1-C6
Seq. ID
                   BLASTX
Method
                   g2702284
NCBI GI
                   239
BLAST score
                   3.0e-20
E value
                   84
Match length
 % identity
                   (AC003033) Argonaute (AG01)-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   295303
 Seq. No.
                   LIB3076-019-Q1-K1-D3
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q1710401
                   536
 BLAST score
                   6.0e-55
 E value
                   130
 Match length
                   79
 % identity
                   RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN
 NCBI Description
                    (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)
```

R2 [Nicotiana tabacum]

>gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase



```
295304
Seq. No.
                  LIB3076-019-Q1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263722
BLAST score
                  624
E value
                  3.0e-65
                  146
Match length
% identity
NCBI Description (AC006223) putative glucan synthase [Arabidopsis thaliana]
                  295305
Seq. No.
                  LIB3076-019-Q1-K1-D7
Seq. ID
                  BLASTX
Method
                  g3176686
NCBI GI
                   205
BLAST score
                   3.0e-22
E value
Match length
                   105
                   50
% identity
                   (AC003671) Similar to high affinity potassium transporter,
NCBI Description
                   HAK1 protein gb U22945 from Schwanniomyces occidentalis.
                   [Arabidopsis thaliana]
                   295306
Seq. No.
                   LIB3076-019-Q1-K1-E1
Seq. ID
                   {\tt BLASTX}
Method
                   g2384671
NCBI GI
                   183
BLAST score
                   8.0e-14
E value
                   95
Match length
                   43
% identity
                   (AF012657) putative potassium transporter AtKT2p
NCBI Description
                   [Arabidopsis thaliana]
                   295307
Seq. No.
                   LIB3076-019-Q1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1296955
                   281
BLAST score
                   4.0e-25
E value
                   92
Match length
% identity
                   (X95402) duplicated domain structure protein [Oryza sativa]
NCBI Description
                   295308
Seq. No.
Seq. ID
                   LIB3076-019-Q1-K1-E4
Method
                   BLASTX
NCBI GI
                   g4467097
BLAST score
                   223
                   3.0e-18
E value
Match length
                   80
                   57
% identity
                   (AL035538) heat shock protein 70 like protein [Arabidopsis
NCBI Description
                   thaliana]
```

295309

LIB3076-019-Q1-K1-F10

Seq. No.

Seq. ID

Seq. ID Method



```
Method
                  BLASTX
NCBI GI
                  q548669
BLAST score
                  163
                  3.0e-11
E value
Match length
                  111
% identity
                  41
                  DNA REPAIR PROTEIN RAD8 >gi 542223 pir__S41478 RAD8 protein
NCBI Description
                  - fission yeast (Schizosaccharomyces pombe)
                  >gi 443973 emb CAA52686 (X74615) rad8 [Schizosaccharomyces
                  pombe]
                  295310
Seq. No.
                  LIB3076-020-Q1-K1-A10
Seq. ID
Method
                  BLASTX
                  g2129774
NCBI GI
BLAST score
                  156
E value
                  2.0e-10
                  110
Match length
% identity
                  xyloglucan endotransglycosylase-related protein XTR4 -
NCBI Description
                  Arabidopsis thaliana (fragment) >gi 1244754 (U43486)
                  xyloglucan endotransglycosylase-related protein
                  [Arabidopsis thaliana]
                   295311
Seq. No.
Seq. ID
                  LIB3076-020-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  g3080427
                   157
BLAST score
E value
                   5.0e-11
                   54
Match length
                   59
% identity
                  (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   295312
                   LIB3076-020-Q1-K1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4220479
BLAST score
                   302
                   2.0e-27
E value
Match length
                   87
                   74
% identity
                  (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                   295313
Seq. No.
                   LIB3076-020-Q1-K1-E6
Seq. ID
                   BLASTX
Method
                   q2655098
NCBI GI
BLAST score
                   195
                   5.0e-15
E value
                   124
Match length
                   35
% identity
                  (AF023472) peptide transporter [Hordeum vulgare]
NCBI Description
                   295314
Seq. No.
```

41303

LIB3076-020-Q1-K1-F2

BLASTX



```
g585876
NCBI GI
                  151
BLAST score
                  5.0e-10
E value
                  65
Match length
% identity
                  60S RIBOSOMAL PROTEIN L23A (L25) >gi_1084424_pir__S48026
NCBI Description
                  ribosomal protein L25 - common tobacco >gi 310935 (L18908)
                  60S ribosomal protein L25 [Nicotiana tabacum]
                  295315
Seq. No.
                  LIB3076-020-Q1-K1-F6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1345132
                  235
BLAST score
                  1.0e-19
E value
                  133
Match length
                  41
% identity
                  (U47029) ERECTA [Arabidopsis thaliana]
NCBI Description
                  >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase
                  [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor
                  protein kinase, ERECTA [Arabidopsis thaliana]
                  295316
Seq. No.
                  LIB3076-020-Q1-K1-G1
Seq. ID
                  BLASTX
Method
                  q3024432
NCBI GI
                  214
BLAST score
                  2.0e-17
E value
                  87
Match length
                   60
% identity
                  PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                   COMPLEX ALPHA SUBUNIT) >qi 1930070 (U92540) proteasome
                   alpha subunit [Oryza sativa]
                   295317
Seq. No.
Seq. ID
                  LIB3076-020-Q1-K1-G12
Method
                   BLASTX
NCBI GI
                   g3757521
                   348
BLAST score
                   6.0e-33
E value
                   92
Match length
% identity
                   (AC005167) unknown protein [Arabidopsis thaliana]
NCBI Description
                   295318
Seq. No.
                   LIB3076-021-Q1-K1-A7
Seq. ID
                   BLASTX
Method
                   g2982259
NCBI GI
BLAST score
                   202
                   5.0e-16
E value
Match length
                   85
```

295319 Seq. No. LIB3076-021-Q1-K1-C4

mariana]

53

% identity

Seq. ID

NCBI Description

(AF051212) probable 60s ribosomal protein L13a [Picea



```
BLASTX
Method
                    q4210332
NCBI GI
BLAST score
                    283
                    3.0e-25
E value
Match length
                    127
% identity
                    52
NCBI Description (AJ223803) 2-oxoglutarate dehydrogenase E2 subunit
                    [Arabidopsis thaliana]
                    295320
Seq. No.
                    LIB3076-021-Q1-K1-F8
Seq. ID
                    BLASTX
Method
                    g4574208
NCBI GI
BLAST score
                    489
                    3.0e-49
E value
Match length
                     98
% identity
                     99
NCBI Description (AF093108) histone H3 [Tortula ruralis]
                    295321
Seq. No.
Seq. ID
                    LIB3076-021-Q1-K1-G6
Method
                    BLASTX
                     g1053057
NCBI GI
                     156
BLAST score
                     2.0e-10
E value
                     88
Match length
% identity
                     48
NCBI Description (U38422) histone H3 [Triticum aestivum]
Seq. No.
                     295322
                     LIB3076-022-Q1-K1-B9
Seq. ID
                     BLASTX
Method
                     g282833
NCBI GI
                     197
BLAST score
                     2.0e-15
E value
                     84
Match length
% identity
                     54
NCBI Description phosphoglycerate kinase (EC 2.7.2.3) - spinach (fragment)
                     295323
Seq. No.
                     LIB3076-022-Q1-K1-D2
Seq. ID
                     BLASTX
Method
                     q135417
NCBI GI
                     187
BLAST score
                     3.0e-14
E value
                     45
Match length
                     78
 % identity
                     TUBULIN ALPHA-3 CHAIN >gi_100946_pir__JN0105 tubulin alpha-3 chain - maize >gi_22150_emb_CAA44861_ (X63176) Alpha-tubulin #3 [Zea mays] >gi_485377 (M60171) alpha-3
 NCBI Description
                     tubulin [Zea mays]
                     295324
 Seq. No.
                     LIB3076-022-Q1-K1-E12
 Seq. ID
                     BLASTX
 Method
```

g3024018

335

NCBI GI BLAST score



```
2.0e-31
E value
                  101
Match length
% identity
                  INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
NCBI Description
                  >gi 1546919 emb CAA69225 (Y07920) translation initiation
                  factor 5A [Zea mays] >gi 2668738 (AF034943) translation
                  initiation factor 5A [Zea mays]
                  295325
Seq. No.
                  LIB3076-022-Q1-K1-F1
Seq. ID
Method
                  BLASTX
                  g4249412
NCBI GI
                  552
BLAST score
                  8.0e-57
E value
                  140
Match length
                  73
% identity
NCBI Description (AC006072) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  295326
                  LIB3076-022-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4467152
BLAST score
                  279
                  5.0e-25
E value
                  95
Match length
% identity
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
                   295327
Seq. No.
Seq. ID
                  LIB3076-022-Q1-K1-G11
                  BLASTX
Method
                   q122007
NCBI GI
BLAST score
                   257
                   3.0e-22
E value
Match length
                   87
                   61
% identity
                  HISTONE H2A >gi_100161_pir _S11498 histone H2A - parsley
NCBI Description
                   >gi_20448_emb_CAA37828^- (X\overline{53}831) H2A histone protein (AA 1
                   - 149) [Petroselinum crispum]
Seq. No.
                   295328
                   LIB3076-023-Q1-K1-C10
Seq. ID
Method
                   BLASTN
                   q3819299
NCBI GI
BLAST score
                   42
                   3.0e-14
E value
                   94
Match length
% identity
                   86
NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG0577
                  295329
Seq. No.
                   LIB3076-023-Q1-K1-E1
Seq. ID
Method
                   BLASTX
                   g1169228
NCBI GI
                   186
BLAST score
```

7.0e-14

49

E value Match length



```
% identity
                  RNA HELICASE-LIKE PROTEIN DB10 >gi 1084413 pir__S42639
NCBI Description
                  helicase-like protein - Wood tobacco
                  >gi 563986_dbj_BAA03763_ (D16247) RNA helicase like protein
                  DB10 [Nicotiana sylvestris]
                  295330
Seq. No.
                  LIB3076-023-Q1-K1-E11
Seq. ID
                  BLASTX
Method
                  q4406792
NCBI GI
                  331
BLAST score
                  8.0e-31
E value
                  142
Match length
                  45
% identity
NCBI Description (AC006304) putative reverse transcriptase [Arabidopsis
                  thaliana]
                  295331
Seq. No.
                  LIB3076-023-Q1-K1-E2
Seq. ID
                  BLASTX
Method
                  g2623310
NCBI GI
                  288
BLAST score
                  8.0e-26
E value
                  82
Match length
                  67
% identity
NCBI Description (AC002409) unknown protein [Arabidopsis thaliana]
                  >gi 3402721 (AC004261) unknown protein [Arabidopsis
                  thaliana]
                  295332
Seq. No.
                  LIB3076-023-Q1-K1-F7
Seq. ID
                  BLASTX
Method
                  q81600
NCBI GI
BLAST score
                  146
                  1.0e-09
E value
                  82
Match length
% identity
                  45
                  chaperonin 60 beta (clone bX) - Arabidopsis thaliana
NCBI Description
                   (fragment)
                   295333
Seq. No.
Seq. ID
                  LIB3076-023-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                   g417360
                   303
BLAST score
                   1.0e-27
E value
                   105
Match length
                   55
% identity
                  HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2
NCBI Description
                   >gi 2131280 pir__S67767 high mobility group-like protein
                   NHP2 - yeast (Saccharomyces cerevisiae)
                   >gi_666101_emb_CAA40885_ (X57714) high mobility group-like
                   nuclear protein 2 [Saccharomyces cerevisiae]
                   >gi 1429348 emb CAA67483 (X99000) high-mobility-group-like
                   protein [Saccharomyces cerevisiae]
```

[Saccharomyces cerevisiae]

>gi_1431346_emb_CAA98786_ (Z74256) ORF YDL208w



Seq. No. 295334

Seq. ID LIB3076-024-Q1-K1-B1

Method BLASTX
NCBI GI g4586255
BLAST score 173
E value 5.0e-13
Match length 57
% identity 63

NCBI Description (AL049640) putative protein [Arabidopsis thaliana]

Seq. No. 295335

Seq. ID LIB3076-024-Q1-K1-B7

Method BLASTX
NCBI GI g417103
BLAST score 644
E value 2.0e-67
Match length 137
% identity 96

NCBI Description HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi_488563
(U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460)
histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone
H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2

[Medicago sativa] >gi 488577 (U09465) histone H3.2

[Medicago sativa] >gi_510911 emb_CAA56153_ (X79714) histone

H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350 dbj_BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469 gb_AAC97380 (AF109910) histone H3 [Porteresia coarctata] >gi_4490754 emb_CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 295336

Seq. ID LIB3076-024-Q1-K1-B8

Method BLASTX
NCBI GI g1053047
BLAST score 218
E value 1.0e-17
Match length 100
% identity 50

NCBI Description (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)

histone H3 [Glycine max] >gi_1053051 (U38427) histone H3

[Glycine max]

Seq. No. 295337

Seq. ID LIB3076-024-Q1-K1-G11

Method BLASTX
NCBI GI g3006145
BLAST score 341
E value 4.0e-32



```
Match length
                  52
% identity
NCBI Description (AL022299) ABC transporter [Schizosaccharomyces pombe]
Seq. No.
                  295338
                  LIB3076-024-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g531829
BLAST score
                  141
                  6.0e-09
E value
Match length
                  63
                   46
% identity
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
                   295339
Seq. No.
                  LIB3076-025-Q1-K1-D2
Seq. ID
Method
                  BLASTX
                   g2088822
NCBI GI
                   170
BLAST score
                   5.0e-12
E value
Match length
                   105
% identity
NCBI Description (AF003384) K07B1.4 gene product [Caenorhabditis elegans]
                   295340
Seq. No.
Seq. ID
                   LIB3076-025-Q1-K1-D4
                   BLASTX
Method
                   q3193316
NCBI GI
BLAST score
                   262
                   7.0e-23
E value
                   101
Match length
% identity
                   57
                   (AF069299) contains similarity to nucleotide sugar
NCBI Description
                   epimerases [Arabidopsis thaliana]
Seq. No.
                   295341
                   LIB3076-025-Q1-K1-F2
Seq. ID
                   BLASTN
Method
                   g1181330
NCBI GI
BLAST score
                   67
E value
                   1.0e-29
Match length
                   87
                   94
% identity
NCBI Description Z.mays CNX mRNA
                   295342
Seq. No.
                   LIB3076-025-Q1-K1-F8
Seq. ID
                   BLASTX
Method
                   g100665
NCBI GI
BLAST score
                   502
                   5.0e-51
E value
                   100
Match length
                   56
 % identity
                   calmodulin 2 (clone lambda DASH) - rice
NCBI Description
                   >gi_20190_emb_CAA78288_ (Z12828) calmodulin [Oryza sativa]
                   >gi 310313 (L18914) calmodulin [Oryza sativa]
```



```
295343
Seq. No.
                  LIB3076-025-Q1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2668742
BLAST score
                  425
                  5.0e-42
E value
Match length
                  86
% identity
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]
                  295344
Seq. No.
                  LIB3076-026-Q1-K1-A10
Seq. ID
                  BLASTX
Method
                  q4538962
NCBI GI
BLAST score
                   143
                   7.0e-09
E value
Match length
                   68
% identity
NCBI Description (AL049488) hypothetical protein [Arabidopsis thaliana]
                   295345
Seq. No.
                   LIB3076-026-Q1-K1-A4
Seq. ID
                   BLASTX
Method
                   g2281090
NCBI GI
                   141
BLAST score
E value
                   3.0e-09
                   45
Match length
% identity
                  (AC002333) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   295346
Seq. No.
                   LIB3076-026-Q1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1519251
BLAST score
                   282
E value
                   2.0e-25
Match length
                   88
 % identity
                   66
                  (U65957) GF14-c protein [Oryza sativa]
NCBI Description
                   295347
Seq. No.
                   LIB3076-026-Q1-K1-D8
 Seq. ID
                   BLASTX
Method
                   q4586111
NCBI GI
                   190
BLAST score
                   9.0e-15
E value
                   74
Match length
                   53
 % identity
                   (AL049638) putative protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                   295348
                   LIB3076-026-Q1-K1-H10
 Seq. ID
                   BLASTX
 Method
                   g1076331
 NCBI GI
```

162

1.0e-17

BLAST score E value



Match length 115 % identity 39 NCBI Description his

histidine transport protein - Arabidopsis thaliana >gi_510238 emb_CAA54634_ (X77503) oligopeptide transporter 1-1 [Arabidopsis thaliana] >gi_744157_prf__2014244A His transporter [Arabidopsis thaliana]

Seq. No. 295349

Seq. ID LIB3076-027-Q1-K1-A3

Method BLASTX
NCBI GI g3927806
BLAST score 217
E value 9.0e-18
Match length 62
% identity 66

NCBI Description (U96439) aminoalcoholphosphotransferase [Pimpinella

brachycarpa]

Seq. No.

295350

Seq. ID LIB3076-027-Q1-K1-F1 Method BLASTN

NCBI GI g2921303 BLAST score 40 E value 3.0e-13 Match length 86 % identity 87

NCBI Description Zea mays herbicide safener binding protein (SBP1) mRNA,

complete cds

Seq. No. 295351

Seq. ID LIB3076-027-Q1-K1-G5

Method BLASTX
NCBI GI g1055130
BLAST score 189
E value 4.0e-14
Match length 111
% identity 44

NCBI Description (U39998) coded for by C. elegans cDNA yk92b11.3; coded for

by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA

yk78c2.3

Seq. No. 295352

Seq. ID LIB3076-028-Q1-K1-D8

Method BLASTX
NCBI GI g3258569
BLAST score 222
E value 3.0e-18
Match length 58
% identity 78

NCBI Description (U89959) Similar to yeast general negative regulator of

transcription subunit 1 [Arabidopsis thaliana]

Seq. No. 295353

Seq. ID LIB3076-029-Q1-K1-C10

Method BLASTN



```
NCBI GI
                   g3821780
                   36
BLAST score
                   6.0e-11
E value
                   36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   295354
Seq. No.
                   LIB3076-029-Q1-K1-C6
Seq. ID
                   BLASTX
Method
                   g3860277
NCBI GI
BLAST score
                   196
                   1.0e-15
E value
                   58
Match length
                   71
% identity
                   (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                   thaliana] >gi 4314394_gb_AAD15604_ (AC006232) putative
                   ribosomal protein L10A [Arabidopsis thaliana]
                   295355
Seq. No.
                   LIB3076-029-Q1-K1-E10
Seq. ID
                   BLASTX
Method
                   g1345838
NCBI GI
                   281
BLAST score
                   3.0e-25
E value
                   94
Match length
                   66
% identity
                   PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATURASE)
NCBI Description
                   >gi_2130143_pir__S65060 phytoene desaturase precursor -
                   \overline{\text{maize}} > \text{gi } 1\overline{0}511\overline{80} (U37285) phytoene desaturase [Zea mays]
                   295356
Seq. No.
Seq. ID
                   LIB3076-029-Q1-K1-E8
Method
                   BLASTX
                   q452593
NCBI GI
                   227
BLAST score
                   3.0e-19
E value
                   70
Match length
                   57
% identity
NCBI Description (D21814) ORF [Lilium longiflorum]
                   295357
Seq. No.
Seq. ID
                   LIB3076-029-Q1-K1-F10
Method
                   BLASTX
                   q1708107
NCBI GI
                    300
BLAST score
                    3.0e-27
E value
                    96
Match length
% identity
NCBI Description HISTONE H2B >gi_473605 (U08226) histone H2B [Zea mays]
                    295358
Seq. No.
Seq. ID
                    LIB3076-029-Q1-K1-F9
Method
                   BLASTX
                    q4586103
NCBI GI
BLAST score
                    539
```

7.0e-56

E value

NCBI Description



```
Match length
% identity
                  (AL049638) putative protein [Arabidopsis thaliana]
NCBI Description
                  295359
Seq. No.
                  LIB3076-029-Q1-K1-G9
Seq. ID
                  BLASTX
Method
                  q2342683
NCBI GI
                  383
BLAST score
                  6.0e-37
E value
Match length
                  75
% identity
                   (AC000106) Contains similarity to Bos beta-mannosidase
NCBI Description
                   (gb U46067). [Arabidopsis thaliana]
                  295360
Seq. No.
Seq. ID
                  LIB3076-029-Q1-K1-H5
                  BLASTN
Method
NCBI GI
                  q398917
BLAST score
                   36
                   6.0e-11
E value
                   64
Match length
                   89
% identity
NCBI Description B.napus cold induced protein (BnC24A) mRNA
                   295361
Seq. No.
Seq. ID
                  LIB3076-030-Q1-K1-D8
                   BLASTX
Method
                   g2146746
NCBI GI
BLAST score
                   201
                   1.0e-15
E value
                   97
Match length
% identity
                   41
                   protein kinase (EC 2.7.1.-) - Arabidopsis thaliana
NCBI Description
                   >gi_166819 (L05562) protein kinase [Arabidopsis thaliana]
                   295362
Seq. No.
Seq. ID
                   LIB3076-030-Q1-K1-E9
Method
                   BLASTX
NCBI GI
                   g642624
BLAST score
                   153
E value
                   3.0e-13
Match length
                   94
                   52
% identity
                   (L39266) phytoene desaturase [Zea mays]
NCBI Description
                   295363
Seq. No.
                   LIB3076-030-Q1-K1-F11
Seq. ID
                   BLASTX
Method
                   q3513727
NCBI GI
                   283
BLAST score
                   2.0e-25
E value
Match length
                   86
% identity
                   69
```

(AF080118) contains similarity to TPR domains (Pfam:

TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis



thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]

```
295364
Seq. No.
Seq. ID
                  LIB3076-030-Q1-K1-G3
Method
                  BLASTX
                  q4006893
NCBI GI
                  501
BLAST score
                  7.0e-51
E value
                  116
Match length
                  78
% identity
NCBI Description (Z99708) aminopeptidase-like protein [Arabidopsis thaliana]
                  295365
Seq. No.
                  LIB3076-031-Q1-K1-B4
Seq. ID
                  BLASTN
Method
NCBI GI
                   q577824
BLAST score
                  126
                   1.0e-64
E value
                   221
Match length
                   89
% identity
NCBI Description Z.mays gene for H2B histone (gH2B3)
                   295366
Seq. No.
Seq. ID
                   LIB3076-031-Q1-K1-E7
                   BLASTX
Method
NCBI GI
                   g3892051
BLAST score
                   228
                   6.0e-19
E value
                   59
Match length
                   69
% identity
                   (AC002330) predicted NADH dehydrogenase 24 kD subunit
NCBI Description
                   [Arabidopsis thaliana]
                   295367
Seq. No.
Seq. ID
                   LIB3076-031-Q1-K1-F8
                   BLASTX
Method
NCBI GI
                   g3482914
                   145
BLAST score
                   3.0e-09
E value
                   58
Match length
% identity
                   57
                   (AC003970) Similar to nodulins and lipase [Arabidopsis
NCBI Description
                   thaliana]
                   295368
Seq. No.
                   LIB3076-031-Q1-K1-G11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2668742
BLAST score
                   441
                   8.0e-44
E value
Match length
                   86
% identity
                   (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
```

LIB3076-031-Q1-K1-H9

295369

Seq. No.

Seq. ID



```
BLASTX
Method
                  g2160161
NCBI GI
                  297
BLAST score
                  7.0e-27
E value
                  146
Match length
% identity
NCBI Description (AC000132) F21M12.7 gene product [Arabidopsis thaliana]
                  295370
Seq. No.
Seq. ID
                  LIB3076-032-Q1-K1-B3
Method
                  BLASTN
                  g168500
NCBI GI
                  132
BLAST score
                  2.0e-68
E value
                  184
Match length
                  93
% identity
NCBI Description Maize (Zea mays) histone H4 gene (H4Cl4), complete cds
Seq. No.
                  295371
                  LIB3076-032-Q1-K1-B4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g122103
BLAST score
                  165
                  9.0e-12
E value
                  59
Match length
                  58
% identity
NCBI Description HISTONE H4 >gi_70776 pir_ HSZP4 histone H4 - fission yeast
                  (Schizosaccharomyces pombe) >gi 4964 emb CAA28853 (X05223)
                  histone H4.2 (AA 1-103) [Schizosaccharomyces pombe]
                  >gi 4967 emb CAA28855 (X05224) histone H4.3 (AA 1 - 103)
                  [Schizosaccharomyces pombe] >gi_4969_emb_CAA28850_ (X05222)
                  Histone H4.1 [Schizosaccharomyces pombe]
                  >gi 2257549 dbj BAA21442 (AB004538) histone H4
                   [Schizosaccharomyces pombe] >gi 2950490 emb CAA17818
                   (AL022072) histone h4 [Schizosaccharomyces pombe]
                  >gi 224836_prf__1202262E histone H4.1 [Schizosaccharomyces
                  pombe]
Seq. No.
                  295372
Seq. ID
                  LIB3076-032-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g3108161
BLAST score
                  149
E value
                   4.0e-10
Match length
                  52
                  56
% identity
                   (AF061106) putative monosaccharide transporter 1 [Petunia x
NCBI Description
                  hybrida]
                   295373
Seq. No.
                  LIB3076-032-Q1-K1-C3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3142294
BLAST score
                  551
                   1.0e-56
E value
                   110
Match length
```

% identity



```
(AC002411) Strong similarity to initiation factor eIF-2,
NCBI Description
                  gb U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and
                  gb_N37529 come from this gene. [Arabidopsis thaliana]
                   295374
Seq. No.
Seq. ID
                  LIB3076-032-Q1-K1-C7
                  BLASTX
Method
                   q4406820
NCBI GI
                   164
BLAST score
                   5.0e-15
E value
                   87
Match length
                   48
% identity
                   (AC006201) putative ras superfamily member [Arabidopsis
NCBI Description
                   thaliana]
                   295375
Seq. No.
Seq. ID
                   LIB3076-032-Q1-K1-D3
                   BLASTX
Method
                   g550438
NCBI GI
                   242
BLAST score
                   1.0e-20
E value
                   67
Match length
                   75
% identity
                   (X81829) cytochrome P450 [Zea mays]
NCBI Description
                   >gi_1870201_emb_CAA72208_ (Y11404) cytochrome p450 [Zea
                   mays]
                   295376
Seq. No.
                   LIB3076-032-Q1-K1-F11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3372230
                   247
BLAST score
                   5.0e-21
E value
                   71
Match length
                   63
% identity
                   (AF017074) RNA polymerase I, II and III 16.5 kDa subunit
NCBI Description
                   [Arabidopsis thaliana] >gi_4585968_gb_AAD25604.1_AC005287_6
                   (AC005287) RNA polymerase \overline{I}, II and \overline{III} 16.5 kDa subunit
                   [Arabidopsis thaliana]
                   295377
Seq. No.
                   LIB3076-032-Q1-K1-G2
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2062705
BLAST score
                   38
                   6.0e-12
E value
                   42
Match length
                   98
% identity
                   Human butyrophilin (BTF5) mRNA, complete cds
NCBI Description
```

Seq. No. 295378

Seq. ID LIB3076-032-Q1-K1-G5

Method BLASTX
NCBI GI g2832649
BLAST score 211
E value 2.0e-22
Match length 97



% identity

NCBI Description

```
% identity
                  (AL021710) adenylosuccinate lyase - like protein
NCBI Description
                  [Arabidopsis thaliana]
                  295379
Seq. No.
Seq. ID
                  LIB3076-032-Q1-K1-G9
                  BLASTX
Method
                  q3885342
NCBI GI
                  417
BLAST score
E value
                  4.0e-41
Match length
                  105
% identity
NCBI Description (AC005623) putative DNA polymerase [Arabidopsis thaliana]
                  295380
Seq. No.
Seq. ID
                  LIB3076-032-Q1-K1-H11
                  BLASTX
Method
NCBI GI
                  q4507075
                  294
BLAST score
                  2.0e-26
E value
                  133
Match length
                   47
% identity
                  SWI/SNF related, matrix associated, actin dependent
NCBI Description
                  regulator of chromatin, subfamily a, member 5
                  >gi_2967452_dbj_BAA25173_ (AB010882) hSNF2H [Homo sapiens]
                   295381
Seq. No.
                  LIB3076-033-Q1-K1-E12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1076746
BLAST score
                   208
                   6.0e-17
E value
Match length
                   78
% identity
                   59
                   heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
Seq. No.
                   295382
                   LIB3076-033-Q1-K1-E3
Seq. ID
Method
                   BLASTX
                   g3461848
NCBI GI
BLAST score
                   402
E value
                   3.0e - 39
                   130
Match length
                   63
% identity
                   (ACO05315) putative ATPase [Arabidopsis thaliana]
NCBI Description
                   295383
Seq. No.
                   LIB3076-033-Q1-K1-F2
Seq. ID
                   BLASTX
Method
                   g2104959
NCBI GI
                   170
BLAST score
                   9.0e-16
E value
                   74
Match length
```

(U96925) immunophilin [Vicia faba]

BLAST score



```
295384
Seq. No.
                  LIB3076-033-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3242659
BLAST score
                  173
                  2.0e-12
E value
                  55
Match length
% identity
NCBI Description (AB015599) spermidine synthase [Coffea arabica]
                  295385
Seq. No.
                  LIB3076-034-Q1-K1-C3
Seq. ID
                  BLASTX
Method
                  g2281705
NCBI GI
BLAST score
                  426
E value
                  4.0e-42
                  122
Match length
% identity
NCBI Description (AF013979) ethylene responsive factor [Oryza sativa]
                  295386
Seq. No.
Seq. ID
                  LIB3076-034-Q1-K1-D3
                  BLASTX
Method
NCBI GI
                  g3004950
                  408
BLAST score
E value
                   4.0e-40
                  101
Match length
% identity
NCBI Description (AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays]
                   295387
Seq. No.
Seq. ID
                   LIB3076-034-Q1-K1-G4
                   BLASTX
Method
                   q4056502
NCBI GI
BLAST score
                   244
E value
                   8.0e-23
Match length
                   75
                   74
% identity
                  (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
NCBI Description
                   295388
Seq. No.
                   LIB3076-035-Q1-K1-A3
Seq. ID
                   BLASTX
Method
                   q4426627
NCBI GI
                   199
BLAST score
                   2.0e-15
E value
Match length
                   48
                   77
% identity
                   (AF099969) sterol-C5(6)-desaturase homolog [Nicotiana
NCBI Description
                   tabacum]
Seq. No.
                   295389
                   LIB3076-035-Q1-K1-B12
Seq. ID
                   BLASTX
Method
                   g2245125
NCBI GI
```



```
2.0e-10
E value
Match length
                  44
% identity
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  295390
                  LIB3076-035-Q1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3819164
BLAST score
                  261
E value
                  9.0e-23
                  94
Match length
% identity
                  (AJ012318) cytosolic chaperonin, delta-subunit [Glycine
NCBI Description
                  max]
Seq. No.
                  295391
Seq. ID
                  LIB3076-036-Q1-K1-A12
                  BLASTX
Method
                  q3150407
NCBI GI
BLAST score
                  241
E value
                  2.0e-20
                  57
Match length
                  77
% identity
NCBI Description (AC004165) hypothetical protein [Arabidopsis thaliana]
                  295392
Seq. No.
                  LIB3076-036-Q1-K1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3121848
BLAST score
                  521
                  2.0e-53
E value
Match length
                  106
                  96
% identity
                  CALMODULIN >gi 1835521 (U83402) calmodulin [Capsicum
NCBI Description
                  annuum]
                  295393
Seq. No.
                  LIB3076-036-Q1-K1-D5
Seq. ID
                  BLASTX
                  g3298548
                  215
```

Method NCBI GI BLAST score E value 6.0e-18 Match length 62 73 % identity

(AC004681) putative spliceosomal protein [Arabidopsis NCBI Description

thaliana]

295394 Seq. No.

LIB3076-036-Q1-K1-D9 Seq. ID

BLASTN Method g3747049 NCBI GI BLAST score 57 2.0e-23 E value Match length 181 83 % identity

NCBI Description Zea mays ribosomal protein L26 mRNA, partial cds



```
295395
Seq. No.
Seq. ID
                  LIB3076-036-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g2668742
BLAST score
                  274
E value
                  2.0e-24
Match length
                  79
                  72
% identity
NCBI Description
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
                  295396
Seq. No.
Seq. ID
                  LIB3076-036-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  q3142300
BLAST score
                  360
E value
                  2.0e-34
Match length
                  113
% identity
                  62
                  (AC002411) Contains similarity to pre-mRNA processing
NCBI Description
                  protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb R64908
                  and gb T88158, gb N38703 and gb AA651043 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  295397
Seq. ID
                  LIB3076-036-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  q3850999
BLAST score
                  280
E value
                  2.0e-25
Match length
                  70
% identity
                  79
                  (AF069908) pyruvate dehydrogenase El beta subunit isoform 1
NCBI Description
                   [Zea mays]
                   295398
Seq. No.
Seq. ID
                  LIB3076-037-Q1-K1-B9
                  BLASTX
Method
NCBI GI
                  g3269293
                  277
BLAST score
                  1.0e-24
E value
Match length
                  112
% identity
                   47
                  (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                  295399
Seq. No.
                  LIB3076-037-Q1-K1-F11
Seq. ID
Method
                  BLASTX
                   g1707928
NCBI GI
BLAST score
                  198
```

E value 1.0e-15 Match length 80 % identity 61

GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT 2 NCBI Description

PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE

PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE

ADENYL TRANSFERASE) >gi 1076806 pir__S49439





glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) maize >gi_558365_emb_CAA86227_ (Z38111) ADP-glucose
pyrophosphorylase [Zea mays]

Seq. No. 295400

Seq. ID LIB3076-037-Q1-K1-F5

Method BLASTN
NCBI GI g2737972
BLAST score 129
E value 3.0e-66
Match length 189
% identity 92

NCBI Description Zea mays protein kinase ZmMEK1 mRNA, complete cds

Seq. No. 295401

Seq. ID LIB3076-037-Q1-K1-H12

Method BLASTX
NCBI GI g4539292
BLAST score 197
E value 2.0e-15
Match length 79
% identity 56

NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis

thaliana]

Seq. No. 295402

Seq. ID LIB3076-038-Q1-K1-B2

Method BLASTX
NCBI GI g1729938
BLAST score 165
E value 7.0e-12
Match length 64
% identity 47

NCBI Description THIOREDOXIN-LIKE PROTEIN SLR0233 >gi 1001610_dbj_BAA10238_

(D64000) thioredoxin M [Synechocystis sp.]

Seq. No. 295403

Seq. ID LIB3076-038-Q1-K1-C6

Method BLASTX
NCBI GI g1076348
BLAST score 210
E value 9.0e-23
Match length 69
% identity 84

NCBI Description myosin MYA1, class V - Arabidopsis thaliana

>gi_433663_emb_CAA82234_ (Z28389) myosin [Arabidopsis

thaliana]

Seq. No. 295404

Seq. ID LIB3076-038-Q1-K1-E11

Method BLASTX
NCBI GI 94406761
BLAST score 312
E value 9.0e-29
Match length 110
% identity 55

NCBI Description (AC006836) putative ubiquinone biosynthesis protein

Method

BLASTX



[Arabidopsis thaliana]

```
Seq. No.
                  295405
Seq. ID
                  LIB3076-038-Q1-K1-E4
Method
                  BLASTN
NCBI GI
                  q168547
BLAST score
                  73
E value
                  6.0e-33
Match length
                  77
% identity
                  99
                  Zea mays putative brain specific 14-3-3 protein, tau
NCBI Description
                  protein homolog mRNA, partial cds
Seq. No.
                  295406
Seq. ID
                  LIB3076-039-Q1-K1-A11
Method
                  BLASTN
NCBI GI
                  q2984708
BLAST score
                  56
E value
                  1.0e-22
Match length
                  63
                  97
% identity
                  Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
NCBI Description
Seq. No.
                  295407
Seq. ID
                  LIB3076-039-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  g3757521
BLAST score
                  170
E value
                   4.0e-12
Match length
                  78
% identity
                   41
                  (AC005167) unknown protein [Arabidopsis thaliana]
NCBI Description
                  295408
Seq. No.
                  LIB3076-039-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2668742
BLAST score
                   229
                   3.0e-19
E value
Match length
                  70
% identity
                   67
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                   295409
Seq. No.
                  LIB3076-039-Q1-K1-B8
Seq. ID
Method
                  BLASTX
                   g4206309
NCBI GI
BLAST score
                   239
                   2.0e-20
E value
                   83
Match length
% identity
                   59
NCBI Description (AF049112) prpol [Zea mays]
                   295410
Seq. No.
                   LIB3076-039-Q1-K1-D5
Seq. ID
```



NCBI GI g2500380 BLAST score 398 1.0e-38 E value Match length 86 % identity 60S RIBOSOMAL PROTEIN L44 >gi 2119128 pir JC4923 ribosomal NCBI Description protein RL44 - upland cotton >gi 1553129 (U64677) ribosomal protein L44 isoform a [Gossypium hirsutum] >gi 1553131 (U64678) ribosomal protein L44 isoform b [Gossypium hirsutum] 295411 Seq. No. LIB3076-039-Q1-K1-D7 Seq. ID

Method BLASTX
NCBI GI g2500380
BLAST score 398
E value 9.0e-39
Match length 86
% identity 85

NCBI Description 60S RIBOSOMAL PROTEIN L44 >gi 2119128 pir__JC4923 ribosomal

protein RL44 - upland cotton >gi_1553129 (U64677) ribosomal protein L44 isoform a [Gossypium hirsutum] >gi_1553131 (U64678) ribosomal protein L44 isoform b [Gossypium

hirsutum]

Seq. No. 295412

Seq. ID LIB3076-039-Q1-K1-G2

Method BLASTX
NCBI GI g2668742
BLAST score 207
E value 1.0e-16
Match length 66
% identity 70

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 295413

Seq. ID LIB3076-040-Q1-K1-C12

Method BLASTX
NCBI GI g1076758
BLAST score 151
E value 9.0e-14
Match length 60
% identity 72

NCBI Description heat-shock protein precursor - rye >gi 2130093 pir S65776

heat-shock protein, 82K, precursor - rye

>gi_556673_emb_CAA82945_ (Z30243) heat-shock protein

[Secale cereale]

Seq. No. 295414

Seq. ID LIB3076-041-Q1-K1-C7

Method BLASTX
NCBI GI g2959767
BLAST score 404
E value 2.0e-39
Match length 133
% identity 58

NCBI Description (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292



(AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]

 Seq. No.
 295415

 Seq. ID
 LIB3076-041-Q1-K1-H10

 Method
 BLASTN

 NCBI GI
 g2665535

 BLAST score
 202

 E value
 1.0e-110

Match length 399 % identity 88

NCBI Description Zea mays HCF106 precursor protein (Hcf106) mRNA, nuclear

gene encoding chloroplast protein, complete cds

Seq. No. 295416

Seq. ID LIB3076-041-Q1-K1-H2

Method BLASTN
NCBI GI g1657766
BLAST score 34
E value 8.0e-10
Match length 50
% identity 46

NCBI Description Zea mays retrotransposon Opie-2 5' LTR, primer binding

site, gag gene, pol gene, complete cds, polypurine tract

and 3' LTR

Seq. No. 295417

Seq. ID LIB3076-041-Q1-K1-H4

Method BLASTX
NCBI GI g3341679
BLAST score 156
E value 2.0e-10
Match length 68
% identity 51

NCBI Description (AC003672) dynamin-like protein phragmoplastin 12

[Arabidopsis thaliana]

Seq. No. 295418

Seq. ID LIB3076-042-Q1-K1-A12

Method BLASTN
NCBI GI g22292
BLAST score 80
E value 2.0e-37
Match length 120
% identity 92

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 295419

Seq. ID LIB3076-042-Q1-K1-A3

Method BLASTX
NCBI GI g2673868
BLAST score 173
E value 9.0e-13
Match length 44
% identity 75

NCBI Description (Y14856) fimbriata-associated protein [Antirrhinum majus]

E value

Match length

7.0e-34

82



```
295420
Seq. No.
                  LIB3076-042-Q1-K1-C2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  33
                  5.0e-09
E value
Match length
                  33
                  100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  295421
                  LIB3076-042-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076678
BLAST score
                  179
E value
                   1.0e-13
Match length
                   45
% identity
                   84
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)
                   295422
Seq. No.
                  LIB3076-042-Q1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3785978
BLAST score
                   346
                   1.0e-32
E value
Match length
                   87
% identity
                  (AC005560) unknown protein [Arabidopsis thaliana]
NCBI Description
                   295423
Seq. No.
Seq. ID
                   LIB3076-042-Q1-K1-H11
Method
                   BLASTX
                   g121974
NCBI GI
                   158
BLAST score
                   6.0e-23
E value
Match length
                   67
                   90
% identity
NCBI Description HISTONE H2A.2.1 >gi_70710_pir__HSWT2A histone H2A.2 - wheat
Seq. No.
                   295424
                   LIB3076-042-Q1-K1-H9
Seq. ID
Method
                   BLASTX
                   q1498053
NCBI GI
                   398
BLAST score
                   8.0e-39
E value
Match length
                   94
                   80
% identity
                  (U64436) ribosomal protein S8 [Zea mays]
NCBI Description
                   295425
Seq. No.
                   LIB3076-043-Q1-K1-B11
Seq. ID
Method
                   BLASTX
                   g2347198
NCBI GI
BLAST score
                   357
```



% identity 77 NCBI Description (AC002338) hypothetical protein [Arabidopsis thaliana]

Seq. No. 295426

Seq. ID LIB3076-043-Q1-K1-E5

Method BLASTX
NCBI GI g417103
BLAST score 145
E value 1.0e-18
Match length 89
% identity 64

NCBI Description HISTONE H3.2, MINOR >gi 282871 pir S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi_488563
(U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460)
histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone
H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2

[Medicago sativa] >gi 488577 (U09465) histone H3.2

[Medicago sativa] >gi_510911 emb_CAA56153 (X79714) histone H3 [Lolium temulentum] >qi 1435157 emb_CAA58445 (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum]

>gi_2558944 (AF024716) histone 3 [Gossypium hirsutum]

>gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa]

>gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755 emb_CAB38917.1

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 295427

Seq. ID LIB3076-043-Q1-K1-H9

Method BLASTX
NCBI GI g2213612
BLAST score 150
E value 9.0e-10
Match length 31
% identity 84

NCBI Description (AC000103) F21J9.6 [Arabidopsis thaliana]

Seq. No. 295428

Seq. ID LIB3076-044-Q1-K1-B4

Method BLASTX
NCBI GI g1168654
BLAST score 422
E value 1.0e-41
Match length 132
% identity 58

NCBI Description BETA-GALACTOSIDASE PRECURSOR (LACTASE)

>gi_542198_pir__S41889 beta-galactosidase (EC 3.2.1.23) -

garden asparagus >gi 452712 emb CAA54525 (X77319)

beta-galactosidase [Asparagus officinalis]

Seq. No. 295429

Seq. ID LIB3076-044-Q1-K1-G3

Method BLASTX



```
g462243
NCBI GI
BLAST score
                  327
E value
                  2.0e-30
Match length
                  86
% identity
NCBI Description
                  HISTONE H4 >qi 421921 pir S32769 histone H4 - tomato
                  >gi 297150 emb CAA48923 (X69179) histone H4 [Lycopersicon
                  esculentum] >qi 297152 emb CAA48924 (X69180) histone H4
                  [Lycopersicon esculentum] >gi 2746721 (AF038387) histone H4
                  [Capsicum annuum]
                  295430
Seq. No.
                  LIB3076-045-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1666173
BLAST score
                  187
                  3.0e-14
E value
Match length
                  75
% identity
NCBI Description
                  (Y09106) transcription factor [Nicotiana plumbaginifolia]
Seq. No.
                  295431
Seq. ID
                  LIB3076-045-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  g584893
BLAST score
                  164
E value
                  1.0e-11
Match length
                  56
% identity
                  71
                  SERINE CARBOXYPEPTIDASE III PRECURSOR
NCBI Description
                  >gi 283002 pir S22530 carboxypeptidase III (EC 3.4.16.-) -
                  rice >gi 218153 dbj_BAA01757_ (D10985) serine
                  carboxypeptidase III [Oryza sativa]
                  295432
Seq. No.
                  LIB3076-045-Q1-K1-G11
Seq. ID
Method
                  BLASTX
                  g3128188
NCBI GI
                  291
BLAST score
                  3.0e-26
E value
Match length
                  106
% identity
                  48
                  (AC004521) putative beta-glucosidase [Arabidopsis thaliana]
NCBI Description
                  295433
Seq. No.
                  LIB3076-046-Q1-K1-D9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2832242
BLAST score
                  59
                  2.0e-24
E value
Match length
                  107
% identity
                  89
                  Zea mays 22-kDa alpha zein gene cluster, complete sequence
NCBI Description
```

Seq. No. 295434

Seq. ID LIB3076-046-Q1-K1-E9

Method BLASTX

Method

NCBI GI

BLASTX

g2267006



```
g730510
NCBI GI
                  238
BLAST score
E value
                  4.0e-20
Match length
                  46
% identity
                  100
                  RAS-RELATED PROTEIN RIC1 >gi 542150 pir__S38740 GTP-binding
NCBI Description
                  protein - rice >qi 432607 gb AAB28535 (S66160) ras-related
                  GTP binding protein possessing GTPase activity=ric1 [Oryza
                  sativa=rice, var. Yamahoushi, callus, Peptide, 202 aa]
                  [Oryza sativa]
                  295435
Seq. No.
Seq. ID
                  LIB3076-046-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  q2244939
BLAST score
                  256
E value
                  4.0e-22
Match length
                  135
% identity
                  (Z97339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  295436
Seq. ID
                  LIB3076-046-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  g399854
BLAST score
                  258
E value
                  2.0e-22
Match length
                  91
% identity
                  HISTONE H2B.2 >gi 283042 pir S28049 histone H2B - maize
NCBI Description
                  >gi 22325 emb CAA40565 (X57313) H2B histone [Zea mays]
Seq. No.
                  295437
                  LIB3076-047-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g134598
BLAST score
                  161
                  1.0e-17
E value
Match length
                  63
                  79
% identity
NCBI Description SUPEROXIDE DISMUTASE-4AP (CU-ZN)
                  295438
Seq. No.
                  LIB3076-047-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4508021
                  152
BLAST score
                  4.0e-10
E value
                  98
Match length
                  40
% identity
NCBI Description
                  UNKNOWN >qi 3510462 (AF019767) zinc finger protein [Homo
                  sapiens]
                  295439
Seq. No.
                  LIB3076-047-Q1-K1-D5
Seq. ID
```

NCBI Description



```
BLAST score
                  3.0e-15
E value
                  69
Match length
% identity
                  61
                  (AF006825) endosperm lumenal binding protein [Oryza sativa]
NCBI Description
                  295440
Seq. No.
Seq. ID
                  LIB3076-047-Q1-K1-H2
Method
                  BLASTN
                  g5091496
NCBI GI
BLAST score
                  51
                  1.0e-19
E value
                  99
Match length
                  88
% identity
                  Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
NCBI Description
                  complete sequence
                  295441
Seq. No.
                  LIB3076-048-Q1-E1-D2
Seq. ID
                  BLASTX
Method
                  g2244771
NCBI GI
                  280
BLAST score
                  4.0e-25
E value
                  62
Match length
                  90
% identity
                  (Z97335) kinesin homolog [Arabidopsis thaliana]
NCBI Description
                  295442
Seq. No.
                  LIB3076-048-Q1-E1-H3
Seq. ID
                  BLASTX
Method
                  g3080372
NCBI GI
                   307
BLAST score
                   4.0e-28
E value
                   91
Match length
% identity
                   62
                   (AL022580) putative pectinacetylesterase [Arabidopsis
NCBI Description
                  thaliana]
                   295443
Seq. No.
                  LIB3076-049-Q1-K1-A11
Seq. ID
Method
                  BLASTX
                   g4262250
NCBI GI
BLAST score
                   261
                   8.0e-23
E value
                   107
Match length
% identity
                   52
                  (AC006200) putative aldolase [Arabidopsis thaliana]
NCBI Description
                   295444
Seq. No.
                   LIB3076-049-Q1-K1-C9
Seq. ID
Method
                   BLASTX
                   g531829
NCBI GI
BLAST score
                   148
                   9.0e-10
E value
Match length
                   86
% identity
                   42
                  (U12390) beta-galactosidase alpha peptide [cloning vector
```



pSport1]

```
295445
Seq. No.
                  LIB3076-049-Q1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4454464
                  221
BLAST score
                  2.0e-18
E value
                  69
Match length
% identity
                  62
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
                  295446
Seq. No.
Seq. ID
                  LIB3076-052-Q1-E1-G6
Method
                  BLASTX
NCBI GI
                  g135411
BLAST score
                  622
                  6.0e-65
E value
Match length
                  116
% identity
                  TUBULIN ALPHA-2 CHAIN >gi 82732 pir S15772 tubulin alpha-2
NCBI Description
                  chain - maize >qi 22148 emb CAA33733 (X15704)
                  alpha2-tubulin [Zea mays]
                   295447
Seq. No.
                  LIB3076-052-Q1-E1-H4
Seq. ID
Method
                  BLASTX
                   g1737492
NCBI GI
                   177
BLAST score
E value
                   3.0e-15
Match length
                   72
% identity
                  (U81318) poly(A)-binding protein [Triticum aestivum]
NCBI Description
Seq. No.
                   295448
                   LIB3076-053-Q1-E1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g417154
BLAST score
                   345
                   1.0e-32
E value
Match length
                   72
% identity
                   88
                  HEAT SHOCK PROTEIN 82 >gi 100685_pir__S25541 heat shock
NCBI Description
                   protein 82 - rice (strain Taichung Native One)
                   >gi 20256 emb CAA77978 (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
Seq. No.
                   295449
                   LIB3076-053-Q1-E1-C10
Seq. ID
                   BLASTX
Method
                   g2511531
NCBI GI
BLAST score
                   229
E value
                   1.0e-31
Match length
                   88
                   81
% identity
                   (AF008120) alpha tubulin 1 [Eleusine indica]
NCBI Description
                   >gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1
```

Method

BLASTX



[Eleusine indica]

```
295450
Seq. No.
                  LIB3076-053-Q1-E1-D9
Seq. ID
Method
                  BLASTX
                  g1732519
NCBI GI
BLAST score
                  170
                  3.0e-15
E value
Match length
                  96
% identity
                  51
                  (U62746) Rho1Ps homolog [Arabidopsis thaliana]
NCBI Description
                  295451
Seq. No.
                  LIB3076-053-Q1-E1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3341511
BLAST score
                  147
E value
                  3.0e-13
Match length
                  82
% identity
                  53
                  (AJ231134) cinnamoyl-CoA reductase [Saccharum officinarum]
NCBI Description
Seq. No.
                  295452
                  LIB3076-053-Q1-E1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3738293
BLAST score
                  265
E value
                  2.0e-23
Match length
                  63
% identity
                  83
                  (AC005309) putative CCAAT-binding transcription factor
NCBI Description
                  subunit A (CBF-A) [Arabidopsis thaliana]
                  295453
Seq. No.
                  LIB3076-053-Q1-E1-F2
Seq. ID
Method
                  BLASTX
                  g82696
NCBI GI
BLAST score
                  148
                   4.0e-11
E value
Match length
                  53
% identity
                  75
                  glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
Seq. No.
                  295454
                  LIB3076-053-Q1-E1-F8
Seq. ID
Method
                  BLASTX
                   g2661179
NCBI GI
BLAST score
                   358
                   4.0e-34
E value
                  127
Match length
% identity
                   50
NCBI Description (U80984) AtZW10 [Arabidopsis thaliana]
                   295455
Seq. No.
Seq. ID
                  LIB3076-053-Q1-E1-F9
```



```
NCBI GI
                  g2062167
BLAST score
                  320
                  3.0e-36
E value
Match length
                  143
% identity
                  52
                  (ACO01645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                  thaliana]
                  295456
Seq. No.
                  LIB3076-055-Q1-K1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3511235
BLAST score
                  116
E value
                  2.0e-58
Match length
                  312
% identity
                  92
NCBI Description Zea mays starch branching enzyme IIb (ae) gene, complete
                  295457
Seq. No.
Seq. ID
                  LIB3076-055-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g3201994
BLAST score
                  188
E value
                  2.0e-14
Match length
                  71
% identity
NCBI Description (AF068483) chaperonin Cct6 [Oryctolagus cuniculus]
                  295458
Seq. No.
                  LIB3076-055-Q1-K1-D10
Seq. ID
Method
                  BLASTX
                  g4580395
NCBI GI
                  204
BLAST score
                  5.0e-16
E value
Match length
                  126
% identity
                  (AC007171) putative kinesin-related protein [Arabidopsis
NCBI Description
                  thaliana]
                  295459
Seq. No.
                  LIB3076-055-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3445212
BLAST score
                   205
                  2.0e-16
E value
Match length
                  93
                   51
% identity
NCBI Description (AC004786) putative chloroplast envelope Ca2+-ATPase
                   [Arabidopsis thaliana]
```

Seq. No. 295460

LIB3076-055-Q1-K1-G5 Seq. ID

Method BLASTX NCBI GI q3775985 BLAST score 217 E value 6.0e-18

Match length

NCBI Description

% identity

98 91



```
Match length
                  53
% identity
                  (AJ010456) RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  295461
                  LIB3077-002-Q1-K1-A11
Seq. ID
Method
                  BLASTX
                  q3687223
NCBI GI
BLAST score
                  242
E value
                  2.0e-20
Match length
                  80
% identity
                  69
NCBI Description (AC005169) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  295462
                  LIB3077-002-Q1-K1-D11
Seq. ID
Method
                  BLASTX
                  g1483230
NCBI GI
BLAST score
                  244
E value
                  1.0e-20
Match length
                  88
% identity
                  62
NCBI Description (X99654) MADS4 protein [Betula pendula]
Seq. No.
                  295463
Seq. ID
                  LIB3077-002-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  g531829
BLAST score
                  159
E value
                  5.0e-11
Match length
                  69
% identity
                  54
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
Seq. No.
                  295464
                  LIB3078-001-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4585882
BLAST score
                  471
E value
                  2.0e-47
Match length
                  102
                  81
% identity
                   (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                  295465
Seq. No.
                  LIB3078-001-Q1-K1-A8
Seq. ID
Method
                  BLASTX
                   g3036942
NCBI GI
BLAST score
                   350
E value
                   8.0e-39
```

[Nicotiana sylvestris]

(AB012636) light harvesting chlorophyll a/b-binding protein

Seq. No.

Seq. ID

295471

LIB3078-001-Q1-K1-G5



```
295466
Seq. No.
Seq. ID
                  LIB3078-001-Q1-K1-B6
Method
                  BLASTN
NCBI GI
                  g167084
BLAST score
                  35
                  2.0e-10
E value
Match length
                  43
                  95
% identity
                  Barley PSI-D subunit of photosystem I (PsaD) mRNA, complete
NCBI Description
                  295467
Seq. No.
                  LIB3078-001-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352200
BLAST score
                  381
E value
                  7.0e-37
Match length
                  105
% identity
                  71
NCBI Description
                  CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)
                  >gi 480909 pir S37497 triose
                  phosphate/3-phosphoglycerate/phosphate translocator - maize
                  >gi 405635 emb CAA81349 (Z26595) triose
                  phosphate/phosphate translocator [Zea mays]
Seq. No.
                  295468
Seq. ID
                  LIB3078-001-Q1-K1-D2
Method
                  BLASTN
NCBI GI
                  g22292
BLAST score
                  124
                  3.0e-63
E value
Match length
                  128
                  99
% identity
NCBI Description Z.mays mRNA for glycine-rich protein
Seq. No.
                  295469
                  LIB3078-001-Q1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g459895
BLAST score
                  525
E value
                  1.0e-53
Match length
                  113
% identity
                  89
NCBI Description
                 (L29418) sus1 gene product [Zea mays]
Seq. No.
                  295470
                  LIB3078-001-Q1-K1-F10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3005931
BLAST score
                  389
E value
                  2.0e-39
Match length
                  117
% identity
NCBI Description (AJ005016) ABC transporter [Homo sapiens]
```

E value

Match length

6.0e-10



```
BLASTX
Method
                  g2583129
NCBI GI
                  551
BLAST score
                  1.0e-56
E value
Match length
                  126
% identity
                  81
                  (AC002387) putative methionine aminopeptidase [Arabidopsis
NCBI Description
                  thaliana]
                  295472
Seq. No.
                  LIB3078-001-Q1-K1-G9
Seq. ID
Method
                  BLASTX
                  g3036951
NCBI GI
                  470
BLAST score
E value
                  2.0e-47
Match length
                  91
                  97
% identity
                  (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
Seq. No.
                  295473
                  LIB3078-001-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220514
BLAST score
                  168
E value
                  5.0e-12
                  90
Match length
% identity
                  41
                  (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
                  295474
Seq. No.
                  LIB3078-002-Q1-K1-A2
Seq. ID
Method
                  BLASTX
                  g4105561
NCBI GI
BLAST score
                  291
E value
                  3.0e-41
                  123
Match length
                  77
% identity
NCBI Description (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]
                  295475
Seq. No.
                  LIB3078-002-Q1-K1-B2
Seq. ID
Method
                  BLASTX
                   g3928142
NCBI GI
BLAST score
                   551
E value
                  1.0e-56
Match length
                  134
                  80
% identity
NCBI Description (AJ131045) protein phosphatase [Cicer arietinum]
Seq. No.
                   295476
                  LIB3078-002-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1710838
BLAST score
                   152
```

E value

Match length

2.0e-12

85



```
% identity
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                  HYDROLASE) (ADOHCYASE) >gi 535584 (L36119)
                  adenosylhomocysteinase [Medicago sativa]
Seq. No.
                  295477
                  LIB3078-002-Q1-K1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q22223
BLAST score
                  116
E value
                  1.0e-58
Match length
                  152
% identity
NCBI Description Maize cab-1 gene for chlorophyll a/b-binding protein
Seq. No.
                  295478
Seq. ID
                  LIB3078-002-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  q1169528
BLAST score
                  298
E value
                  3.0e-27
Match length
                  88
                  72
% identity
                  ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi_602253 (U17973)
                  enolase [Zea mays]
Seq. No.
                  295479
Seq. ID
                  LIB3078-002-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  q2773154
BLAST score
                  226
E value
                  2.0e-18
Match length
                  56
% identity
                  73
                  (AF039573) abscisic acid- and stress-inducible protein
NCBI Description
                   [Oryza sativa]
                  295480
Seq. No.
                  LIB3078-002-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2117937
BLAST score
                  408
                  2.0e-41
E value
Match length
                  96
                   96
% identity
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
NCBI Description
                  barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose
                  pyrophosphorylase [Hordeum vulgare]
                  295481
Seq. No.
Seq. ID
                  LIB3078-002-Q1-K1-F9
Method
                  BLASTX
                  g4539292
NCBI GI
BLAST score
                  173
```



% identity 47
NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No. 295482

Seq. ID LIB3078-002-Q1-K1-G1

Method BLASTX
NCBI GI 94506489
BLAST score 262
E value 8.0e-23
Match length 111
% identity 46

NCBI Description replication factor C (activator 1) 3 (38kD)

>gi 3915601 sp P40938 AC13 HUMAN ACTIVATOR 1 38 KD SUBUNIT (REPLICATION FACTOR C 38 KD SUBUNIT) (A1 38 KD SUBUNIT) (RF-C 38 KD SUBUNIT) (RFC38) >gi 1498259 (L07541)

(RF-C 38 KD SUBUNIT) (RFC38) >gi_1498259 (L07541) replication factor C, 38-kDa subunit [Homo sapiens]

Seq. No. 295483

Seq. ID LIB3078-002-Q1-K1-G7

Method BLASTX
NCBI GI g4586111
BLAST score 155
E value 2.0e-10
Match length 87
% identity 43

NCBI Description (AL049638) putative protein [Arabidopsis thaliana]

Seq. No. 295484

Seq. ID LIB3078-002-Q1-K1-H4

Method BLASTX
NCBI GI g2281095
BLAST score 397
E value 7.0e-56
Match length 136
% identity 84

NCBI Description (AC002333) cysteine synthase, cpACS1 [Arabidopsis thaliana]

Seq. No. 295485

Seq. ID LIB3078-002-Q1-K1-H5

Method BLASTX
NCBI GI g538596
BLAST score 212
E value 5.0e-24
Match length 120
% identity 57

NCBI Description translation elongation factor EF-Tu.A - Escherichia coli

>gi_606273 (U18997) CG Site No. 61 [Escherichia coli]
>gi_1789737 (AE000410) protein chain elongation factor

EF-Tu (duplicate of tufB) [Escherichia coli]

Seq. No. 295486

Seq. ID LIB3078-002-Q1-K1-H6

Method BLASTX
NCBI GI g1167953
BLAST score 162
E value 3.0e-11



```
Match length
                   62
% identity
NCBI Description
                   (U43496) putative 32.6 kDa jasmonate-induced protein
                   [Hordeum vulgare] >gi 2465426 (AF021256) 32 kDa protein
                   [Hordeum vulgare]
                  295487
Seq. No.
                  LIB3078-003-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1706551
BLAST score
                  394
E value
                  3.0e-38
Match length
                  133
% identity
                  55
NCBI Description
                  GLUCAN ENDO-1, 3-BETA-GLUCOSIDASE PRECURSOR
                   ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
                   (BETA-1,3-ENDOGLUCANASE) >gi 924953 (U30323) beta
                  1,3-glucanase [Triticum aestivum]
Seq. No.
                  295488
Seq. ID
                  LIB3078-003-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  g4585576
BLAST score
                  327
E value
                  7.0e-45
Match length
                  105
% identity
NCBI Description
                  (AF134051) fructose-1,6-bisphosphatase precursor [Solanum
                  tuberosum]
Seq. No.
                  295489
Seq. ID
                  LIB3078-003-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g2641619
BLAST score
                  173
                  2.0e-12
E value
Match length
                  92
                  49
% identity
                  (AF032468) ubiquitin-conjugating enzyme protein E2 [Zea
NCBI Description
Seq. No.
                  295490
                  LIB3078-003-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q99486
BLAST score
                  212
                  6.0e-17
E value
Match length
                  99
```

52 % identity

NCBI Description

chlorophyll a/b-binding protein (clone pINEab 31) - Scotch pine >gi_20792_emb_CAA41406 (X58516) Type II chlorophyll a

/b-binding protein [Pinus sylvestris]

Seq. No.

LIB3078-003-Q1-K1-G5 Seq. ID

295491

Method BLASTX NCBI GI g3024503

Match length



```
BLAST score
                  7.0e-13
E value
                  75
Match length
% identity
                  52
                  RAS-RELATED PROTEIN RAB11C >gi 623576 (L29268) putative
NCBI Description
                  [Nicotiana tabacum]
                  295492
Seq. No.
                  LIB3078-003-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g393116
BLAST score
                  271
                  6.0e-24
E value
                  123
Match length
% identity
                  26
NCBI Description
                 (L23922) P-glycoprotein 5 [Entamoeba histolytica]
                  295493
Seq. No.
                  LIB3078-004-Q1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q693918
BLAST score
                  139
                  5.0e-09
E value
Match length
                  60
% identity
                  50
NCBI Description
                  (U21112) chlorophyll a/b binding protein [Solanum
                  tuberosum]
Seq. No.
                  295494
                  LIB3078-004-Q1-K1-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22312
BLAST score
                  64
                  2.0e-27
E value
Match length
                  151
% identity.
                  87
NCBI Description Maize ABA-inducible gene for glycine-rich protein ( ABA =
                  abscisic acid)
                  295495
Seq. No.
Seq. ID
                  LIB3078-004-Q1-K1-B11
Method
                  BLASTX
                  g551167
NCBI GI
BLAST score
                  206
E value
                  2.0e-16
Match length
                  97
                  45
% identity
NCBI Description
                  (L35241) moesin actin-binding domain homologue [Arabidopsis
                  thaliana]
Seq. No.
                  295496
Seq. ID
                  LIB3078-004-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  q3914465
BLAST score
                  156
E value
                  1.0e-10
```



% identity 47

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)

>gi_2981207 (AF052076) photosystem I complex PsaH subunit precursor [Zea mays]

Seq. ID LIB3078-004-Q1-K1-D2 Method BLASTX NCBI GI g548605 BLAST score 392 E value 5.0e-38 Match length 105 % identity 81

Seq. No.

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

Seq. No. 295498
Seq. ID LIB307

LIB3078-004-Q1-K1-E3

Method BLASTX
NCBI GI g4099919
BLAST score 280
E value 6.0e-25
Match length 97
% identity 56

NCBI Description (U91981) pollen allergen homolog [Triticum aestivum]

Seq. No. 295499

Seq. ID LIB3078-004-Q1-K1-E7

Method BLASTX
NCBI GI g3329368
BLAST score 437
E value 2.0e-43
Match length 125
% identity 64

NCBI Description (AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 295500

Seq. ID LIB3078-004-Q1-K1-G8

Method BLASTN
NCBI GI 94140643
BLAST score 88
E value 1.0e-41
Match length 237
% identity 90

NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

complete sequence

Seq. No. 295501

Seq. ID LIB3078-004-Q1-K1-H4

Method BLASTX
NCBI GI g4090257
BLAST score 240
E value 3.0e-28



```
Match length
                  71
% identity
                  (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
NCBI Description
Seq. No.
                  295502
                  LIB3078-004-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2293568
BLAST score
                  151
                  8.0e-10
E value
Match length
                  64
                  50
% identity
NCBI Description (AF012897) HvB12D homolog [Oryza sativa]
                  295503
Seq. No.
Seq. ID
                  LIB3078-006-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  g2494320
                  260
BLAST score
                  4.0e-23
E value
Match length
                  64
% identity
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5)
NCBI Description
                  >gi 1806575 emb CAA67868 (X99517) Eukaryotic initiation
                  factor-5 [Zea mays]
Seq. No.
                   295504
                  LIB3078-006-Q1-K1-C3
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4454056
BLAST score
                   200
E value
                   6.0e-16
Match length
                   74
% identity
                   55
                  (AJ000930) ClpP [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   295505
                   LIB3078-006-Q1-K1-D8
Seq. ID
Method
                   BLASTX
                   g3004950
NCBI GI
BLAST score
                   375
                   4.0e-42
E value
Match length
                   91
                   96
% identity
                  (AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays]
NCBI Description
                   295506
Seq. No.
                   LIB3078-006-Q1-K1-F9
Seq. ID
                   BLASTX
Method
                   g3298538
NCBI GI
BLAST score
                   186
                   7.0e-14
E value
Match length
                   123
% identity
                   41
                  (AC004681) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

41341

295507

Seq. No.

BLAST score

E value

244

1.0e-20



```
Seq. ID
                  LIB3078-006-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  g2827526
BLAST score
                  320
E value
                  1.0e-29
Match length
                  121
% identity
NCBI Description (AL021633) AIG2-like protein [Arabidopsis thaliana]
Seq. No.
                  295508
                  LIB3078-006-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  252
E value
                  1.0e-21
Match length
                  95
% identity
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                  295509
Seq. No.
Seq. ID
                  LIB3078-006-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  q3080407
BLAST score
                  291
E value
                   3.0e-26
Match length
                   142
% identity
NCBI Description
                  (AL022604) hypothetical protein (fragment) [Arabidopsis
                  thaliana]
Seq. No.
                   295510
Seq. ID
                  LIB3078-007-Q1-K1-A5
Method
                   BLASTX
                   g21693
NCBI GI
BLAST score
                   407
                   6.0e-40
E value
Match length
                  88
                  83
% identity
NCBI Description (X66012) cathepsin B [Triticum aestivum]
Seq. No.
                   295511
                   LIB3078-007-Q1-K1-B9
Seq. ID
Method
                  BLASTN
                   q3800748
NCBI GI
BLAST score
                   37
                   3.0e-11
E value
Match length
                   49
                   94
% identity
NCBI Description Cuphea hookeriana 3-ketoacyl-ACP synthase (Kas4) mRNA,
                   complete cds
Seq. No.
                   295512
                   LIB3078-007-Q1-K1-C12
Seq. ID
Method
                  BLASTX
                   g398845
NCBI GI
```



```
Match length
% identity
                  52
                  (X74654) beta3 tubulin [Zea mays]
NCBI Description
                  295513
Seq. No.
                  LIB3078-007-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1708108
BLAST score
                  329
E value
                  7.0e-31
Match length
                  80
% identity
                  84
                  HISTONE H3.3 >gi_860702 (U28732) similar to histone H3
NCBI Description
                  [Caenorhabditis elegans]
Seq. No.
                  295514
                  LIB3078-007-Q1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82696
BLAST score
                  232
E value
                  6.0e-27
Match length
                  75
% identity
                  91
                  glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                  (X61121) glycine-rich protein [Zea mays]
                  295515
Seq. No.
                  LIB3078-008-Q1-K1-A3
Seq. ID
Method
                  BLASTX
                  q266578
NCBI GI
BLAST score
                  286
                  1.0e-25
E value
                  56
Match length
                  93
% identity
                  METALLOTHIONEIN-LIKE PROTEIN 1 >gi_100898_pir__S17560
NCBI Description
                  metallothionein-like protein - maize >gi_236730_bbs_57629
                  (S57628) metallothionein homologue [Zea mays, Peptide, 76
                  aa] [Zea mays] >gi_559536_emb_CAA57676_ (X82186)
                  metallothionein- like protein [Zea mays]
                  >gi 228095 prf 1717215A metallothionein-like protein [Zea
                  mays]
                  295516
Seq. No.
                  LIB3078-008-Q1-K1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3421090
BLAST score
                  164
                  2.0e-11
E value
Match length
                  32
                  100
% identity
                  (AF043525) 20S proteasome subunit PAE2 [Arabidopsis
NCBI Description
```

thaliana]

295517 Seq. No.

Seq. ID LIB3078-008-Q1-K1-B3

Method BLASTX NCBI GI g4557627



```
BLAST score
E value
                  1.0e-16
Match length
                  105
% identity
                  43
NCBI Description
                  GLE1-like, RNA export mediator >gi 3288817 (AF058922) GLE1
                  [Homo sapiens]
                  295518
Seq. No.
                  LIB3078-008-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3687251
BLAST score
                  150
E value
                  4.0e-10
Match length
                  45
% identity
NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]
Seq. No.
                  295519
Seq. ID
                  LIB3078-008-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  q1172809
BLAST score
                  291
E value
                  4.0e-26
Match length
                  85
% identity
                  66
NCBI Description
                  60S RIBOSOMAL PROTEIN L10 (QM PROTEIN HOMOLOG) >gi 468056
                  (U06108) QM protein [Zea mays]
Seq. No.
                  295520
Seq. ID
                  LIB3078-008-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  q122007
BLAST score
                  217
E value
                  8.0e-18
Match length
                  44
% identity
                  98
NCBI Description
                  HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley
                  >gi 20448 emb CAA37828 (X53831) H2A histone protein (AA 1
                  - 149) [Petroselinum crispum]
Seq. No.
                  295521
                  LIB3078-008-Q1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132918
BLAST score
                  174
                  1.0e-12
E value
Match length
                  54
% identity
                  74
NCBI Description
                  50S RIBOSOMAL PROTEIN L35, CHLOROPLAST PRECURSOR (CL35)
                  >gi 81486 pir A36107 ribosomal protein L35 precursor,
                  chloroplast - spinach >gi 170139 (M60449) ribosomal protein
                  L35 [Spinacia oleracea]
```

Seq. No. 295522

LIB3078-008-Q1-K1-E9 Seq. ID

Method BLASTX NCBI GI g4126809



```
BLAST score
E value
                  5.0e-38
Match length
                  95
% identity
NCBI Description
                  (AB017042) glyoxalase I [Oryza sativa]
                  295523
Seq. No.
Seq. ID
                  LIB3078-008-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  q733456
BLAST score
                  188
                  3.0e-17
E value
Match length
                  65
                  80
% identity
                  (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
Seq. No.
                  295524
                  LIB3078-008-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4185143
BLAST score
                  141
E value
                  5.0e-09
Match length
                  72
                  43
% identity
                  (AC005724) putative signal recognition particle receptor
NCBI Description
                  beta subunit [Arabidopsis thaliana]
Seq. No.
                  295525
Seq. ID
                  LIB3078-008-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  q3252866
BLAST score
                  239
E value
                  3.0e-20
Match length
                  75
% identity
NCBI Description (AF033535) putative zinc transporter [Arabidopsis thaliana]
Seq. No.
                  295526
Seq. ID
                  LIB3078-008-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  q3335341
BLAST score
                  339
E value
                  7.0e-32
Match length
                  116
% identity
                  57
NCBI Description (AC004512) T8F5.10 [Arabidopsis thaliana]
Seq. No.
                  295527
                  LIB3078-008-Q1-K1-G6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1498596
BLAST score
                  158
E value
                  1.0e-83
Match length
                  258
% identity
                  90
NCBI Description Zea mays phospholipid transfer protein mRNA, complete cds
```

Seq. ID

Method NCBI GI



```
295528
Seq. No.
                  LIB3078-008-Q1-K1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2760330
BLAST score
                  152
                  6.0e-10
E value
                  94
Match length
% identity
NCBI Description (AC002130) F1N21.15 [Arabidopsis thaliana]
                  295529
Seq. No.
                  LIB3078-009-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1673456
BLAST score
                  221
                  1.0e-18
E value
Match length
                  46
% identity
                  87
NCBI Description (Y09214) rubisco small subunit [Zea mays]
                  295530
Seq. No.
                  LIB3078-009-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3386569
BLAST score
                  184
E value
                   7.0e-14
                  74
Match length
% identity
                   51
NCBI Description (AF079590) photosystem II type II chlorophyll a/b binding
                  protein [Sorghum bicolor]
Seq. No.
                   295531
                  LIB3078-009-Q1-K1-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3738208
BLAST score
                   161
E value
                   4.0e-11
Match length
                   118
                   37
% identity
                  (AL031853) strong similarity to human Rev interacting
NCBI Description
                   protein Rip-1 [Schizosaccharomyces pombe]
Seq. No.
                   295532
                   LIB3078-009-Q1-K1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2293568
BLAST score
                   227
                   4.0e-19
E value
                   55
Match length
                   75
% identity
NCBI Description
                  (AF012897) HvB12D homolog [Oryza sativa]
                   295533
Seq. No.
```

41346

LIB3078-009-Q1-K1-H4

BLASTX

g2773154



```
BLAST score
                  2.0e-19
E value
Match length
                  61
% identity
                  67
                  (AF039573) abscisic acid- and stress-inducible protein
NCBI Description
                  [Oryza sativa]
                  295534
Seq. No.
                  LIB3078-011-Q1-K1-A5
Seq. ID
Method
                  BLASTX
                  g2795809
NCBI GI
BLAST score
                  246
                  5.0e-21
E value
Match length
                  53
% identity
                  (AC003674) putative expansin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  295535
                  LIB3078-011-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4126473
BLAST score
                  341
E value
                  5.0e-32
Match length
                  94
                  71
% identity
                  (AB014884) adenylyl cyclase associated protein [Gossypium
NCBI Description
                  hirsutum]
Seq. No.
                  295536
                  LIB3078-011-Q1-K1-C12
Seq. ID
Method
                  BLASTN
                  g1944204
NCBI GI
BLAST score
                  52
                  3.0e-20
E value
                  68
Match length
                  94
% identity
NCBI Description Oryza sativa mRNA for RicMT, complete cds
                  295537
Seq. No.
                  LIB3078-011-Q1-K1-D9
Seq. ID
Method
                  BLASTN
                  g902200
NCBI GI
                  155
BLAST score
                  8.0e-82
E value
                  279
Match length
                  89
% identity
NCBI Description Z.mays complete chloroplast genome
                  295538
Seq. No.
                  LIB3078-011-Q1-K1-G5
Seq. ID
Method
                  BLASTX
                  g606811
NCBI GI
                  195
BLAST score
                  4.0e-15
E value
Match length
                  75
                  29
% identity
NCBI Description (U08401) carbonic anhydrase [Zea mays]
```



```
295539
Seq. No.
Seq. ID
                  LIB3078-011-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  q730526
BLAST score
                  291
E value
                  2.0e-26
Match length
                   97
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
                  >qi 480787 pir S37271 ribosomal protein L13 - Arabidopsis
                   thaliana >gi 404166 emb CAA53005 (X75162) BBC1 protein
                   [Arabidopsis thaliana]
                  295540
Seq. No.
Seq. ID
                  LIB3078-011-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g3763916
BLAST score
                  220
                   5.0e-18
E value
                  89
Match length
% identity
                   45
                  (AC004450) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4531439 gb AAD22124.1 AC006224 6 (AC006224) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  295541
                  LIB3078-012-Q1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1661160
BLAST score
                   245
E value
                   3.0e-21
Match length
                  79
% identity
                   65
                  (U74295) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   295542
                  LIB3078-012-Q1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4337195
BLAST score
                   152
E value
                   2.0e-10
Match length
                   45
                   76
% identity
                  (AC006403) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   295543
                  LIB3078-012-Q1-K1-D12
Seq. ID
Method
                  BLASTN
NCBI GI
                   g287829
BLAST score
                   64
E value
                   2.0e-27
Match length
                   147
```

Seq. No. 295544

86

NCBI Description Z.mays gene for polygalacturonase

% identity



```
LIB3078-012-Q1-K1-D3
Seq. ID
Method
                  BLASTX
                  g1063276
NCBI GI
BLAST score
                  381
                  8.0e-37
E value
                  118
Match length
% identity
                  68
                  (X92893) geranylgeranyl pyrophosphate synthase
NCBI Description
                  [Catharanthus roseus]
Seq. No.
                  295545
                  LIB3078-012-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3763918
BLAST score
                  177
E value
                  7.0e-13
Match length
                  41
% identity
                  80
NCBI Description
                  (AC004450) putative isopropylmalate dehydratase
                  [Arabidopsis thaliana]
Seq. No.
                  295546
Seq. ID
                  LIB3078-012-Q1-K1-G8
Method
                  BLASTN
NCBI GI
                  g881474
BLAST score
                  35
E value
                  4.0e-10
Match length
                  39
% identity
                  97
NCBI Description Human pephBGT-1 betaine-GABA transporter mRNA, complete cds
Seq. No.
                  295547
                LIB3078-013-Q1-K1-D9
Seq. ID
Method
                  BLASTX
                  g3776579
NCBI GI
BLAST score
                  352
                  4.0e-34
E value
Match length
                  105
% identity
NCBI Description
                  (AC005388) Strong similarity to F22013.22 gi 3063460 myosin
                  homolog from A. thaliana BAC gb AC003981. [Arabidopsis
                  thaliana]
                  295548
Seq. No.
Seq. ID
                  LIB3078-013-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g4204278
BLAST score
                  324
                  5.0e-30
E value
Match length
                  126
% identity
NCBI Description
                  (AC004146) putative Cytochrome P450 protein [Arabidopsis
                  thaliana]
```

Seq. No. 295549

Seq. ID LIB3078-013-Q1-K1-H6

Method BLASTX

Match length

126



```
q2231046
NCBI GI
BLAST score
                  186
E value
                  6.0e-14
Match length
                  57
% identity
                  70
NCBI Description (Y12618) PPF-1 protein [Pisum sativum]
Seq. No.
                  295550
Seq. ID
                  LIB3078-013-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g1747310
BLAST score
                  639
E value
                  4.0e-74
Match length
                  144
% identity
                  95
NCBI Description
                  (D58424) Myb-like DNA binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  295551
Seq. ID
                  LIB3078-014-Q1-K1-C6
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  295552
Seq. ID
                  LIB3078-014-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  q3861402
BLAST score
                  165
E value
                  2.0e-11
                  53
Match length
% identity
                  60
NCBI Description
                  (AJ235273) 50S RIBOSOMAL PROTEIN L33 (rpmG) [Rickettsia
                  prowazekii]
Seq. No.
                  295553
Seq. ID
                  LIB3078-014-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  g2618704
BLAST score
                  560
                  9.0e-58
E value
Match length
                  133
% identity
                  77
NCBI Description
                  (AC002510) putative thioredoxin reductase [Arabidopsis
                  thaliana]
Seq. No.
                  295554
Seq. ID
                  LIB3078-014-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  g3348077
BLAST score
                  392
E value
                  4.0e-38
```



% identity NCBI Description (AF078080) isochorismate synthase [Arabidopsis thaliana] Seq. No. 295555 LIB3078-015-Q1-K1-E10 Seq. ID Method BLASTX g3335333 NCBI GI BLAST score 154 E value 3.0e-10 Match length 114 39 % identity NCBI Description (AC004512) Similar to chloroplast membrane-associated 30KD protein precursor (IM30) gb M73744 from Pisum sativum. ESTs gb N37557, gb W43887 and gb AA042479 come from this gene. [Arabidopsis thaliana] 295556 Seq. No. Seq. ID LIB3078-015-Q1-K1-F2 Method BLASTX NCBI GI g1931643 BLAST score 148 7.0e-10 E value Match length 59 % identity 51 NCBI Description (U95973) DnaJ isolog [Arabidopsis thaliana] 295557 Seq. No. LIB3078-015-Q1-K1-F6 Seq. ID Method BLASTX NCBI GI q2088652 BLAST score 320 E value 1.0e-29 Match length 117 51 % identity (AF002109) 26S proteasome regulatory subunit S12 isolog NCBI Description [Arabidopsis thaliana] >gi_2351376 (U54561) translation initiation factor eIF2 p47 subunit homolog [Arabidopsis thaliana] Seq. No. 295558 LIB3078-015-Q1-K1-G10 Seq. ID Method BLASTX NCBI GI g2465430 BLAST score 166 2.0e-11 E value Match length 91 % identity 42 NCBI Description (AF021258) 32 kDa protein [Hordeum vulgare]

Seq. No. 295559

Seq. ID LIB3078-015-Q1-K1-G7

Method BLASTX
NCBI GI g1419370
BLAST score 270
E value 1.0e-23
Match length 57
% identity 96





```
NCBI Description (X97726) actin depolymerizing factor [Zea mays]
```

Seq. No. 295560

Seq. ID LIB3078-015-Q1-K1-H12

Method BLASTX
NCBI GI g2088734
BLAST score 166
E value 1.0e-11
Match length 55
% identity 60

NCBI Description (AF003141) Similar to dihydroorotate dehydrogenase

[Caenorhabditis elegans]

Seq. No. 295561

Seq. ID LIB3078-016-Q1-K1-C10

Method BLASTN
NCBI GI g2062705
BLAST score 36
E value 9.0e-11
Match length 36
% identity 100

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 295562

Seq. ID LIB3078-016-Q1-K1-E6

Method BLASTX
NCBI GI g3169883
BLAST score 327
E value 2.0e-30
Match length 113
% identity 59

NCBI Description (AF033194) dehydroquinate dehydratase/shikimate:NADP

oxidoreductase [Lycopersicon esculentum] >gi_3169888 (AF034411) dehydroquinate dehydratase/shikimate:NADP

oxidoreductase [Lycopersicon esculentum]

Seq. No. 295563

Seq. ID LIB3078-016-Q1-K1-H9

Method BLASTX
NCBI GI g515377
BLAST score 171
E value 2.0e-12
Match length 50
% identity 72

NCBI Description (X79715) histone H4 [Lolium temulentum]

Seq. No. 295564

Seq. ID LIB3078-017-Q1-K1-A9

Method BLASTX
NCBI GI g3377820
BLAST score 275
E value 2.0e-24
Match length 81
% identity 67

NCBI Description (AF076275) contains similarity to coatomer zeta chains

[Arabidopsis thaliana]



```
Seq. No.
                  LIB3078-017-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4262180
BLAST score
                  295
E value
                  3.0e-27
Match length
                  76
% identity
                  72
NCBI Description (AC005508) 29621 [Arabidopsis thaliana]
Seq. No.
                  295566
Seq. ID
                  LIB3078-017-Q1-K1-E10
Method
                  BLASTN
NCBI GI
                  q1667388
BLAST score
                  274
E value
                  1.0e-153
Match length
                  367
% identity
                  93
NCBI Description Z.mays gene encoding 3-hydroxy-3-methylglutaryl-CoA
                  reductase
Seq. No.
                  295567
                  LIB3078-018-Q1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006900
BLAST score
                  162
E value
                  5.0e-11
Match length
                  139
% identity
NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  295568
Seq. ID
                  LIB3078-018-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  g4309741
BLAST score
                  269
E value
                  1.0e-23
Match length
                  96
% identity
NCBI Description (AC006439) hypothetical protein [Arabidopsis thaliana]
                  295569
Seq. No.
Seq. ID
                  LIB3078-018-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g2746079
BLAST score
                  182
E value
                  2.0e-13
Match length
                  100
                  46
% identity
NCBI Description (AF015310) BTH1 [Brassica napus]
Seq. No.
                  295570
Seq. ID
                  LIB3078-018-Q1-K1-E3
Method
                  BLASTN
```

41353

g625147

34 1.0e-09

NCBI GI BLAST score

E value



Match length 66 % identity 88

NCBI Description Zea mays protein disulfide isomerase (pdi) mRNA, complete

cds

Seq. No. 295571

Seq. ID LIB3078-018-Q1-K1-E8

Method BLASTX
NCBI GI g4539452
BLAST score 439
E value 2.0e-43
Match length 146
% identity 51

NCBI Description (AL049500) putative phosphoribosylanthranilate transferase

[Arabidopsis thaliana]

Seq. No. 295572

Seq. ID LIB3078-018-Q1-K1-G12

Method BLASTX
NCBI GI g231404
BLAST score 713
E value 1.0e-75
Match length 136
% identity 98

NCBI Description HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-44(B-12) B*4402

ALPHA CHAIN PRECURSOR (B44.2) >gi_2118755_pir__I61861 MHC HLA-B44.2 chain - human >gi_386900 (M24038) MHC HLA-B44.2

chain [Homo sapiens]

Seq. No. 295573

Seq. ID LIB3078-018-Q1-K1-H12

Method BLASTX
NCBI GI g309233
BLAST score 158
E value 2.0e-13
Match length 107
% identity 47

NCBI Description (M24509) ferritin heavy chain [Mus musculus] >qi 1435203

(U58829) ferritin-H subunit [Rattus norvegicus]

Seq. No. 295574

Seq. ID LIB3078-019-Q1-K1-A11

Method BLASTX
NCBI GI 94589960
BLAST score 299
E value 4.0e-27
Match length 126
% identity 51

NCBI Description (AC007169) unknown protein [Arabidopsis thaliana]

Seq. No. 295575

Seq. ID LIB3078-019-Q1-K1-B3

Method BLASTX
NCBI GI g549986
BLAST score 237
E value 3.0e-20
Match length 53



```
% identity
                  (U13149) possible apospory-associated protein [Pennisetum
NCBI Description
                  ciliare]
Seq. No.
                  295576
                  LIB3078-019-Q1-K1-B6
Seq. ID
Method
                  BLASTN
                  g169818
NCBI GI
BLAST score
                  82
                  4.0e-38
E value
Match length
                  82
% identity
                  100
NCBI Description Rice 25S ribosomal RNA gene
Seq. No.
                  295577
Seq. ID
                  LIB3078-019-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  q1084457
BLAST score
                  265
E value
                  4.0e-23
Match length
                  138
% identity
                  43
                  elongation factor 1-beta - Rice >gi 432368 dbj BAA04903
NCBI Description
                  (D23674) elongation factor 1 beta [Oryza sativa]
Seq. No.
                  295578
Seq. ID
                  LIB3078-019-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g445612
BLAST score
                  177
E value
                  6.0e-13
Match length
                  112
% identity
                  38
NCBI Description ribosomal protein S19 [Solanum tuberosum]
                  295579
Seq. No.
                  LIB3078-019-Q1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913641
BLAST score
                  368
                  3.0e-35
E value
Match length
                  73
                  96
% identity
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                  (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi 3041777 dbj BAA25423 (AB007194)
                  fructose-1,6-bisphosphatase [Oryza sativa]
                  295580
Seq. No.
Seq. ID
                  LIB3078-019-Q1-K1-H11
Method
                  BLASTX
```

Method BLASTX
NCBI GI g1154954
BLAST score 264
E value 2.0e-23
Match length 81
% identity 69

NCBI Description (X94693) histone H2A [Triticum aestivum]

Match length

NCBI Description

% identity

103

76

```
Seq. No.
                  295581
Seq. ID
                  LIB3078-020-Q1-K1-A11
Method
                  BLASTN
NCBI GI
                  g433038
BLAST score
                  41
E value
                  8.0e-14
Match length
                  65
% identity
                  Zea mays W-22 clone cDNA7 retroelement PREM-1-containing
NCBI Description
                  mRNA
                  295582
Seq. No.
Seq. ID
                  LIB3078-020-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g3122071
BLAST score
                  346
E value
                  9.0e-33
                  119
Match length
% identity
                  66
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >qi 2130148 pir S66339 translation elongation factor eEF-1
                  alpha chain - maize >gi 1321656 dbj BAA08249 (D45408)
                  alpha subunit of tlanslation elongation factor 1 [Zea mays]
Seq. No.
                  295583
Seq. ID
                  LIB3078-021-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  g733456
BLAST score
                  219
E value
                  7.0e-22
Match length
                  78
% identity
                  77
                  (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
Seq. No.
                  295584
                  LIB3078-022-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1398999
BLAST score
                  383
E value
                  3.0e-37
Match length
                  84
                  85
% identity
NCBI Description
                   (D49713) 23 kDa polypeptide of photosystem II [Oryza
                  sativa]
                  295585
Seq. No.
                  LIB3078-022-Q1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g974850
BLAST score
                  328
                  1.0e-35
E value
```

(X89023) LHCII type I protein [Hordeum vulgare]

NCBI Description



```
Seq. No.
                  295586
                  LIB3078-022-Q1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q551288
BLAST score
                  145
E value
                  2.0e-09
                  60
Match length
                  50
% identity
                  (Z33611) phosphoglycerate mutase [Zea mays]
NCBI Description
Seq. No.
                  295587
                  LIB3078-022-Q1-K1-F3
Seq. ID
Method
                  BLASTX
                  q118104
NCBI GI
                  386
BLAST score
E value
                  2.0e-37
Match length
                  106
% identity
                  74
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi 68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi 168461 (M55021) cyclophilin [Zea mays]
                  >qi 829148 emb CAA48638 (X68678) cyclophilin [Zea mays]
                  295588
Seq. No.
                  LIB3078-022-Q1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1346033
BLAST score
                  173
E value
                   9.0e-13
Match length
                  81
                   48
% identity
                  FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS)
NCBI Description
                   (FARNESYL DIPHOSPHATE SYNTHETASE) (DIMETHYLALLYLTRANSFERASE
                   / GERANYLTRANSTRANSFERASE >gi_662368 (L39789) farnesyl
                   pyrophosphate synthetase [Zea mays]
                   295589
Seq. No.
                  LIB3078-022-Q1-K1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1171579
BLAST score
                   387
E value
                   2.0e-37
Match length
                   124
                   58
% identity
                  (X95342) cytochrome P450 [Nicotiana tabacum]
NCBI Description
                   295590
Seq. No.
                   LIB3078-022-Q1-K1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3386569
BLAST score
                   326
                   2.0e-30
E value
Match length
                   90
                   74
% identity
```

41357

protein [Sorghum bicolor]

(AF079590) photosystem II type II chlorophyll a/b binding



```
Seq. No.
                  295591
Seq. ID
                  LIB3078-023-Q1-K1-C2
Method
                  BLASTN
NCBI GI
                  g2981206
BLAST score
                  33
E value
                   4.0e-09
Match length
                   45
                   93
% identity
NCBI Description
                   Zea mays photosystem I complex PsaH subunit precursor
                   (psaH) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
Seq. No.
                   295592
                  LIB3078-023-Q1-K1-C4
                  BLASTX
```

Seq. ID Method NCBI GI q2546954 BLAST score 217 E value 5.0e-18

295593

Match length 78 % identity

Seq. No.

NCBI Description (Y15108) translation elongation factor-TU [Glycine max]

LIB3078-023-Q1-K1-C8 Seq. ID Method BLASTX NCBI GI g115771 BLAST score 777 E value 4.0e-83 Match length 149 % identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >qi 82682 pir S04453 chlorophyll

a/b-binding protein precursor - maize

>gi 22224 emb CAA32900 (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No. 295594

LIB3078-023-Q1-K1-D12 Seq. ID

Method BLASTX NCBI GI q283038 BLAST score 150 3.0e-10 E value Match length 54 61 % identity

chlorophyll a/b-binding protein (cab-m7) precursor - maize NCBI Description

>qi 22230 emb CAA37474 (X53398) light harvesting

chlorophyll a /b binding protein [Zea mays]

295595 Seq. No.

Seq. ID LIB3078-023-Q1-K1-D4

Method BLASTX g4584342 NCBI GI BLAST score 290 5.0e-26 E value Match length 146 % identity 46





```
NCBI Description
                   (AC007127) putative ubiquitin protein [Arabidopsis
                  thaliana]
                  295596
Seq. No.
                  LIB3078-023-Q1-K1-E6
Seq. ID
Method
                  BLASTX
                  q4538920
NCBI GI
BLAST score
                  245
E value
                  6.0e-21
Match length
                  86
% identity
                  65
                   (AL049483) nitrogen fixation like protein [Arabidopsis
NCBI Description
                  thaliana]
                  295597
Seq. No.
                  LIB3078-023-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2668742
BLAST score
                  287
                  1.0e-25
E value
Match length
                  86
% identity
                  67
NCBI Description
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
Seq. No.
                  295598
                  LIB3078-023-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2921158
BLAST score
                  293
E value
                  3.0e-29
Match length
                  115
% identity
                  60
                  (AF022909) ClpC [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  295599
                  LIB3078-023-Q1-K1-H12
Seq. ID
Method
                  BLASTX
                  g2961176
NCBI GI
BLAST score
                   416
E value
                  8.0e-41
Match length
                  144
% identity
                  62
NCBI Description
                  (AF050674) ribosomal protein L27 precursor [Oryza sativa]
Seq. No.
                  295600
Seq. ID
                  LIB3078-023-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g3885886
BLAST score
                  182
                  9.0e-14
E value
Match length
                  68
% identity
                  56
```

NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No.

295601

Seq. ID LIB3078-023-Q1-K1-H6

Method BLASTX



```
g3914465
NCBI GI
BLAST score
                  242
                  4.0e-31
E value
Match length
                  114
% identity
                  76
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                  >gi 2981207 (AF052076) photosystem I complex PsaH subunit
                  precursor [Zea mays]
Seq. No.
                  295602
                  LIB3078-024-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  275
                  2.0e-24
E value
Match length
                  72
% identity
                  72
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                  295603
                  LIB3078-024-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3868758
BLAST score
                  140
E value
                  5.0e-11
Match length
                  68
% identity
                  57
NCBI Description
                  (D89802) elongation factor 1B gamma [Oryza sativa]
                  295604
Seq. No.
                  LIB3078-024-Q1-K1-D10
Seq. ID
Method
                  BLASTX
                  g3550483
NCBI GI
BLAST score
                  211
E value
                  5.0e-17
Match length
                  83
% identity
                  54
NCBI Description (AJ224324) cp31BHv [Hordeum vulgare]
                  295605
Seq. No.
                  LIB3078-024-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462828
BLAST score
                  167
                  3.0e-12
E value
Match length
                  70
                  47
% identity
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  295606
                  LIB3078-024-Q1-K1-F8
```

Seq. ID

Method BLASTX

NCBI GI g129591 BLAST score 140 E value 1.0e-08 Match length 70





% identity PHENYLALANINE AMMONIA-LYASE >gi 295824 emb CAA34226 NCBI Description (X16099) phenylalanine ammonia-lyase [Oryza sativa] 295607

Seq. No. LIB3078-025-Q1-K1-D3 Seq. ID Method BLASTX

g2500345 NCBI GI BLAST score 246 E value 5.0e-21 Match length 58 % identity 81

NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG (HIGH MOBILITY NCBI Description

GROUP-LIKE NUCLEAR PROTEIN 2 HOMOLOG)

>gi 2618578 dbj BAA23363 (D50420) OTK27 [Homo sapiens]

>gi 3859990 (AF091076) OTK27 [Homo sapiens]

>gi 1589072 prf 2210268A nuclear protein-NHP2-like protein

[Homo sapiens]

Seq. No. 295608 Seq. ID

LIB3078-025-Q1-K1-F10

Method BLASTX NCBI GI g1173194 BLAST score 160 E value 4.0e-11 Match length 70 % identity 47

NCBI Description 30S RIBOSOMAL PROTEIN S13, CHLOROPLAST PRECURSOR (CS13)

>qi 2119093 pir S59594 ribosomal protein S13 precursor, chloroplast - Arabidopsis thaliana >gi 16767 emb CAA79013 (Z17611) chloroplast 30S ribosomal protein S13 [Arabidopsis

thaliana] >gi_662869_emb_CAA88028_ (Z47986) chloroplast ribosomal protein S13 [Arabidopsis thaliana]

>qi 1107483 emb CAA63021 (X91955) 30S ribosomal protein S13 [Arabidopsis thaliana] >gi 1515107 emb CAA60413 (X86734) plastid ribosomal protein S13 [Arabidopsis

thaliana]

Seq. No. 295609

LIB3078-025-Q1-K1-G1 Seq. ID

Method BLASTX NCBI GI g4587610 BLAST score 428 3.0e-42 E value Match length 107 74 % identity

(AC006951) putative indole-3-glycerol phosphate synthase NCBI Description

precursor [Arabidopsis thaliana]

295610 Seq. No.

LIB3078-025-Q1-K1-G10 Seq. ID

Method BLASTX g2245004 NCBI GI BLAST score 360 E value 2.0e-34 Match length 118 % identity 56



[Arabidopsis thaliana]

NCBI Description (Z97341) similarity to membrane transport protein

Seq. No. 295611

Seq. ID LIB3078-025-Q1-K1-H8

Method BLASTN
NCBI GI g3868757
BLAST score 40
E value 2.0e-13
Match length 100
% identity 85

NCBI Description Oryza sativa mRNA for elongation factor 1B gamma, complete

cds

Seq. No. 295612

Seq. ID LIB3078-026-Q1-K1-B2

Method BLASTX
NCBI GI g3318613
BLAST score 190
E value 3.0e-17
Match length 78
% identity 65

NCBI Description (AB016064) mitochondrial phosphate transporter [Zea mays]

Seq. No. 295613

Seq. ID LIB3078-026-Q1-K1-C11

Method BLASTX
NCBI GI g99755
BLAST score 400
E value 6.0e-39
Match length 141
% identity 55

NCBI Description RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis

thaliana retrotransposon Tal-1 (fragment)

>gi_16356_emb_CAA37917_ (X53973) reverse transcriptase

[Arabidopsis thaliana]

Seq. No. 295614

Seq. ID LIB3078-026-Q1-K1-D1

Method BLASTN
NCBI GI g998429
BLAST score 53
E value 6.0e-21
Match length 153
% identity 84

NCBI Description GRF1=general regulatory factor [Zea mays, XL80, Genomic,

5348 nt]

Seq. No. 295615

Seq. ID LIB3078-026-Q1-K1-D9

Method BLASTX
NCBI GI g3982576
BLAST score 322
E value 6.0e-30
Match length 80
% identity 79

NCBI Description (AF023140) imidazoleglycerol phosphate dehydratase [Thlaspi



goesingense]

```
295616
Seq. No.
Seq. ID
                  LIB3078-026-Q1-K1-F8
Method
                   BLASTX
NCBI GI
                   g4406372
                   157
BLAST score
                   9.0e-11
E value
                   70
Match length
                   49
% identity
NCBI Description
                   (AF109156) thiosulfate sulfurtransferase [Datisca
                   glomerata]
                   295617
Seq. No.
                   LIB3078-026-Q1-K1-G11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g168470
BLAST score
                   40
                   4.0e-13
E value
Match length
                   55
% identity
NCBI Description Maize ferredoxin I (Fd) isoprotein mRNA, pFD1'
                   295618
Seq. No.
Seq. ID
                   LIB3078-026-Q1-K1-H2
Method
                   BLASTX
NCBI GI
                   g733458
BLAST score
                   189
                   2.0e-14
E value
Match length
                   50
% identity
NCBI Description
                   (U23190) chlorophyll a/b-binding apoprotein CP24 precursor
                   [Zea mays]
Seq. No.
                   295619
                   LIB3078-026-Q1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3386569
BLAST score
                   311
E value
                   1.0e-28
Match length
                   107
% identity
                   64
                   (AF079590) photosystem II type II chlorophyll a/b binding
NCBI Description
                   protein [Sorghum bicolor]
                   295620
Seq. No.
                   LIB3078-026-Q1-K1-H6
Seq. ID
Method
                   BLASTX
                   g1084479
NCBI GI
BLAST score
                   448
                   1.0e-44
E value
                   96
Match length
% identity
                   95
                   H+-transporting ATP synthase (EC 3.6.1.34) delta chain -
NCBI Description
                   {\tt maize (fragment) > gi\_311237\_emb\_CAA46804\_ (X66005)}
                   H(+)-transporting ATP synthase [Zea mays]
```



```
295621
Seq. No.
                  LIB3078-027-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2058284
                  212
BLAST score
                  5.0e-17
E value
Match length
                  88
% identity
                  47
NCBI Description (X97378) atranbplb [Arabidopsis thaliana]
Seq. No.
                  295622
                  LIB3078-027-Q1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914006
BLAST score
                  327
E value
                  2.0e-30
Match length
                  126
% identity
                  60
NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi_1816588
                  (U85495) LON2 [Zea mays]
Seq. No.
                  295623
                  LIB3078-027-Q1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2431769
BLAST score
                  205
                                                                  , in,
E value
                  3.0e-16
Match length
                  103
% identity
NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays]
Seq. No.
                  295624
                  LIB3078-027-Q1-K1-B1
Seq. ID
                  BLASTX
Method
                  g4567312
NCBI GI
BLAST score
                  200
                  1.0e-15
E value
                  118
Match length
                   42
% identity
NCBI Description (AC005956) hypothetical protein [Arabidopsis thaliana]
                  295625
Seq. No.
                  LIB3078-027-Q1-K1-B11
Seq. ID
                  BLASTX
Method
                  g3075488
NCBI GI
BLAST score
                   215
                   5.0e-26
E value
Match length
                  84
                   74
% identity
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                   295626
                   LIB3078-027-Q1-K1-D2
Seq. ID
Method
                   BLASTN
```

41364

q3821780

36 1.0e-10

NCBI GI BLAST score

E value



Match length 100 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No.

295627

Seq. ID

LIB3078-027-Q1-K1-F2

Method NCBI GI BLASTX q3236248

BLAST score

246

E value Match length

2.0e-21 74

72

% identity NCBI Description

(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.

295628

Seq. ID

LIB3078-027-Q1-K1-G12

Method NCBI GI BLASTX g2493493 149

BLAST score E value

9.0e-10

Match length % identity

39 74

NCBI Description

SERINE CARBOXYPEPTIDASE II-1 PRECURSOR (CP-MII.1)

>gi 619352 bbs 153538 CP-MII.1=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 324

65

Seq. No.

295629

Seq. ID

LIB3078-027-Q1-K1-G4

Method BLASTX NCBI GI g4506629 BLAST score 182 1.0e-13 E value 52 Match length

% identity

ribosomal protein L29 >gi 1350706 sp P47914_RL29_HUMAN 60S NCBI Description

RIBOSOMAL PROTEIN L29 (CELL SURFACE HEPARIN BINDING PROTEIN HIP) >gi 2136119 pir S65784 ribosomal protein L29 - human >gi 806697 (U10248) ribosomal protein L29 [Homo sapiens]

>gi 1215742 (U49083) HIP [Homo sapiens]

Seq. No.

295630

Seq. ID

LIB3078-028-Q1-K1-D6

Method BLASTX NCBI GI q1710416 BLAST score 226 E value 8.0e-19 69 Match length

NCBI Description

CHLOROPLAST 50S RIBOSOMAL PROTEIN L1

>gi 2147041 pir S73259 50S ribosomal protein L1 - Porphyra purpurea chloroplast >gi 1276804 (U38804) 50S ribosomal

protein L1 [Porphyra purpurea]

Seq. No.

% identity

295631

61

Seq. ID

LIB3078-028-Q1-K1-E8

Method BLASTX



```
NCBI GI
                  g132659
BLAST score
                  195
                  4.0e-18
E value
Match length
                  106
% identity
                  55
                  50S RIBOSOMAL PROTEIN L13, CHLOROPLAST PRECURSOR (CL13)
NCBI Description
                  >gi 81483 pir A32033 ribosomal protein L13 precursor,
                  chloroplast - spinach >gi 170133 (J04461) ribosomal protein
                  L13 [Spinacia oleracea]
                  295632
Seq. No.
                  LIB3078-028-Q1-K1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2981213
BLAST score
                  81
E value
                  9.0e-38
Match length
                  244
                  85
% identity
                  Zea mays photosystem I complex PsaN subunit precursor
NCBI Description
                   (psaN) mRNA, nuclear gene encoding chloroplast protein,
                  partial cds
Seq. No.
                  295633
                  LIB3078-029-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4522007
BLAST score
                  176
E value
                  7.0e-13
Match length
                  48
% identity
                  71
                  (AC007069) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  295634
                  LIB3078-029-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g102330
BLAST score
                  210
E value
                  5.0e-17
Match length
                  67
% identity
                  63
NCBI Description actin - Plasmodium falciparum
                  295635
Seq. No.
Seq. ID
                  LIB3078-029-Q1-K1-C7
Method
                  BLASTX
                  g3334441
NCBI GI
BLAST score
                  177
E value
                  7.0e-13
Match length
                  83
% identity
                  46
```

NCBI Description

HYPOTHETICAL 47.9 KD PROTEIN T517.9 IN CHROMOSOME II >gi 2642161 (AC003000) hypothetical protein [Arabidopsis

thaliana]

Seq. No.

295636

Seq. ID

LIB3078-029-Q1-K1-D9

Method

BLASTX



```
g3789954
NCBI GI
BLAST score
                  364
E value
                  9.0e-35
Match length
                  75
% identity
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
Seq. No.
                  295637
Seq. ID
                  LIB3078-029-Q1-K1-F11
Method
                  BLASTN
NCBI GI
                  g397395
BLAST score
                  92
E value
                  2.0e-44
Match length
                  128
% identity
                  93
NCBI Description Z.mays MNB1b mRNA for DNA-binding protein
Seq. No.
                  295638
Seq. ID
                  LIB3078-029-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  q3913811
BLAST score
                  223
E value
                  7.0e-19
Match length
                  71
                  65
% identity
NCBI Description
                  GLUTAMYL-TRNA REDUCTASE PRECURSOR (GLUTR)
                  >gi 2920320 dbj BAA25003 (AB011416) glutamyl-tRNA
                  reductase [Oryza sativa]
Seq. No.
                  295639
Seq. ID
                  LIB3078-029-Q1-K1-G3
Method
                  BLASTN
NCBI GI
                  g2645165
BLAST score
                  58
                  5.0e-24
E value
Match length
                  70
% identity
                  96
NCBI Description Oryza sativa mRNA, similar to ribosomal protein
Seq. No.
                  295640
                  LIB3078-029-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1707642
BLAST score
                  152
E value
                  5.0e-10
Match length
                  63
% identity
                  54
NCBI Description (Y07748) TMK [Oryza sativa]
                  295641
Seq. No.
```

Seq. ID

LIB3078-029-Q1-K1-H5 Method BLASTX

NCBI GI g606815 BLAST score 262 E value 5.0e-23 94 Match length

BLAST score

E value

169

5.0e-12





عزوزتو

```
% identity
                  (U08403) carbonic anhydrase [Zea mays]
NCBI Description
                  295642
Seq. No.
                  LIB3078-030-Q1-K1-A2
Seq. ID
Method
                  BLASTX
                  g2982268
NCBI GI
                  207
BLAST score
                  2.0e-16
E value
                  71
Match length
                  61
% identity
                  (AF051217) probable 40S ribosomal protein S15 [Picea
NCBI Description
                  mariana]
Seq. No.
                  295643
                  LIB3078-030-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4530591
BLAST score
                  164
                  2.0e-11
E value
Match length
                  49
                  65
% identity
                  (AF132475) heme oxygenase 1 [Arabidopsis thaliana]
NCBI Description
                  >gi 4530593 gb AAD22108.1_ (AF132476) heme oxygenase 1
                   [Arabidopsis thaliana]
Seq. No.
                  295644
                  LIB3078-030-Q1-K1-C11
Seq. ID
Method
                  BLASTX
                  g115813
NCBI GI
BLAST score
                  171
                  2.0e-12
E value
Match length
                  43
                  74
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE III PRECURSOR
NCBI Description
                   (CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                  295645
Seq. No.
                  LIB3078-030-Q1-K1-C12
Seq. ID
Method
                  BLASTX
                  g1174783
NCBI GI
BLAST score
                  332
E value
                   6.0e-31
Match length
                  67
% identity
                  99
                  TRYPTOPHAN SYNTHASE ALPHA CHAIN PRECURSOR
NCBI Description
                  >gi_1362207_pir__S56665 tryptophan synthase (EC 4.2.1.20)
                  alpha chain - maize >gi_440171_emb_CAA54131_ (X76713)
                  tryptophan synthase, alpha subunit [Zea mays]
Seq. No.
                  295646
                  LIB3078-030-Q1-K1-F12
Seq. ID
Method
                  BLASTX
                  g730558
NCBI GI
```



Match length 76 % identity 47

NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi_1076636_pir__S48027 ribosomal

protein L34 - common tobacco >gi_2129964_pir__S48028 ribosomal protein L34.e, cytosolic - common tobacco >gi_436030 (L27089) 60S ribosomal protein L34 [Nicotiana tabacum] >gi_436032 (L27107) 60S ribosomal protein L34

[Nicotiana tabacum]

Seq. No. 295647

Seq. ID LIB3078-030-Q1-K1-G2

Method BLASTN
NCBI GI g22302
BLAST score 47
E value 2.0e-17
Match length 51
% identity 98

NCBI Description Maize Gpc1 gene for glyceraldehyde-3-phosphate

dehydrogenase (GADPH) subunit C

Seq. No. 295648

Seq. ID LIB3078-030-Q1-K1-G7

Method BLASTX
NCBI GI g2245026
BLAST score 259
E value 1.0e-22
Match length 91
% identity 56

NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 295649

Seq. ID LIB3078-031-Q1-K1-A1

Method BLASTX
NCBI GI g115771
BLAST score 256
E value 4.0e-27
Match length 87
% identity 79

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >gi 82682 pir S04453 chlorophyll

a/b-binding protein precursor - maize

>gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No. 295650

Seq. ID LIB3078-031-Q1-K1-A4

Method BLASTX
NCBI GI 9733456
BLAST score 575
E value 1.0e-70
Match length 144
% identity 97

NCBI Description (U23189) chlorophyll a/b-binding apoprotein CP26 precursor

[Zea mays]

Seq. No. 295651

Seq. ID LIB3078-031-Q1-K1-B1

Method

NCBI GI

BLASTX

g729478

```
BLASTX
Method
NCBI GI
                  g4263712
                                            4
                  254
BLAST score
                  4.0e-22
E value
Match length
                  94
                  53
% identity
                  (AC006223) putative ribosomal protein S12 [Arabidopsis
NCBI Description
                  thaliana]
                  295652
Seq. No.
                  LIB3078-031-Q1-K1-C2
Seq. ID
Method
                  BLASTX
                  g3292814
NCBI GI
BLAST score
                  155
E value
                  2.0e-10
Match length
                  51
% identity
                  55
                  (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  295653
Seq. ID
                  LIB3078-031-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g1262849
BLAST score
                  224
                  1.0e-18
E value
Match length
                  74
% identity
                  61
                  (U51633) type 1 light-harvesting chlorophyll a/b-binding
NCBI Description
                  polypeptide [Pinus palustris]
Seq. No.
                  295654
                  LIB3078-031-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3047116
BLAST score
                  429
                  1.0e-42
E value
Match length
                  104
                  78
% identity
                  (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  295655
                  LIB3078-031-Q1-K1-F2
Seq. ID
Method
                  BLASTX
                  g115786
NCBI GI
BLAST score
                  156
E value
                  2.0e-10
Match length
                  28
                  100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB) (LHCP) >gi_82680_pir__A29119 chlorophyll a/b-binding
                  protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea
                  mays]
                  295656
Seq. No.
                  LIB3078-031-Q1-K1-G8
Seq. ID
```



```
BLAST score
                  2.0e-63
E value
Match length
                  122
                  94
% identity
                  FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
NCBI Description
                  >qi 442481 dbj BAA04616 (D17790) ferredoxin-NADP+
                  reductase [Oryza sativa]
                  295657
Seq. No.
                  LIB3078-032-Q1-K1-C2
Seq. ID
Method
                  BLASTN
                  g2062705
NCBI GI
BLAST score
                  36
                  8.0e-11
E value
                   36
Match length
% identity
                  100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  295658
Seq. ID
                  LIB3078-032-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                   q2529668
                   149
BLAST score
                   1.0e-09
E value
                   58
Match length
% identity
                   (AC002535) putative photolyase/blue-light receptor
NCBI Description
                   [Arabidopsis thaliana] >gi 3319288 (AF053366)
                   photolyase/blue light photoreceptor PHR2 [Arabidopsis
                   thaliana]
                   295659
Seq. No.
Seq. ID
                   LIB3078-032-Q1-K1-C7
Method
                   BLASTX
NCBI GI
                   g2565436
BLAST score
                   142
E value
                   4.0e-09
Match length
                   76
% identity
                   42
                  (AF028842) DegP protease precursor [Arabidopsis thaliana]
NCBI Description
                   295660
Seq. No.
                   LIB3078-032-Q1-K1-H10
Seq. ID
Method
                   BLASTX
                   q2191165
NCBI GI
                   196
BLAST score
                   5.0e-15
E value
Match length
                   50
                   70
% identity
                   (AF007270) A IG002P16.14 gene product [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   295661
                   LIB3078-033-Q1-K1-A5
Seq. ID
                   BLASTN
Method
```

41371

g168606

106

NCBI GI BLAST score



E value 9.0e-53 Match length 198 % identity 88

NCBI Description Zea mays mitochondrial Rieske Fe-S protein mRNA, complete

cds

Seq. No.

Seq. ID LIB3078-033-Q1-K1-B10

295662

Method BLASTX
NCBI GI g136063
BLAST score 398
E value 1.0e-38
Match length 103
% identity 75

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)

>gi_68426_pir__ISZMT triose-phosphate isomerase (EC
5.3.1.1) - maize >gi_168647 (L00371) triosephosphate
isomerase 1 [Zea mays] >gi_217974_dbj_BAA00009_ (D00012)

triosephosphate isomerase [Zea mays]

Seq. No. 295663

Seq. ID LIB3078-033-Q1-K1-B3

Method BLASTX
NCBI GI g430947
BLAST score 157
E value 1.0e-10
Match length 62
% identity 53

NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 295664

Seq. ID LIB3078-033-Q1-K1-B4

Method BLASTN
NCBI GI g559531
BLAST score 236
E value 1.0e-130
Match length 252
% identity 98

NCBI Description Z.mays mRNA for cysteine proteinase

Seq. No. 295665

Seq. ID LIB3078-033-Q1-K1-C10

Method BLASTX
NCBI GI g2565010
BLAST score 512
E value 4.0e-52
Match length 145
% identity 68

NCBI Description (AC002983) putative microfibril-associated protein

[Arabidopsis thaliana] >gi_3377811 (AF076275) contains similarity to ATP synthase B/B' (Pfam: ATP-synt_B.hmm,

score: 11.71) [Arabidopsis thaliana]

Seq. No. 295666

Seq. ID LIB3078-033-Q1-K1-D4

Method BLASTX

NCBI GI

BLAST score





```
g1706261
NCBI GI
BLAST score
                  478
E value
                  1.0e-49
Match length
                  153
% identity
                  73
NCBI Description CYSTEINE PROTEINASE 2 PRECURSOR >gi 2118129 pir S59598
                  cysteine proteinase 2 precursor - maize
                  >gi 644490 dbj BAA08245 (D45403) cysteine proteinase [Zea
                  mays]
Seq. No.
                  295667
Seq. ID
                  LIB3078-033-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  g1491774
BLAST score
                  280
E value
                  7.0e-28
Match length
                  105
% identity
                  61
NCBI Description (X99936) cysteine protease [Zea mays]
Seq. No.
                  295668
Seq. ID
                  LIB3078-033-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g3334376
BLAST score
                  407
E value
                  8.0e-40
Match length
                  117
% identity
                  74
NCBI Description THIOREDOXIN M-TYPE PRECURSOR (TRX-M) >qi 725276 (L40957)
                  thioredoxin M [Zea mays]
Seq. No.
                  295669
Seq. ID
                  LIB3078-033-Q1-K1-F12
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  35
E value
                  3.0e-10
Match length
                  35
% identity
                  100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  295670
Seq. No.
Seq. ID
                  LIB3078-033-Q1-K1-F3
                 BLASTX
Method
NCBI GI
                  g2773154
BLAST score
                  162
                  5.0e-11
E value
Match length
                  74
% identity
                  41
NCBI Description (AF039573) abscisic acid- and stress-inducible protein
                  [Oryza sativa]
Seq. No.
                  295671
Seq. ID
                  LIB3078-033-Q1-K1-H2
Method
                  BLASTX
```

41373

g4263712



8

```
E value
                  3.0e-22
Match length
                  71
% identity
NCBI Description
                  (AC006223) putative ribosomal protein S12 [Arabidopsis
                  thaliana]
                  295672
Seq. No.
                  LIB3078-033-Q1-K1-H6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4165340
BLAST score
                  39
E value
                  2.0e-12
Match length
                  59
% identity
                  92
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F11M15 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  295673
Seq. ID
                  LIB3078-034-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  q2943792
BLAST score
                  363
E value
                  4.0e-36
Match length
                  124
                  65
% identity
NCBI Description (AB006809) PV72 [Cucurbita sp.]
Seq. No.
                  295674
Seq. ID
                  LIB3078-034-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g1778149
BLAST score
                  210
                  8.0e-17
E value
Match length
                  91
                  51
% identity
                  (U66404) phosphate/phosphoenolpyruvate translocator
NCBI Description
                  precursor [Zea mays]
Seq. No.
                  295675
                  LIB3078-034-Q1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4105561
BLAST score
                  269
                  1.0e-23
E value
                  94
Match length
                  64
% identity
NCBI Description (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]
                  295676
Seq. No.
                  LIB3078-035-Q1-K1-A12
Seq. ID
Method
                  BLASTX
                  g730536
NCBI GI
BLAST score
                  186
E value
                  9.0e-14
Match length
                  48
                  79
% identity
```

41374

NCBI Description 60S RIBOSOMAL PROTEIN L23 >gi 310933 (L18915) 60S ribosomal

Match length

87





protein subunit L17 [Nicotiana tabacum]

```
295677
Seq. No.
Seq. ID
                  LIB3078-035-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  q3057150
                  296
BLAST score
                  8.0e-27
E value
                  75
Match length
% identity
NCBI Description (AF059037) chaperonin 10 [Arabidopsis thaliana]
                  295678
Seq. No.
                  LIB3078-035-Q1-K1-A3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g116167
BLAST score
                  177
E value
                  1.0e-18
                  116
Match length
                  47
% identity
                  G2/MITOTIC-SPECIFIC CYCLIN C13-1 (A-LIKE CYCLIN)
NCBI Description
                  >gi 100153 pir S16521 cyclin, mitotic - carrot (fragment)
                  >gi 829260 emb CAA44631 (X62819) mitotic cyclin [Daucus
                  carota]
                  295679
Seq. No.
Seq. ID
                  LIB3078-035-Q1-K1-F10
                  BLASTX
Method
                  g1001650
NCBI GI
BLAST score
                  187
                  5.0e-14
E value
Match length
                  89
% identity
                  (D64002) hypothetical protein [Synechocystis sp.]
NCBI Description
                  295680
Seq. No.
                  LIB3078-035-Q1-K1-F12
Seq. ID
                  BLASTX
Method
                  g1729896
NCBI GI
                  154
BLAST score
                  2.0e-10
E value
                  61
Match length
% identity
                  66
                  TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE HOMOLOG 1
NCBI Description
                   (P97/CDC48 HOMOLOG 1) >gi 3874005 emb_CAA90050_ (Z49886)
                  similar to transitional endoplasmic reticulum ATPase
                  homolog 1 (P97 protein); cDNA EST EMBL:D67689 comes from
                  this gene; cDNA EST EMBL:D37049 comes from this gene; cDNA
                  EST EMBL:D37645 comes from this gene; cDNA EST EM
                  295681
Seq. No.
                  LIB3078-035-Q1-K1-F5
Seq. ID
Method
                  BLASTX
                  g3121731
NCBI GI
BLAST score
                  200
E value
                  7.0e-16
```

Match length

% identity

78





```
% identity
NCBI Description ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
                   (ACONITASE) >gi 2145473 emb_CAA65735_ (X97012) aconitate
                  hydratase [Solanum tuberosum]
                  295682
Seq. No.
                  LIB3078-035-Q1-K1-H1
Seq. ID
                  BLASTX
Method
                  g1483563
NCBI GI
BLAST score
                  145
                  1.0e-09
E. value
Match length
                  48
% identity
                  67
NCBI Description (X99825) leucine aminopeptidase [Petroselinum crispum]
Seq. No.
                  295683
                  LIB3078-035-Q1-K1-H5
Seq. ID
Method
                  BLASTN
                  g168527
NCBI GI
BLAST score
                  88
E value
                  2.0e-42
Match length
                  100
% identity
                  98
NCBI Description Maize NADP-dependent malic enzyme (Me1) mRNA, complete cds
Seq. No.
                  295684
                  LIB3078-036-Q1-K1-D10
Seq. ID
Method
                  BLASTX
                  g4587610
NCBI GI
                  270
BLAST score
                  1.0e-23
E value
Match length
                   107
                   53
% identity
                  (AC006951) putative indole-3-glycerol phosphate synthase
NCBI Description
                   precursor [Arabidopsis thaliana]
                   295685
Seq. No.
                   LIB3078-036-Q1-K1-F4
Seq. ID
                   BLASTX
Method
                   g2618704
NCBI GI
BLAST score
                   186
                   5.0e-14
E value
                   75
Match length
                   51
% identity
                   (AC002510) putative thioredoxin reductase [Arabidopsis
NCBI Description
                   thaliana]
                   295686
Seq. No.
                   LIB3078-036-Q1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2984709
                   244
BLAST score
E value
                   8.0e-21
                   68
```

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

NCBI GI BLAST score

E value



```
Seq. No.
                  295687
                  LIB3078-036-Q1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3550483
BLAST score
                  151
E value
                   5.0e-10
Match length
                   56
                   59
% identity
                  (AJ224324) cp31BHv [Hordeum vulgare]
NCBI Description
Seq. No.
                   295688
                  LIB3078-036-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4220476
BLAST score
                   161
E value
                   4.0e-11
Match length
                   106
% identity
                  (AC006069) ribophorin I-like protein [Arabidopsis thaliana]
NCBI Description
                   295689
Seq. No.
Seq. ID
                   LIB3078-037-Q1-K1-E6
Method
                   BLASTX
NCBI GI
                   q2668742
BLAST score
                   193
                   2.0e-23
E value
Match length
                   73
% identity
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
Seq. No.
                   295690
Seq. ID
                   LIB3078-038-Q1-K1-A10
Method
                   BLASTN
                   g644491
NCBI GI
BLAST score
                   37
                   2.0e-11
E value
Match length
                   65
                   89
% identity
                  Corn mRNA for elongation factor 1A
NCBI Description
Seq. No.
                   295691
                   LIB3078-038-Q1-K1-A12
Seq. ID
Method
                   BLASTX
                   g3386569
NCBI GI
BLAST score
                   403
                   1.0e-39
E value
                   90
Match length
                   89
% identity
                   (AF079590) photosystem II type II chlorophyll a/b binding
NCBI Description
                   protein [Sorghum bicolor]
Seq. No.
                   295692
                   LIB3078-038-Q1-K1-A9
Seq. ID
                   BLASTX
Method
```

41377

g3915826

2.0e-15





```
Match length
% identity
                   51
                   60S RIBOSOMAL PROTEIN L5
NCBI Description
                   295693
Seq. No.
                   LIB3078-038-Q1-K1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q122022
BLAST score
                   212
E value
                   4.0e-17
Match length
                   67
% identity
                   67
                   \verb|HISTONE| | H2B| > \verb|gi_283025_pir_s| \\ | S22323| | histone| | H2B| - wheat| \\
NCBI Description
                   >gi 21801 emb CAA42530 (X59873) histone H2B [Triticum
                   aestivum]
                   295694
Seq. No.
                   LIB3078-038-Q1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3334320
BLAST score
                   151
E value
                   2.0e-10
Match length
                   49
                   59
% identity
                  40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
NCBI Description
                   ribosome-associated protein p40 [GTycine max]
Seq. No.
                   295695
Seq. ID
                   LIB3078-038-Q1-K1-C4
Method
                   BLASTX
                   g82696
NCBI GI
BLAST score
                   192
                   3.0e-15
E value
Match length
                   45
                   82
% identity
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
Seq. No.
                   295696
```

glycine-rich protein - maize >gi_22293_emb_CAA43431__

Seq. ID LIB3078-038-Q1-K1-D9

Method BLASTX NCBI GI q3309583 BLAST score 157 4.0e-11 E value 58 Match length 55 % identity

(AF073830) fructose-6-phosphate NCBI Description

2-kinase/fructose-2,6-bisphosphatase [Solanum tuberosum]

Seq. No. 295697

Seq. ID LIB3078-038-Q1-K1-E4

Method BLASTX NCBI GI g3421104 BLAST score 383 5.0e-37 E value Match length 84 % identity 81

```
(AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  295698
Seq. ID
                  LIB3078-038-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  g168586
BLAST score
                  340
E value
                  4.0e-32
Match length
                  104
% identity
                  (M58656) pyruvate, orthophosphate dikinase [Zea mays]
NCBI Description
                  295699
Seq. No.
Seq. ID
                  LIB3078-038-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g3914685
BLAST score
                  269
E value
                  5.0e-24
Match length
                  59
                  90
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L17 >gi 2668748 (AF034948) ribosomal
                  protein L17 [Zea mays]
                  295700
Seq. No.
                  LIB3078-038-Q1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g461753
BLAST score
                  207
E value
                  1.0e-16
Match length
                  81
% identity
                  ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
NCBI Description
                  PRECURSOR >qi 419773 pir S31164 ATP-dependent ClpB
                  proteinase regulatory chain homolog precursor, chloroplast
                  - garden pea >gi 169128 (L09547) nuclear encoded precursor
                  to chloroplast protein [Pisum sativum]
```

Seq. No. 295701

LIB3078-038-Q1-K1-H11 Seq. ID

Method BLASTN NCBI GI g311236 BLAST score 44 1.0e-15 E value Match length 112 % identity 85

NCBI Description Z.mays mRNA for ATPase (delta subunit)

295702 Seq. No.

LIB3078-039-Q1-K1-A2 Seq. ID

Method BLASTX NCBI GI q82166 BLAST score 282 2.0e-25 E value Match length 84 73 % identity

NCBI Description glyceraldehyde-3-phosphate dehydrogenase (NADP+)





```
(phosphorylating) (EC 1.2.1.13) B, chloroplast - common
tobacco (fragment)
```

Seq. No. 295703

Seq. ID LIB3078-039-Q1-K1-B12

Method BLASTN
NCBI GI g2065239
BLAST score 35
E value 3.0e-10
Match length 39
% identity 97

NCBI Description M.musculus mRNA for coxsackie and adenovirus receptor

homologue

Seq. No. 295704

Seq. ID LIB3078-039-Q1-K1-C12

Method BLASTX
NCBI GI g2196770
BLAST score 151
E value 5.0e-10
Match length 40
% identity 72

NCBI Description (AF003127) chlorophyll a/b-binding protein

[Mesembryanthemum crystallinum]

Seq. No. 295705

Seq. ID LIB3078-039-Q1-K1-G7

Method BLASTN
NCBI GI g3821780
BLAST score 35
E value 3.0e-10
Match length 35
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 295706

Seq. ID LIB3078-039-Q1-K1-H1

Method BLASTX
NCBI GI g2493046
BLAST score 165
E value 1.0e-11
Match length 81
% identity 47

NCBI Description ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR

>gi_82297_pir__A41740 H+-transporting ATP synthase (EC

3.6.1.34) delta' chain precursor - sweet potato

>gi 217938 dbj BAA01511 (D10660) mitochondrial F1-ATPase

delta subunit [Ipomoea batatas]

Seq. No. 295707

Seq. ID LIB3078-039-Q1-K1-H3

Method BLASTX
NCBI GI g1206013
BLAST score 206
E value 1.0e-29
Match length 101
% identity 71

Method

BLASTX





```
NCBI Description (U44087) beta-D-glucosidase precursor [Zea mays]
                  295708
Seq. No.
                  LIB3078-039-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2651310
BLAST score
                  222
                  4.0e-18
E value
                  95
Match length
% identity
                  40
                  (AC002336) putative PTR2-B peptide transporter [Arabidopsis
NCBI Description
                  thaliana]
                  295709
Seq. No.
Seq. ID
                  LIB3078-039-Q1-K1-H9
Method
                  BLASTX
                  g3915847
NCBI GI
BLAST score
                  180
E value
                  8.0e-14
Match length
                  60
% identity
                  63
                  40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
NCBI Description
                  40S ribosomal protein S2 [Arabidopsis thaliana]
                  295710
Seq. No.
Seq. ID
                  LIB3078-040-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g2582639
BLAST score
                  157
                  1.0e-10
E value
Match length
                  67
% identity
                  51
NCBI Description (AJ002414) hnRNP-like protein [Arabidopsis thaliana]
                  295711
Seq. No.
                  LIB3078-040-Q1-K1-A6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2306767
BLAST score
                  40
                  4.0e-13
E value
Match length
                  108
% identity
                  84
NCBI Description Triticum aestivum eIF-2 beta subunit mRNA, complete cds
Seq. No.
                  295712
Seq. ID
                  LIB3078-040-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g3915826
BLAST score
                  169
E value
                  2.0e-12
Match length
                  40
% identity
                  82
NCBI Description 60S RIBOSOMAL PROTEIN L5
Seq. No.
                  295713
                  LIB3078-040-Q1-K1-D7
Seq. ID
```

NCBI GI

E value

BLAST score

q1632768

237 9.0e-31



```
NCBI GI
                  g2246378
BLAST score
                  217
E value
                  1.0e-17
Match length
                  47
                  87
% identity
                  (Z86094) plastid protein [Arabidopsis thaliana]
NCBI Description
                  295714
Seq. No.
                  LIB3078-040-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3548802
BLAST score
                  344
                  1.0e-32
E value
Match length
                  97
% identity
                  65
NCBI Description
                  (AC005313) axi 1-like protein [Arabidopsis thaliana]
                  >gi 4335769 qb AAD17446 (AC006284) putative axi1 protein
                  [Nicotiana tabacum] [Arabidopsis thaliana]
Seq. No.
                  295715
Seq. ID
                  LIB3078-040-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g4049345
BLAST score
                  190
                  2.0e-14
E value
Match length
                  78
% identity
                  47
NCBI Description
                  (AL034567) putative protein [Arabidopsis thaliana]
Seq. No.
                  295716
                  LIB3078-045-Q1-K1-D6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1419369
BLAST score
                  208
                  1.0e-113
E value
Match length
                  212
                  100
% identity
NCBI Description Z.mays ZmABP3 mRNA for actin depolymerizing factor
Seq. No.
                  295717
Seq. ID
                  LIB3078-046-Q1-K1-B7
Method
                  BLASTN
                  g1657766
NCBI GI
BLAST score
                  36
                  5.0e-11
E value
Match length
                  48
% identity
                  47
NCBI Description
                  Zea mays retrotransposon Opie-2 5' LTR, primer binding
                  site, gag gene, pol gene, complete cds, polypurine tract
                  and 3' LTR
Seq. No.
                  295718
Seq. ID
                  LIB3078-046-Q1-K1-C1
Method
                  BLASTX
```





```
Match length
                  78
% identity
                  (D84408) calcium dependent protein kinase [Zea mays]
NCBI Description
Seq. No.
                  295719
                  LIB3078-046-Q1-K1-C10
Seq. ID
Method
                  BLASTX
                  g2290400
NCBI GI
BLAST score
                  209
E value
                  3.0e-17
Match length
                  58
% identity
                  69
                  (U91339) stearoyl-ACP desaturase [Helianthus annuus]
NCBI Description
Seq. No.
                  295720
                  LIB3078-046-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3372233
BLAST score
                  166
                  1.0e-12
E value
Match length
                  46
% identity
                  87
                  (AF019248) RNA polymerase I, II and III 24.3 kDa subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  295721
                  LIB3078-046-Q1-K1-D7
Seq. ID
Method
                  BLASTX
                  g1078406
NCBI GI
BLAST score
                  153
                  5.0e-10
E value
Match length
                  53
                  53
% identity
                  SWH1 protein (version 2) - yeast (Saccharomyces cerevisiae)
NCBI Description
                  >gi 402658 emb CAA52646 (X74552) SWH1 [Saccharomyces
                  cerevisiae] >gi 1090523 prf 2019253A oxysterol-binding
                  protein-like protein [Saccharomyces cerevisiae]
Seq. No.
                  295722
Seq. ID
                  LIB3078-046-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  q4508068
BLAST score
                  142
                  8.0e-09
E value
Match length
                  50
% identity
                  64
NCBI Description
                  (AC005882) 3063 [Arabidopsis thaliana]
                  295723
Seq. No.
Seq. ID
                  LIB3078-046-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g467996
BLAST score
                  277
                  2.0e-41
E value
Match length
                  119
% identity
                  81
                  (U04434) flavanone 3-beta-hydroxylase [Zea mays]
NCBI Description
```

NCBI Description





```
Seq. No.
                  295724
Seq. ID
                  LIB3078-046-Q1-K1-E9
Method
                  BLASTX
                  g4335761
NCBI GI
                  156
BLAST score
E value
                  2.0e-10
Match length
                  88
% identity
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]
Seq. No.
                  295725
                  LIB3078-046-Q1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3068714
BLAST score
                  452
E value
                  5.0e-45
Match length
                  145
% identity
                  59
NCBI Description (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                  295726
Seq. ID
                  LIB3078-046-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  g131192
BLAST score
                  321
E value
                  1.0e-29
Match length
                  111
% identity
                  59
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR
                  (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >qi 100606 pir S20937
                  photosystem I chain V precursor - barley
                  >gi 19091 emb CAA42727 (X60158) photosystem I polypeptide
                  PSI-G precursor [Hordeum vulgare]
Seq. No.
                  295727
Seq. ID
                  LIB3078-046-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  g1710841
BLAST score
                  237
E value
                  6.0e-23
Match length
                  98
                  61
% identity
NCBI Description
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
                  HYDROLASE) (ADOHCYASE) >gi_758247_emb_CAA56278_ (X79905)
                  S-adenosylhomocysteine hydrolase [Phalaenopsis sp.]
Seq. No.
                  295728
Seq. ID
                  LIB3078-046-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  g68029
BLAST score
                  301
E value
                  2.0e-27
Match length
                  110
% identity
                  63
```

phosphoenolpyruvate carboxylase (EC 4.1.1.31) - maize

>gi 22408 emb CAA33317 (X15239) PEP carboxylase [Zea mays]





>gi_228619_prf__1807332A phosphoenolpyruvate carboxylase
[Zea mays]

Seq. No. 295729

Seq. ID LIB3078-046-Q1-K1-H9

Method BLASTN
NCBI GI g3452299
BLAST score 74
E value 1.0e-33
Match length 171
% identity 87

NCBI Description Zea mays retrotransposon Ji-6 3' LTR, partial sequence

Seq. No. 295730

Seq. ID LIB3078-047-Q1-K1-C6

Method BLASTX
NCBI GI g4127456
BLAST score 344
E value 2.0e-32
Match length 100
% identity 36

NCBI Description (AJ010818) Cpn21 protein [Arabidopsis thaliana]

Seq. No. 295731

Seq. ID LIB3078-047-Q1-K1-D5

Method BLASTX
NCBI GI g548605
BLAST score 463
E value 3.0e-46
Match length 123
% identity 82

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR

(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi_539055_pir__A48527 photosystem I protein psaK precursor
- barley >gi_304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

Seq. No. 295732

Seq. ID LIB3078-047-Q1-K1-E6

Method BLASTX
NCBI GI g266578
BLAST score 236
E value 1.0e-19
Match length 56
% identity 75

NCBI Description METALLOTHIONEIN-LIKE PROTEIN 1 >gi_100898_pir__S17560

metallothionein-like protein - maize >gi_236730_bbs_57629 (S57628) metallothionein homologue [Zea mays, Peptide, 76

aa] [Zea mays] >gi_559536_emb_CAA57676_ (X82186)

metallothionein- like protein [Zea mays]

>gi_228095_prf__1717215A metallothionein-like protein [Zea

mays]

Seq. No. 295733

Seq. ID LIB3078-047-Q1-K1-F5

Method BLASTX NCBI GI g467996



BLAST score 5.0e-57 E value 109 Match length % identity 97 (U04434) flavanone 3-beta-hydroxylase [Zea mays] NCBI Description 295734 Seq. No. LIB3078-047-Q1-K1-G12 Seq. ID BLASTX Method g115765

NCBI GI g115765
BLAST score 343
E value 3.0e-32
Match length 78
% identity 82

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__ S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding

protein [Lycopersicon esculentum] >gi_226546_prf__1601518A

chlorophyll a/b binding protein II [Lycopersicon

esculentum]

Seq. No. 295735

Seq. ID LIB3078-048-Q1-K1-C7

Method BLASTX
NCBI GI g1217601
BLAST score 150
E value 6.0e-10
Match length 45
% identity 71

NCBI Description (D42070) PSI-E subunit of photosystem I [Nicotiana

sylvestris]

Seq. No. 295736

Seq. ID LIB3078-048-Q1-K1-D7

Method BLASTX
NCBI GI g320622
BLAST score 343
E value 2.0e-32
Match length 113
% identity 59

NCBI Description probable protein kinase - maize (fragment) >gi_168618

(M62985) protein kinase [Zea mays]

Seq. No. 295737

Seq. ID LIB3078-048-Q1-K1-E4

Method BLASTN
NCBI GI g22239
BLAST score 57
E value 1.0e-23
Match length 149
% identity 85

NCBI Description Maize cytosolic mRNA for subunit A of chloroplast GAPDH

(GapA) glyceraldehyde-3-phosphate dehydrogenase

Seq. No. 295738



```
Seq. ID
                  LIB3078-048-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g2244915
BLAST score
                  199
E value
                  2.0e-15
Match length
                  132
% identity
                  35
NCBI Description
                  (Z97339) strong homology to reverse transcriptase
                  [Arabidopsis thaliana]
                  295739
Seq. No.
Seq. ID
                  LIB3078-048-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  g2911073
BLAST score
                  214
E value
                  3.0e-17
Match length
                  84
% identity
                  49
NCBI Description (AL021960) putative protein [Arabidopsis thaliana]
                  295740
Seq. No.
                  LIB3078-048-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g118104
BLAST score
                  437
E value
                  2.0e-43
Match length
                  98
% identity
                  86
NCBI Description
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
                  (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi 68408 pir CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi 168461 (M55021) cyclophilin [Zea mays]
                  >gi 829148 emb CAA48638 (X68678) cyclophilin [Zea mays]
Seq. No.
                  295741
Seq. ID
                  LIB3078-048-Q1-K1-G10
                  BLASTN
Method
NCBI GI
                  g452340
BLAST score
                  73
E value
                  5.0e-33
Match length
                  201
% identity
                  91
NCBI Description
                  Z.mays mRNA for type II light-harvesting chlorophyll
                  a/b-binding protein
Seq. No.
                  295742
                  LIB3078-048-Q1-K1-G12
Seq. ID
Method
                  BLASTX
                  g3126854
                  315
                  4.0e-29
```

NCBI GI BLAST score E value Match length 111 % identity

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 295743

Seq. ID LIB3078-049-Q1-K1-B5



Method BLASTX
NCBI GI g3510256
BLAST score 200
E value 1.0e-15
Match length 62

NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]

Seq. No. 295744

% identity

Seq. ID LIB3078-049-Q1-K1-C10

53

Method BLASTX
NCBI GI g1172818
BLAST score 289
E value 4.0e-26
Match length 110
% identity 58

NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal

protein S16 [Oryza sativa] >gi_1096552_prf__2111468A

ribosomal protein S16 [Oryza sativa]

Seq. No. 295745

Seq. ID LIB3078-049-Q1-K1-C12

Method BLASTX
NCBI GI g3695392
BLAST score 235
E value 1.0e-19
Match length 151
% identity 34

NCBI Description (AF096371) No definition line found [Arabidopsis thaliana]

Seq. No. 295746

Seq. ID LIB3078-049-Q1-K1-G12

Method BLASTX
NCBI GI g132147
BLAST score 328
E value 9.0e-31
Match length 106
% identity 65

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 68089 pir RKZMS

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor - maize >gi_22474_emb_CAA29784_ (X06535) ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor [Zea mays] >gi_217964_dbj_BAA00120_ (D00170) ribulose 1,5-bisphosphate carboxylase small subunit [Zea mays] >gi_359512_prf__1312317A ribulosebisphosphate carboxylase

[Zea mays]

Seq. No. 295747

Seq. ID LIB3078-049-Q1-K1-H3

Method BLASTX
NCBI GI 94544399
BLAST score 455
E value 2.0e-45
Match length 125
% identity 63

NCBI Description (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis



thaliana]

```
Seq. No.
                   295748
                   LIB3078-049-Q1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2773154
BLAST score
                   164
E value
                   3.0e-11
Match length
                   78
                   45
% identity
                  (AF039573) abscisic acid- and stress-inducible protein
NCBI Description
                   [Oryza sativa]
Seq. No.
                   295749
                   LIB3078-050-Q1-K1-A6
Seq. ID
Method
                   BLASTX
                   q729135
NCBI GI
                   473
BLAST score
                   1.0e-47
E value
Match length
                   126
% identity
                   72
                   CAFFEIC ACID 3-O-METHYLTRANSFERASE
NCBI Description
                   (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                   3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir__S28612
                   catechol O-methyltransferase (EC \overline{2}.1.1.6) - \overline{\text{maize}}
                   >gi 168532 (M73235) O-methyltransferase [Zea mays]
                   295750
Seq. No.
                   LIB3078-050-Q1-K1-A9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g671737
BLAST score
                   321
                   5.0e-30
E value
                   87
Match length
% identity
                   74
                  (X74731) Chloropyll a/b binding protein [Amaranthus
NCBI Description
                   hypochondriacus]
Seq. No.
                   295751
Seq. ID
                   LIB3078-050-Q1-K1-C12
Method
                   BLASTX
NCBI GI
                   q1835731
BLAST score
                   270
E value
                   7.0e-24
Match length
                   84
% identity
                   65
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                   295752
Seq. No.
                   LIB3078-050-Q1-K1-F11
Seq. ID
Method
                   BLASTX
                   g2688824
NCBI GI
BLAST score
                   148
E value
                   1.0e-09
Match length
                   71
% identity
                   49
NCBI Description (U93273) putative auxin-repressed protein [Prunus
```

Seq. ID

Method



armeniaca]

```
Seq. No.
                  295753
Seq. ID
                  LIB3078-050-Q1-K1-F9
Method
                  BLASTN
                  q2984708
NCBI GI
BLAST score
                  66
E value
                  5.0e-29
Match length
                  122
% identity
                  89
NCBI Description
                  Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
Seq. No.
                  295754
Seq. ID
                  LIB3078-050-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  347
E value
                  3.0e-33
Match length
                  79
% identity
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                  295755
Seq. ID
                  LIB3078-051-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  q2809249
BLAST score
                  190
E value
                  3.0e-14
Match length
                  147
% identity
                  15
NCBI Description (AC002560) F21B7.18 [Arabidopsis thaliana]
                  295756
Seq. No.
                  LIB3078-051-Q1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3935167
BLAST score
                  361
E value
                  2.0e-34
Match length
                  96
% identity
                  71
NCBI Description
                  (AC004557) F17L21.10 [Arabidopsis thaliana]
                  295757
Seq. No.
                  LIB3078-051-Q1-K1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3925238
BLAST score
                  72
                  3.0e-32
E value
Match length
                  191
% identity
                  85
NCBI Description
                  Zea mays 6-phosphogluconate dehydrogenase isoenzyme A gene,
                  partial cds
Seq. No.
                  295758
```

41390

LIB3078-051-Q1-K1-C3

BLASTX

% identity





```
NCBI GI
                   g3901268
BLAST score
                   212
E value
                   6.0e-17
Match length
                   126
% identity
                   38
                   (AF060173) SV2 related protein [Rattus norvegicus]
NCBI Description
Seq. No.
                   295759
Seq. ID
                   LIB3078-051-Q1-K1-C6
Method
                   BLASTX
NCBI GI
                   g3738230
BLAST score
                   196
E value
                   3.0e-15
Match length
                   88
% identity
                   45
NCBI Description
                   (AB007790) DREB2A [Arabidopsis thaliana]
                   >gi 4126706 dbj_BAA36705_ (AB016570) DREB2A [Arabidopsis
                   thaliana]
Seq. No.
                   295760
Seq. ID
                   LIB3078-051-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                   g4589961
BLAST score
                   454
E value
                   3.0e-45
Match length
                   132
% identity
                   61
NCBI Description (AC007169) unknown protein [Arabidopsis thaliana]
Seq. No.
                   295761
Seq. ID
                  LIB3078-051-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                   g295855
BLAST score
                   363
E value
                   5.0e-35
Match length
                  86
% identity
                  80
NCBI Description (X15642) P-pyruvate carboxylase [Zea mays]
Seq. No.
                  295762
Seq. ID
                  LIB3078-051-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  g2668742
BLAST score
                  282
E value
                  3.0e-25
Match length
                  61
% identity
                  92
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]
Seq. No.
                  295763
Seq. ID
                  LIB3078-051-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  g168586
BLAST score
                  350
E value
                  4.0e-33
Match length
                  113
```





```
NCBI Description
                  (M58656) pyruvate, orthophosphate dikinase [Zea mays]
Seq. No.
                   295764
Seq. ID
                   LIB3078-052-Q1-K1-B10
Method
                   BLASTX
NCBI GI
                   q2055273
BLAST score
                   229
E value
                   2.0e-19
Match length
                   56
                   77
% identity
NCBI Description
                  (D85339) hydroxypyruvate reductase [Arabidopsis thaliana]
Seq. No.
                   295765
Seq. ID
                  LIB3078-052-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                   q4056502
BLAST score
                   147
E value
                  1.0e-09
Match length
                  50
% identity
                   60
NCBI Description
                  (ACO05896) 40S ribosomal protein S5 [Arabidopsis thaliana]
Seq. No.
                  295766
Seq. ID
                  LIB3078-052-Q1-K1-G5
Method
                  BLASTN
                  g3821780
NCBI GI
BLAST score
                  36
E value
                  1.0e-10
Match length
                  48
% identity
                  67
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  295767
Seq. ID
                  LIB3078-052-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  g1848210
BLAST score
                  143
E value
                  5.0e-09
Match length
                  39
% identity
                  74
NCBI Description
                  (Y11208) histone H2B1 [Nicotiana tabacum]
Seq. No.
                  295768
Seq. ID
                  LIB3078-052-Q1-K1-H10
Method
                  BLASTN
NCBI GI
                  g2981206
BLAST score
                  38
E value
                  5.0e-12
Match length
                  102
% identity
                  84
                  Zea mays photosystem I complex PsaH subunit precursor
NCBI Description
                  (psaH) mRNA, nuclear gene encoding chloroplast protein,
```

Seq. No. 295769 Seq. ID LIB3078-053-Q1-K1-B1

complete cds

Method BLASTX





NCBI GI g132147 BLAST score 209 E value 7.0e-21 Match length 87 % identity 69

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_68089_pir__RKZMS

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor - maize >gi 22474 emb CAA29784 (X06535)

ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor [Zea mays] >gi_217964_dbj_BAA00120_ (D00170) ribulose 1,5-bisphosphate carboxylase small subunit [Zea mays] >gi_359512_prf__1312317A ribulosebisphosphate carboxylase

[Zea mays]

Seq. No. 295770

Seq. ID LIB3078-053-Q1-K1-F12

Method BLASTX
NCBI GI g2493650
BLAST score 411
E value 2.0e-40
Match length 85
% identity 98

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD

CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)

>gi_1167858_emb_CAA93139_ (Z68903) chaperonin [Secale

cereale]

Seq. No. 295771

Seq. ID LIB3078-053-Q1-K1-H6

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 295772

Seq. ID LIB3078-054-Q1-K1-B5

Method BLASTX
NCBI GI g3293555
BLAST score 145
E value 3.0e-09
Match length 82
% identity 45

NCBI Description (AF072931) chlorophyll a/b binding protein [Medicago

sativa]

Seq. No. 295773

Seq. ID LIB3078-054-Q1-K1-E1

Method BLASTN
NCBI GI g3777599
BLAST score 53
E value 4.0e-21
Match length 89
% identity 90





NCBI Description Oryza sativa clone LS101 50S ribosomal protein L5 (rpl5)
mRNA, nuclear gene encoding chloroplast protein, partial
cds

Seq. No. 295774
Seq. ID LIB3078-054-Q1-K1-E8
Method BLASTX
NCBI GI 93386569

Method BLASTX
NCBI GI g3386569
BLAST score 294
E value 1.0e-26
Match length 64
% identity 86

NCBI Description (AF079590) photosystem II type II chlorophyll a/b binding

protein [Sorghum bicolor]

Seq. No. 295775

Seq. ID LIB3078-054-Q1-K1-F9

Method BLASTX
NCBI GI g3912917
BLAST score 296
E value 9.0e-27
Match length 138
% identity 43

NCBI Description (AF001308) putative NAK-like ser/thr protein kinase

[Arabidopsis thaliana]

Seq. No. 295776

Seq. ID LIB3078-054-Q1-K1-H12

Method BLASTX
NCBI GI g4572674
BLAST score 368
E value 3.0e-35
Match length 104
% identity 64

NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]

Seq. No. 295777

Seq. ID LIB3078-054-Q1-K1-H3

Method BLASTX
NCBI GI g548770
BLAST score 494
E value 4.0e-50
Match length 107
% identity 87

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal

protein L3 - rice >gi 303853 dbj BAA02155 (D12630)

ribosomal protein L3 [Oryza sativa]

Seq. No. 295778

Seq. ID LIB3078-055-Q1-K1-A10

Method BLASTX
NCBI GI g1899188
BLAST score 150
E value 1.0e-09
Match length 44
% identity 64

NCBI Description (U90212) DNA binding protein ACBF [Nicotiana tabacum]



Seq. No. 295779

Seq. ID LIB3078-055-Q1-K1-E1

Method BLASTX
NCBI GI g3183079
BLAST score 271
E value 6.0e-24
Match length 122
% identity 48

NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR

>gi_1375075_dbj_BAA12870_ (D85763) glyoxysomal malate

dehydrogenase [Oryza sativa]

Seq. No. 295780

Seq. ID LIB3078-055-Q1-K1-E12

Method BLASTX
NCBI GI g135181
BLAST score 157
E value 6.0e-11
Match length 52
% identity 58

NCBI Description VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS)

>gi_143797 (M16318) valyl-tRNA synthetase [Bacillus

stearothermophilus]

Seq. No. 295781

Seq. ID LIB3078-055-Q1-K1-F9

Method BLASTX
NCBI GI g122083
BLAST score 228
E value 7.0e-23
Match length 98
% identity 63

NCBI Description HISTONE H3 >gi_70751_pir__HSEAH3 histone H3 - Altenstein's

bread tree >gi_224865_prf_ 1202289A histone H3

[Encephalartos sp.]

Seq. No. 295782

Seq. ID LIB3078-055-Q1-K1-G7

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 295783

Seq. ID LIB3078-056-Q1-K1-A5

Method BLASTN
NCBI GI g3821780
BLAST score 37
E value 1.0e-11
Match length 49

Match length 49 % identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1



295784

Seq. No. LIB3078-056-Q1-K1-D10 Seq. ID

Method BLASTX g4505873 NCBI GI BLAST score 340 6.0e-32 E value 129 Match length % identity 50

NCBI Description phospholipase D1, phophatidylcholine-specific (NOTE: redefinition of symbol) >gi_2499703_sp_Q13393_PLD1_HUMAN

PHOSPHOLIPASE D1 (PLD 1) (CHOLINE PHOSPHATASE 1) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D1) >gi_1185463 (U38545) phospholipase D1 [Homo sapiens]

Seq. No. 295785

Seq. ID LIB3078-056-Q1-K1-D9

Method BLASTX NCBI GI q3025329 BLAST score 173 E value 2.0e-12 Match length 88 45 % identity

HYPOTHETICAL 25.4 KD PROTEIN F53F4.3 IN CHROMOSOME V NCBI Description

> >gi 3877534 emb CAB01212 (Z77663) Similarity to S.pombe hypothetical proteinSPAC4G9.01 (TR: E223656) [Caenorhabditis

elegans]

295786 Seq. No.

LIB3078-056-Q1-K1-F6 Seq. ID

Method BLASTX NCBI GI q4006902 BLAST score 190 2.0e-14 E value 138 Match length % identity 31

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

295787 Seq. No.

LIB3078-056-Q1-K1-H1 Seq. ID

Method BLASTX g3550485 NCBI GI BLAST score 265 E value 1.0e-23 Match length 83 % identity 65

NCBI Description (AJ224325) cp33Hv [Hordeum vulgare]

Seq. No. 295788

LIB3078-056-Q1-K1-H7 Seq. ID

Method BLASTX NCBI GI g4522009 BLAST score 247 5.0e-21 E value Match length 106 % identity 45

NCBI Description (AC007069) unknown protein [Arabidopsis thaliana]

Seq. No. Seq. ID

Method ~





```
Seq. No.
                  295789
                  LIB3078-057-Q1-K1-A10
Seq. ID
Method
                  BLASTX
                  g2160182
NCBI GI
BLAST score
                  145
                  1.0e-09
E value
Match length
                  70
                  50
% identity
                  (AC000132) ESTs gb_ATTS1236, gb_T43334, gb_N97019, gb_AA395203
NCBI Description
                  come from this gene. [Arabidopsis thaliana]
                  295790
Seq. No.
                  LIB3078-057-Q1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4581856
                  199
BLAST score
                  1.0e-15
E value
Match length
                  110
                  48
% identity
                   (AF116825) 1-deoxy-D-xylulose-5-phosphate reductoisomerase
NCBI Description
                   [Mentha x piperita]
                  295791
Seq. No.
                  LIB3078-057-Q1-K1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g537403
BLAST score
                  145
                  3.0e-09
E value
Match length
                  63
                  52
% identity
                  (D26538) WSI724 protein induced by water stress [Oryza
NCBI Description
                  sativa]
                  295792
Seq. No.
                  LIB3078-057-Q1-K1-D11
Seq. ID
Method
                  BLASTN
                  g1498052
NCBI GI
BLAST score
                  66
                  7.0e-29
E value
Match length
                  82
                  95
% identity
NCBI Description
                  Zea mays ribosomal protein S8 mRNA, complete cds
                  295793
Seq. No.
                  LIB3078-057-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82696
BLAST score
                   353
                   1.0e-33
E value
Match length
                   86
                   80
% identity
NCBI Description
                  glycine-rich protein - maize >gi_22293_emb_CAA43431_
                   (X61121) glycine-rich protein [Zea mays]
                   295794
```

41397

LIB3078-057-Q1-K1-H10

BLASTN

NCBI GI

BLAST score

g1770515

176





```
NCBI GI
                  g2062705
BLAST score
                  38
                  5.0e-12
E value
Match length
                  38
% identity
                  100
NCBI Description
                  Human butyrophilin (BTF5) mRNA, complete cds
                  295795
Seq. No.
                  LIB3079-001-Q1-K1-C11
Seq. ID
Method
                  BLASTN
                  g799029
NCBI GI
BLAST score
                  74
                  2.0e-33
E value
Match length
                  109
% identity
                  94
NCBI Description Z.mays BET1 mRNA
Seq. No.
                  295796
Seq. ID
                  LIB3079-001-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  q732207
BLAST score
                  193
E value
                  1.0e-14
Match length
                  92
% identity
                  42
NCBI Description
                  HYPOTHETICAL 75.4 KD PROTEIN IN AUT1-CSE2 INTERGENIC REGION
                  >gi 626466 pir S45131 probable membrane protein YNR008w -
                  yeast (Saccharomyces cerevisiae) >gi 496725 emb CAA54576
                  (X77395) N2042 [Saccharomyces cerevisiae]
                  >gi 1302482 emb CAA96285 (Z71623) ORF YNR008w
                  [Saccharomyces cerevisiae]
Seq. No.
                  295797
Seq. ID
                  LIB3079-001-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  g1209703
BLAST score
                  371
E value
                  1.0e-35
Match length
                  126
% identity
                  56
NCBI Description (U40489) maize gl1 homolog [Arabidopsis thaliana]
                  295798
Seq. No.
                  LIB3079-001-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2708532
BLAST score
                  182
E value
                  9.0e-15
                  95
Match length
% identity
                  46
NCBI Description (AF029351) putative RNA binding protein [Nicotiana tabacum]
                  295799
Seq. No.
                  LIB3079-001-Q1-K1-F11
Seq. ID
Method
                  BLASTX
```

BLAST score

E value

339

6.0e-32





```
E value
                  1.0e-12
Match length
                  47
% identity
                  66
NCBI Description
                   (X99459) sigma 3 protein [Homo sapiens] >gi 1923272
                   (U91933) AP-3 complex sigma3B subunit [Mus musculus]
Seq. No.
                  295800
                  LIB3079-001-Q1-K1-H2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22544
BLAST score
                  64
                  1.0e-27
E value
Match length
                  156
% identity
                  85
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
Seq. No.
                  295801
                  LIB3079-002-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3126967
BLAST score
                  272
E value
                  1.0e-24
Match length
                  69
% identity
                  15
                  (AF061807) polyubiquitin [Elaeagnus umbellata]
NCBI Description
                  295802
Seq. No.
                  LIB3079-002-Q1-K1-C4
Seq. ID
Method
                  BLASTX
                  g3183079
NCBI GI
BLAST score
                  350
                  4.0e-33
E value
Match length
                  73
% identity
                  93
                  MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
NCBI Description
                  >gi_1375075_dbj_BAA12870_ (D85763) glyoxysomal malate
                  dehydrogenase [Oryza sativa]
Seq. No.
                  295803
Seq. ID
                  LIB3079-002-Q1-K1-E12
Method
                  BLASTX
                  g2842704
NCBI GI
BLAST score
                  195
E value
                  4.0e-15
Match length
                  88
% identity
                  42
NCBI Description
                  HYPOTHETICAL 73.3 KD PROTEIN C6G9.14 IN CHROMOSOME I
                  >gi_1644326_emb_CAB03616.1_ (Z81317) serine rich pumilio
                  family rna binding domain pr otein [Schizosaccharomyces
                  pombe]
Seq. No.
                  295804
Seq. ID
                  LIB3079-002-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g2119187
```

Match length

% identity

84

46





```
Match length
% identity
                  83
NCBI Description
                  transmembrane protein, glucose starvation-induced - maize
                  >gi 575731 emb CAA57955 (X82633) transmembrane protein
                  [Zea mays]
                  295805
Seq. No.
Seq. ID
                  LIB3079-003-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  g82695
BLAST score
                  250
                  2.0e-21
E value
Match length
                  118
% identity
                  48
                  glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) 3 -
NCBI Description
                  maize (fragment) >gi 293887 (L13431)
                  glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
Seq. No.
                  295806
                  LIB3079-003-Q1-K1-B7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g442525
BLAST score
                  82
E value
                  3.0e-38
Match length
                  218
% identity
                  84
NCBI Description ZmERabp4=auxin-binding protein [Zea mays=corn, seedling,
                  mRNA, 917 nt]
Seq. No.
                  295807
                  LIB3079-003-Q1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2624498
BLAST score
                  201
                  1.0e-15
E value
Match length
                  145
                  39
% identity
NCBI Description Crystal Structure Of Barley Grain Peroxidase
Seq. No.
                  295808
                  LIB3079-003-Q1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4512682
BLAST score
                  282
E value
                  4.0e-25
Match length
                  121
% identity
NCBI Description
                  (AC006931) unknown protein [Arabidopsis thaliana]
                  295809
Seq. No.
Seq. ID
                  LIB3079-003-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  q1172818
BLAST score
                  145
E value
                  3.0e-09
```





```
40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal protein S16 [Oryza sativa] >gi_1096552_prf__2111468A
NCBI Description
                   ribosomal protein S16 [Oryza sativa]
Seq. No.
                   295810
                   LIB3079-003-Q1-K1-G2
Seq. ID
                   BLASTX
Method
                   q1370172
NCBI GI
BLAST score
                   152
E value
                   6.0e-10
Match length
                   66
                   53
% identity
NCBI Description (Z73935) RAB1X [Lotus japonicus]
Seq. No.
                   295811
                   LIB3079-004-Q1-K1-A2
Seq. ID
Method
                   BLASTX
                   q3953595
NCBI GI
BLAST score
                   176
E value
                   9.0e-13
Match length
                   76
% identity
                   51
NCBI Description (AB008486) response regulator 3 [Arabidopsis thaliana]
                   295812
Seq. No.
                   LIB3079-004-Q1-K1-A8
Seq. ID
Method
                   BLASTX
                   g2218152
NCBI GI
BLAST score
                    652
                   1.0e-68
E value
Match length
                   131
% identity
                    89
                   (AF005279) type IIIa membrane protein cp-wap13 [Vigna
NCBI Description
                   unguiculata]
                    295813
Seq. No.
                    LIB3079-004-Q1-K1-A9
Seq. ID
                    BLASTX
Method
                    g2580499
NCBI GI
                    506
BLAST score
                    2.0e-51
E value
Match length
                    120
                    72
% identity
                   (U67186) NADPH: ferrihemoprotein oxidoreductase
NCBI Description
                    [Eschscholzia californica]
                    295814
Seq. No.
                    LIB3079-004-Q1-K1-F10
Seq. ID
                    BLASTX
Method
```

Method BLASTX
NCBI GI g4508068
BLAST score 156
E value 2.0e-10
Match length 57
% identity 56

NCBI Description (AC005882) 3063 [Arabidopsis thaliana]

Seq. No. 295815



LIB3079-004-Q1-K1-F11 BLASTN

Method BLASTN
NCBI GI g168484
BLAST score 254
E value 1.0e-141

Match length 294 % identity 97

Seq. ID

NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 295816

Seq. ID LIB3079-005-Q1-K1-B7

Method BLASTN
NCBI GI g1597722
BLAST score 352
E value 0.0e+00
Match length 388
% identity 98

NCBI Description Zea mays CRINKLY4 precursor (cr4) mRNA, complete cds

Seq. No. 295817

Seq. ID LIB3079-005-Q1-K1-C12

Method BLASTX
NCBI GI g3015621
BLAST score 298
E value 1.0e-37
Match length 97
% identity 83

NCBI Description (AF035460) low molecular weight heat shock protein

precursor [Zea mays]

Seq. No. 295818

Seq. ID LIB3079-005-Q1-K1-C3

Method BLASTX
NCBI GI g1076283
BLAST score 195
E value 7.0e-15
Match length 54
% identity 67

NCBI Description adenylylsulfate kinase (EC 2.7.1.25) precursor -

Arabidopsis thaliana >gi_414737_emb_CAA53426_ (X75782) APS kinase [Arabidopsis thaliana] >gi_450235 (U05238) APS kinase [Arabidopsis thaliana] >gi_1575322 (U59759) APS kinase [Arabidopsis thaliana] >gi_3252812 (AC004705) APS

kinase [Arabidopsis thaliana]

Seq. No. 295819

Seq. ID LIB3079-005-Q1-K1-E8

Method BLASTX
NCBI GI g2494140
BLAST score 236
E value 4.0e-20
Match length 77
% identity 56

NCBI Description (AC003002) R29515_1 [Homo sapiens] >gi_3068727 (AF058918)

unknown [Homo sapiens]

Seq. No. 295820



```
LIB3079-005-Q1-K1-G10
Seq. ID
                  BLASTX
Method
                  g1620753
NCBI GI
                  189
BLAST score
                  2.0e-14
E value
                  57
Match length
% identity
                  (U72942) proteinase inhibitor [Oryza sativa]
NCBI Description
                  >gi 2829212 gb_AAC00503_ (AF044059) proteinase inhibitor
                   [Oryza sativa]
                  295821
Seq. No.
                  LIB3079-005-Q1-K1-H5
Seq. ID
                  BLASTX
Method
                  g4567312
NCBI GI
                  157
BLAST score
                   2.0e-10
E value
                   51
Match length
% identity
NCBI Description (AC005956) hypothetical protein [Arabidopsis thaliana]
                   295822
Seq. No.
                  LIB3079-006-Q1-K1-B7
Seq. ID
                   BLASTX
Method
                   q131773
NCBI GI
                   204
BLAST score
                   5.0e-16
E value
                   55
Match length
                   76
% identity
                   40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
NCBI Description
                   >gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) -
                   maize
                   295823
Seq. No.
                   LIB3079-007-Q1-K1-A6
Seq. ID
                   BLASTX
Method
                   q4455276
NCBI GI
BLAST score
                   157
                   2.0e-10
E value
Match length
                   132
 % identity
                   (AL035527) peptide transporter-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   295824
 Seq. No.
                   LIB3079-007-Q1-K1-A8
 Seq. ID
                   BLASTX
Method
NCBI GI
                   g100490
 BLAST score
                   471
                   2.0e-47
E value
                   104
Match length
                   25
 % identity
                   polyubiquitin - garden snapdragon (fragment)
 NCBI Description
                   >gi 16071 emb_CAA48140_ (X67957) ubiquitin [Antirrhinum
                   majus]
```

41403

295825

Seq. No.



```
LIB3079-007-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3912917
BLAST score
                  252
E value
                  1.0e-21
Match length
                  49
% identity
                  (AF001308) putative NAK-like ser/thr protein kinase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  295826
Seq. ID
                  LIB3079-007-Q1-K1-B9
                  BLASTX
Method
                  q4539350
NCBI GI
                  191
BLAST score
E value
                  2.0e-14
Match length
                  53
% identity
NCBI Description (AL035539) putative pectinesterase [Arabidopsis thaliana]
                  295827
Seq. No.
                  LIB3079-007-Q1-K1-C2
Seq. ID
                  BLASTX
Method
                  g451193
NCBI GI
                  524
BLAST score
                  2.0e-53
E value
Match length
                  142
% identity
NCBI Description (L28008) wali7 [Triticum aestivum]
                  >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]
                   295828
Seq. No.
                  LIB3079-007-Q1-K1-E7
Seq. ID
                  BLASTX
Method
                   g22216
NCBI GI
BLAST score
                   341
E value
                   5.0e-32
Match length
                   125
                   59
% identity
NCBI Description (X55722) 22kD zein [Zea mays]
Seq. No.
                   295829
                   LIB3079-007-Q1-K1-G2
Seq. ID
                   BLASTX
Method
                   q2980765
NCBI GI
                   229
BLAST score
                   6.0e-19
E value
Match length
                   107
                   50
% identity
                  (AL022198) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   295830
Seq. No.
                   LIB3079-008-Q1-K1-B11
Seq. ID
                   BLASTX
Method
                   g4544451
NCBI GI
```

41404

164

7.0e-25

BLAST score

E value



Match length 105 % identity 57

% identity 57
NCBI Description (AC006592) unknown protein [Arabidopsis thaliana]

Seq. No. 295831

Seq. ID LIB3079-008-Q1-K1-B7

Method BLASTX
NCBI GI g1345587
BLAST score 511
E value 5.0e-52
Match length 103
% identity 99

NCBI Description 14-3-3-LIKE PROTEIN GF14-6 >gi_998430_bbs_164522 (S77133) GF14-6=14-3-3 protein homolog [Zea mays, XL80, Peptide, 261

aa] [Zea mays]

Seq. No. 295832

Seq. ID LIB3079-008-Q1-K1-C2

Method BLASTX
NCBI GI g1076534
BLAST score 294
E value 1.0e-26
Match length 102
% identity 59

NCBI Description monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - garden

pea >gi_497120 (U06461) monodehydroascorbate reductase

[Pisum sativum]

Seq. No. 295833

Seq. ID LIB3079-008-Q1-K1-C5

Method BLASTX
NCBI GI g1491710
BLAST score 192
E value 1.0e-14
Match length 65
% identity 54

NCBI Description (X96506) alpha subunit; forms heterodimer with NC2

alpha/Dr1 [Homo sapiens]

Seq. No. 295834

Seq. ID LIB3079-008-Q1-K1-D8

Method BLASTN
NCBI GI g311238
BLAST score 50
E value 3.0e-19
Match length 94
% identity 88

NCBI Description Z.mays cat1 gene for catalase

Seq. No. 295835

Seq. ID LIB3079-008-Q1-K1-E2

Method BLASTX
NCBI GI g2760325
BLAST score 237
E value 6.0e-20
Match length 70
% identity 70





```
(AC002130) F1N21.10 [Arabidopsis thaliana]
NCBI Description
                  295836
Seq. No.
Seq. ID
                  LIB3079-008-Q1-K1-E5
                  BLASTX
Method
NCBI GI
                  q16073
                  159
BLAST score
                  8.0e-11
E value
                                                                     · ....
                  35
Match length
% identity
NCBI Description (X59526) zein protein [Acetabularia mediterranea]
                  295837
Seq. No.
Seq. ID
                  LIB3079-008-Q1-K1-E8
                  BLASTX
Method
                  g2501492
NCBI GI
                  142
BLAST score
                  8.0e-09
E value
                  89
Match length
                  36
% identity
                  FLAVONOL 3-O-GLUCOSYLTRANSFERASE 2 (UDP-GLUCOSE FLAVONOID
NCBI Description
                  3-O-GLUCOSYLTRANSFERASE 2) >gi_542018_pir__S41954
                  UTP-glucose glucosyltransferase - cassava (fragment)
                  >gi 453255_emb_CAA54611_ (X77461) UTP-glucose
                  glucosyltransferase [Manihot esculenta]
                   295838
Seq. No.
Seq. ID
                  LIB3079-008-Q1-K1-G1
                   BLASTN
Method
NCBI GI
                   g312180
                   67
BLAST score
                   2.0e-29
E value
Match length
                   71
                   99
% identity
NCBI Description Z.mays GapC4 gene
                   295839
Seq. No.
                   LIB3079-008-Q1-K1-G11
Seq. ID
                   BLASTX
Method
                   g141597
NCBI GI
BLAST score
                   206
E value
                   3.0e-16
Match length
                   114
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi 72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
                   295840
Seq. No.
                   LIB3079-008-Q1-K1-G2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2842494
BLAST score
                   286
                   1.0e-25
E value
                   60
Match length
```

88

% identity



NCBI Description



(AL021749) prohibitin-like protein [Arabidopsis thaliana]

>gi 4097688 (U66591) prohibitin 1 [Arabidopsis thaliana]

```
>gi 4097694 (U66594) prohibitin 1 [Arabidopsis thaliana]
                  295841
Seq. No.
                  LIB3079-008-Q1-K1-G5
Seq. ID
                  BLASTX
Method
                  g3858935
NCBI GI
                  354
BLAST score
                  1.0e-33
E value
                  108
Match length
                  63
% identity
                  (AL021636) synaptobrevin-like protein [Arabidopsis
NCBI Description
                  thaliana] >gi 4103357 (AF025332) vesicle-associated
                  membrane protein 7C; synaptobrevin 7C [Arabidopsis
                  thaliana]
                  295842
Seq. No.
                  LIB3079-008-Q1-K1-G7
Seq. ID
                  BLASTX
Method
                  g3236240
NCBI GI
                  242
BLAST score
                   4.0e-30
E value
                   96
Match length
% identity
                   (AC004684) unknown protein [Arabidopsis thaliana]
NCBI Description
                   295843
Seq. No.
                   LIB3079-009-Q1-K1-C5
Seq. ID
                   BLASTX
Method
                   g3309082
NCBI GI
                   158
BLAST score
                   1.0e-10
E value
                   59
Match length
% identity
                   (AF076251) calcineurin B-like protein 1 [Arabidopsis
NCBI Description
                   thaliana]
                   295844
Seq. No.
                   LIB3079-009-Q1-K1-F3
Seq. ID
                   BLASTN
Method
                   q3452306
NCBI GI
                   99
BLAST score
                   2.0e-48
E value
                   127
Match length
                   94
% identity
NCBI Description Zea mays retrotransposon Opie-3 5' LTR, partial sequence
                   295845
Seq. No.
                   LIB3079-009-Q1-K1-G8
Seq. ID
Method
                   BLASTX
                   g3193290
NCBI GI
BLAST score
                   205
                   2.0e-16
E value
                   80
Match length
                   49
% identity
NCBI Description (AF069298) contains similarity to a protein kinase domain
```



(Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin_legA.hmm, score: 16.72) [Arabido

Seq. No. 295846

Seq. ID LIB3079-010-Q1-K1-A11

Method BLASTN
NCBI GI g2811133
BLAST score 161
E value 2.0e-85
Match length 353
% identity 86

NCBI Description Zea mays starch synthase isoform zSTSII-1 (zSSIIa) mRNA,

partial cds

Seq. No. 295847

Seq. ID LIB3079-010-Q1-K1-A3

Method BLASTX
NCBI GI g3355483
BLAST score 253
E value 9.0e-22
Match length 62
% identity 68

NCBI Description (AC004218) gibberellin-regulated protein (GASA5)-like

[Arabidopsis thaliana]

Seq. No. 295848

Seq. ID LIB3079-010-Q1-K1-A8

Method BLASTN
NCBI GI g596022
BLAST score 106
E value 1.0e-52
Match length 114
% identity 98

NCBI Description Zea mays glucose-6 phosphate isomerase (phi1) mRNA,

complete cds

Seq. No. 295849

Seq. ID LIB3079-010-Q1-K1-D7

Method BLASTX
NCBI GI g2245124
BLAST score 200
E value 2.0e-15
Match length 82
% identity 55

NCBI Description (Z97343) protein kinase [Arabidopsis thaliana]

Seq. No. 295850

Seq. ID LIB3079-010-Q1-K1-G4

Method BLASTX
NCBI GI g3176726
BLAST score 315
E value 4.0e-29
Match length 101
% identity 56

NCBI Description (AC002392) putative serine proteinase [Arabidopsis



thaliana]

```
Seq. No.
                   295851
Seq. ID
                   LIB3079-011-Q1-K1-B6
Method
                   BLASTX
                   q1346281
NCBI GI
                   196
BLAST score
                   4.0e-15
E value
Match length
                   74
                   50
% identity
                   CHITOOLIGOSACCHARIDOLYTIC BETA-N-ACETYLGLUCOSAMINIDASE
NCBI Description
                   PRECURSOR (BETA-GLCNACASE) (BETA-HEXOSAMINIDASE)
                   (BETA-N-ACETYLHEXOSAMINIDASE) >gi_1078988_pir__JC2539 beta-N-acetylglucosaminidase (EC 3.2.1.-) - silkworm
                   >gi_998377_bbs_165703 (S77548) chitooligosaccharidolytic
                   beta-N-acetylglucosaminidase, beta-GlcNAcase=beta 1 enzyme
                    [Bombyx mori=silkworms, larvae, Kinshu X Shouwa, Peptide,
                   596 aa] [Bombyx mori] >gi_1094927_prf__2107188A
                   chitooligosaccharidolytic beta-N-acetylglucosaminidase
                    [Bombyx mori]
Seq. No.
                   295852
                   LIB3079-011-Q1-K1-H2
Seq. ID
Method
                   BLASTX
                   g4249386
NCBI GI
BLAST score
                   178
E value
                    6.0e-13
                    115
Match length
% identity
                    (AC005966) Strong similarity to gb AF061286 gamma-adaptin 1
NCBI Description
                    from Arabidopsis thaliana. EST gb_H37393 comes from this
                    gene. [Arabidopsis thaliana]
                    295853
Seq. No.
                    LIB3079-012-Q1-K1-A12
Seq. ID
                    BLASTX
Method
NCBI GI
                    g141605
                    225
BLAST score
                    7.0e-22
E value
                    89
Match length
% identity
                    70
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                    >gi 72312 pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                    maize > gi_{168\overline{68}0} (M12145) 19 kDa zein protein [Zea mays]
                    295854
Seq. No.
                    LIB3079-012-Q1-K1-C10
Seq. ID
                    BLASTN
Method
                    g531828
NCBI GI
                    43
BLAST score
                    2.0e-15
E value
Match length
                    75
                    89
% identity
NCBI Description Cloning vector pSport1, complete cds
```

41409

295855

LIB3079-012-Q1-K1-F9

Seq. No.

Seq. ID



```
Method
                  g2511531
NCBI GI
                  370
BLAST score
                  1.0e-35
E value
                  94
Match length
% identity
                  (AF008120) alpha tubulin 1 [Eleusine indica]
NCBI Description
                  >gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1
                   [Eleusine indica]
                   295856
Seq. No.
                  LIB3079-012-Q1-K1-H7
Seq. ID
                  BLASTX
Method
                   g531829
NCBI GI
                   157
BLAST score
                   1.0e-10
E value
                   53
Match length
                   60
% identity
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                   pSport1]
                   295857
Seq. No.
                   LIB3079-013-Q1-K1-C11
Seq. ID
                   BLASTX
Method
                   g2541876
NCBI GI
                   245
BLAST score
                   7.0e-21
E value
                   113
Match length
                   43
% identity
                   (D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                   [Nicotiana tabacum]
                   295858
Seq. No.
                   LIB3079-013-Q1-K1-C9
Seq. ID
                   BLASTX
Method
                   q3021268
 NCBI GI
                   302
BLAST score
                   2.0e-27
 E value
                   130
 Match length
 % identity
NCBI Description (AL022347) putative protein [Arabidopsis thaliana]
                   295859
 Seq. No.
 Seq. ID
                   LIB3079-013-Q1-K1-D12
                   BLASTX
 Method
                   q3158372
 NCBI GI
                   207
 BLAST score
                   6.0e-17
 E value
                   60
 Match length
                   73
 % identity
                   (AF035383) polyubiquitin [Arabidopsis thaliana]
 NCBI Description
                   295860
```

Seq. No. 2958

Seq. ID LIB3079-013-Q1-K1-F10

Method BLASTX
NCBI GI g598073
BLAST score 193



```
9.0e-15
E value
Match length
                   65
% identity
                   57
                  (L36806) GT-1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   295861
                   LIB3079-013-Q1-K1-H10
Seq. ID
                   BLASTX
Method
                   q1041815
NCBI GI
                   172
BLAST score
                   3.0e-12
E value
                   87
Match length
% identity
NCBI Description (U16721) lipid transfer protein [Oryza sativa]
                   295862
Seq. No.
                   LIB3079-014-Q1-K1-A6
Seq. ID
Method
                   BLASTX
                   q4582787
NCBI GI
                   165
BLAST score
                   2.0e-11
E value
Match length
                   115
% identity
                   (AJ012281) adenosine kinase [Zea mays]
NCBI Description
                   295863
Seq. No.
                   LIB3079-014-Q1-K1-F10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g629861
BLAST score
                   482
                   9.0e-49
E value
                   125
Match length
% identity
                   86
                   zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
NCBI Description
                   zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                   295864
                   LIB3079-014-Q1-K1-F11
Seq. ID
                   BLASTX
Method
                   g22166
NCBI GI
BLAST score
                   213
                   3.0e-17
E value
Match length
                   43
                   98
 % identity
                   (X15711) adenine nucleotide translocator [Zea mays]
NCBI Description
                    295865
 Seq. No.
                   LIB3079-015-Q1-K1-A10
 Seq. ID
                    BLASTX
 Method
                   g563235
 NCBI GI
```

Method BLASTX
NCBI GI g563235
BLAST score 455
E value 9.0e-51
Match length 141
% identity 78

NCBI Description (U15964) xyloglucan endo-transglycosylase homolog; similar to Triticum aestivum endo-xyloglucan transferase, PIR

Accession Number E49539 [Zea mays] >gi_563927 (U15781)



84

68

Match length

NCBI Description

% identity

8

```
xyloglucan endo-transglycosylase homolog [Zea mays]
>gi_1097378_prf__2113418A xyloglucan endotransglycosylase
homolog [Zea mays]
```

```
295866
Seq. No.
Seq. ID
                  LIB3079-015-Q1-K1-C1
                  BLASTX
Method
                  q4101473
NCBI GI
                  143
BLAST score
                  7.0e-09
E value
                  39
Match length
                  72
% identity
NCBI Description (AF003382) KEA1 [Arabidopsis thaliana]
                  295867
Seq. No.
                  LIB3079-015-Q1-K1-D7
Seq. ID
Method
                  BLASTX
                  q1173104
NCBI GI
                  376
BLAST score
                  3.0e-36
E value
                  133
Match length
                   52
% identity
                  RIBONUCLEASE 2 PRECURSOR >gi_289210 (M98336) ribonuclease
NCBI Description
                   [Arabidopsis thaliana] >gi 2\overline{6}42160 (AC003000) ribonuclease,
                  RNS2 [Arabidopsis thaliana]
                   295868
Seq. No.
Seq. ID
                   LIB3079-015-Q1-K1-G9
                   BLASTX
Method
NCBI GI
                   q1946355
                   555
BLAST score
                   4.0e-57
E value
                   141
Match length
% identity
                   (U93215) maize transposon MuDR mudrA protein isolog
NCBI Description
                   [Arabidopsis thaliana] >gi_2880040 (AC002340) maize
                   transposon MuDR mudrA-like protein [Arabidopsis thaliana]
                   295869
Sèq. No.
                   LIB3079-015-Q1-K1-H10
Seq. ID
Method
                   BLASTN
                   g2062705
NCBI GI
BLAST score
                   36
E value
                   1.0e-10
Match length
                   40
                   97
% identity
                   Human butyrophilin (BTF5) mRNA, complete cds
NCBI Description
                   295870
Seq. No.
                   LIB3079-016-Q1-K1-A12
Seq. ID
                   BLASTX
Method
                   g1362086
NCBI GI
BLAST score
                   271
                   4.0e-24
E value
```

5-methyltetrahydropteroyltriglutamate--homocysteine





```
S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir__S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]
```

 Seq. No.
 295871

 Seq. ID
 LIB3079-016-Q1-K1-A7

 Method
 BLASTX

 NCBI GI
 g2494120

 BLAST score
 313

 E value
 8.0e-29

E value 8.0e-Match length 133 % identity 47

NCBI Description (AC002376) Similar to Synechocystis integral membrane

protein (gb_D64002). [Arabidopsis thaliana]

Seq. No. 295872

Seq. ID LIB3079-016-Q1-K1-B6

Method BLASTN
NCBI GI g4416300
BLAST score 151
E value 2.0e-79
Match length 321
% identity 46

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster

region, complete sequence

Seq. No. 295873

Seq. ID LIB3079-016-Q1-K1-C4

Method BLASTX
NCBI GI g417154
BLAST score 215
E value 2.0e-17
Match length 83
% identity 54

NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 295874

Seq. ID LIB3079-016-Q1-K1-E6

Method BLASTX
NCBI GI g520544
BLAST score 258
E value 1.0e-22
Match length 71
% identity 76

NCBI Description (U12195) betaine aldehyde dehydrogenase [Sorghum bicolor]

Seq. No. 295875

Seq. ID LIB3079-016-Q1-K1-F1

Method BLASTX
NCBI GI g1076678
BLAST score 325



4.0e-30

Match length 65 % identity

NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No.

295876

Seq. ID

E value

LIB3079-016-Q1-K1-F12

BLASTX Method NCBI GI g134598 BLAST score 275 3.0e-24 E value

Match length 78 73 % identity

NCBI Description SUPEROXIDE DISMUTASE-4AP (CU-ZN)

Seq. No.

295877

Seq. ID

LIB3079-016-Q1-K1-F7

BLASTX Method NCBI GI q1619602 298 BLAST score E value 4.0e-27 124 Match length 48 % identity

NCBI Description (Y08726) MtN3 [Medicago truncatula]

Seq. No.

295878 LIB3079-016-Q1-K1-H12

Seq. ID Method BLASTX NCBI GI g1076390 BLAST score 228 7.0e-19 E value 130 Match length % identity 43

NCBI Description

protein phosphatase 2A pDF2 - Arabidopsis thaliana

>gi 683504 emb_CAA57529_ (X82003) protein phosphatase 2A 65

kDa regulatory subunit [Arabidopsis thaliana]

Seq. No. 295879

Seq. ID LIB3079-017-Q1-K1-A4

Method BLASTX NCBI GI g4503523 BLAST score 145 E value 2.0e-09 Match length 51 % identity

UNKNOWN >gi 2351378 (U54558) translation initiation factor NCBI Description

eIF3 p66 subunit [Homo sapiens] >gi_4200328_emb_CAA18440_

(AL022313) EIF3-P66 [Homo sapiens]

Seq. No. 295880

LIB3079-017-Q1-K1-B4 Seq. ID

Method BLASTX NCBI GI g3334259 BLAST score 210 3.0e-17 E value Match length 56 70 % identity



NCBI Description WD-40 REPEAT PROTEIN MSI4 >gi_2599092 (AF028711) WD-40 repeat protein MSI4 [Arabidopsis thaliana]

Seq. No. 295881

Seq. ID LIB3079-017-Q1-K1-B8

Method BLASTX
NCBI GI 94587584
BLAST score 219
E value 3.0e-18
Match length 68
% identity 62

NCBI Description (AC007232) unknown protein [Arabidopsis thaliana]

Seq. No. 295882

Seq. ID LIB3079-017-Q1-K1-D5

Method BLASTN
NCBI GI g168694
BLAST score 62
E value 1.0e-26
Match length 154
% identity 86

NCBI Description Maize gamma zein mRNA, partial cds

Seq. No. 295883

Seq. ID LIB3079-017-Q1-K1-D8

Method BLASTX
NCBI GI g1632831
BLAST score 158
E value 5.0e-11
Match length 64
% identity 55

NCBI Description (Z49698) orf [Ricinus communis]

Seq. No. 295884

Seq. ID LIB3079-017-Q1-K1-E7

Method BLASTN
NCBI GI g799029
BLAST score 180
E value 9.0e-97
Match length 215
% identity 97

NCBI Description Z.mays BET1 mRNA

Seq. No. 295885

Seq. ID LIB3079-017-Q1-K1-F3

Method BLASTX
NCBI GI g3334112
BLAST score 253
E value 5.0e-22
Match length 66
% identity 76

NCBI Description ACYL-COA-BINDING PROTEIN (ACBP) >gi_1938236_emb_CAA70200_

(Y08996) acyl-CoA-binding protein [Ricinus communis]

Seq. No. 295886

Seq. ID LIB3079-017-Q1-K1-G3

Method BLASTX



```
q2696804
NCBI GI
                  186
BLAST score
                  2.0e-14
E value
                  74
Match length
% identity
NCBI Description (AB009665) water channel protein [Oryza sativa]
                  295887
Seq. No.
                  LIB3079-017-Q1-K1-H9
Seq. ID
                  BLASTN
Method
                  q3821780
NCBI GI
```

36 BLAST score 9.0e-11 E value 36 Match length 100 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

295888

Seq. No. Seq. ID LIB3079-018-Q1-K1-B11 BLASTX Method q3551247 NCBI GI 240 BLAST score 3.0e-20E value 62 Match length % identity

NCBI Description (AB012703) 181 [Daucus carota]

295889 Seq. No. LIB3079-018-Q1-K1-C9 Seq. ID BLASTX Method NCBI GI q2245012 207 BLAST score 2.0e-16 E value 125

Match length % identity

NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

295890 Seq. No.

LIB3079-018-Q1-K1-G5 Seq. ID

BLASTX Method g2944389 NCBI GI BLAST score 149 E value 2.0e-09 Match length 93 42 % identity

NCBI Description (AF049106) actin 4 [Glycine max]

295891 Seq. No.

LIB3079-019-Q1-K1-B3 Seq. ID

BLASTN Method g3821780 NCBI GI BLAST score 36 E value 1.0e-10 Match length 36 100 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1



```
Seq. No.
                  LIB3079-019-Q1-K1-F5
Seq. ID
                  BLASTN
Method
                   q3452305
NCBI GI
BLAST score
                   106
E value
                   2.0e-52
                   186
Match length
                   90
% identity
NCBI Description Zea mays retrotransposon Opie-3 3' LTR, partial sequence
                   295893
Seq. No.
                   LIB3079-019-Q1-K1-H7
Seq. ID
                   BLASTN
Method
                   g22144
NCBI GI
                   82
BLAST score
                   3.0e-38
E value
Match length
                   230
                   84
% identity
NCBI Description Maize anaerobically regulated gene for fructose
                   bisphosphate aldolase (EC 4.1.2.13)
                   295894
Seq. No.
Seq. ID
                   LIB3079-020-Q1-K1-C10
                   BLASTX
Method
                   g1419370
NCBI GI
                   308
BLAST score
                   2.0e-28
E value
                   96
Match length
% identity
                   (X97726) actin depolymerizing factor [Zea mays]
NCBI Description
                   295895
Seq. No.
                   LIB3079-020-Q1-K1-C11
Seq. ID
                   BLASTN
Method
                   g454880
NCBI GI
BLAST score
                   53
                   7.0e-21
E value
Match length
                   231
                   85
 % identity
                   Rice mRNA for WSI724 protein induced by water stress,
NCBI Description
                   complete cds
 Seq. No.
                   295896
                   LIB3079-020-Q1-K1-C12
Seq. ID
                   BLASTN
Method
                   g2913892
NCBI GI
                   79
BLAST score
                   2.0e-36
E value
                   236
Match length
                   87
 % identity
 NCBI Description Oryza sativa mRNA for LIP5, complete cds
 Seq. No.
                   295897
                   LIB3079-020-Q1-K1-E1
 Seq. ID
```

BLASTX

260

g3176874

Method

NCBI GI BLAST score



```
E value
                  1.0e-22
                  80
Match length
% identity
                  (AF065639) cucumisin-like serine protease [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  295898
                  LIB3079-020-Q1-K1-E10
Seq. ID
                  BLASTX
Method
                  g3927831
NCBI GI
                  173
BLAST score
                  2.0e-12
E value
                  103
Match length
                  39
% identity
NCBI Description (AC005727) similar to mouse ankyrin 3 [Arabidopsis
                  thaliana]
                  295899
Seq. No.
                  LIB3079-021-Q1-K1-A1
Seq. ID
                  BLASTX
Method
                  g4587557
NCBI GI
                  158
BLAST score
                   1.0e-10
E value
                   58
Match length
% identity
                   (AC006577) Similar to gb U21858 transcription initiation
NCBI Description
                   factor TFIID 31KD subunit (TAFII32) from Homo sapiens.
                   [Arabidopsis thaliana]
                   295900
Seq. No.
                   LIB3079-021-Q1-K1-A5
Seq. ID
                   BLASTN
Method
NCBI GI
                   g22524
BLAST score
                   71
                   8.0e-32
E value
                   135
Match length
                   88
% identity
NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)
                   295901
Seq. No.
                   LIB3079-021-Q1-K1-B7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1172557
BLAST score
                   182
                   1.0e-14
E value
                   97
Match length
% identity
                   OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT
NCBI Description
                   ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                   >gi_422030_pir__S34146 porin por1 - maize
                   >gi_626044_pir__A55017 porin, plastid - maize
                   >gi_313136_emb_CAA51828_ (X73429) porin [Zea mays]
```

Seq. No. 295902

Seq. ID LIB3079-021-Q1-K1-E7

Method BLASTN NCBI GI g3319775



BLAST score 3.0e-17 E value 111 Match length 86 % identity NCBI Description Zea mays mRNA for cytosolic seryl-tRNA synthetase 295903 Seq. No. LIB3079-021-Q1-K1-G6 Seq. ID BLASTX Method q16073 NCBI GI BLAST score 164 2.0e-11 E value 70 Match length 56 % identity NCBI Description (X59526) zein protein [Acetabularia mediterranea] 295904 Seq. No. Seq. ID LIB3079-021-Q1-K1-H3 Method BLASTN g3821780 NCBI GI 36 BLAST score 1.0e-10 E value 36 Match length 100 % identity NCBI Description Xenopus laevis cDNA clone 27A6-1 295905 Seq. No. Seq. ID LIB3079-021-Q1-K1-H8 BLASTX Method q72896 NCBI GI BLAST score 149 1.0e-09 E value 86 Match length % identity NCBI Description (K02938) 5S RNA gene transcription factor (putative);

transcription factor IIIA - African clawed frog >gi_214819

putative [Xenopus laevis]

295906 Seq. No.

Seq. ID LIB3079-022-Q1-K1-A12

Method BLASTX NCBI GI q4585976 BLAST score 146 E value 2.0e-09 93 Match length % identity

(AC005287) Unknown protein [Arabidopsis thaliana] NCBI Description

295907 Seq. No.

LIB3079-022-Q1-K1-D4 Seq. ID

Method BLASTX g4006848 NCBI GI BLAST score 207 E value 2.0e-16 Match length 76 53 % identity

(AJ131433) selenocysteine methyltransferase [Astragalus NCBI Description

Seq. No.

Seq. ID

Method



bisulcatus]

```
295908
Seq. No.
                  LIB3079-022-Q1-K1-D8
Seq. ID
                  BLASTX
Method
                  g567893
NCBI GI
BLAST score
                  168
                  8.0e-12
E value
                  97
Match length
                  40
% identity
NCBI Description (L37382) beta-galactosidase-complementation protein
                   [Cloning vector]
                  295909
Seq. No.
                  LIB3079-022-Q1-K1-G3
Seq. ID
                  BLASTX
Method
                  g461498
NCBI GI
                  237
BLAST score
                  2.0e-20
E value
                  61
Match length
% identity
                  ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
NCBI Description
                   TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                   (ALAAT-2) >gi 320619 pir S28429 alanine transaminase (EC
                   2.6.1.2) - proso millet \overline{>}gi_296204 emb_CAA49199 (X69421)
                   alanine aminotransferase [Panicum miliaceum]
                   295910
Seq. No.
                   LIB3079-023-Q1-K1-A6
Seq. ID
                   BLASTX
Method
                   g3510249
NCBI GI
BLAST score
                   209
                   6.0e-25
E value
Match length
                   123
% identity
NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]
                   295911
Seq. No.
                   LIB3079-023-Q1-K1-B1
Seq. ID
Method
                   BLASTX
                   q3449282
NCBI GI
BLAST score
                   179
                   4.0e-13
E value
Match length
                   76
% identity
                   (AB006139) phosphoribosylformimino-5-aminoimidazole
NCBI Description
                   carboxamide ribotide isomerase [Arabidopsis thaliana]
                   >gi 3449284 dbj BAA32457_ (AB008929)
                   N'-5'-phosphoribosyl-formimino-5-aminoimidazole-
                   4-carboxamide ribonucleotide isomerase [Arabidopsis
                   thaliana] >gi 4510353_gb_AAD21442.1_ (AC006921)
                   phosphoribosylformimino-5-aminoimidazole carboxamide
```

41420

LIB3079-023-Q1-K1-E4

295912

BLASTN

ribotide isomerase [Arabidopsis thaliana]



q3821780

NCBI GI 36 BLAST score 9.0e-11 E value 36

Match length % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No.

295913

Seq. ID

LIB3079-023-Q1-K1-E5

BLASTN Method q662367 NCBI GI 53 BLAST score 3.0e-21 E value 125 Match length 86

% identity

NCBI Description Zea mays farnesyl pyrophosphate synthetase (fps) mRNA,

complete cds

Seq. No.

295914

Seq. ID

LIB3079-023-Q1-K1-E9

BLASTX Method q4582787 NCBI GI 246 BLAST score 4.0e-21 E value 75 Match length % identity

NCBI Description (AJ012281) adenosine kinase [Zea mays]

Seq. No.

295915

Seq. ID

LIB3079-023-Q1-K1-H5

BLASTX Method q3912998 NCBI GI BLAST score 165 2.0e-11 E value 122 Match length % identity

NCBI Description FLORAL HOMEOTIC PROTEIN AGL8 >gi_2129536_pir__S71208 AGL8 protein - Arabidopsis thaliana >gi_1004365 (U33473) AGL8

[Arabidopsis thaliana]

Seq. No.

295916

Seq. ID

LIB3079-023-Q1-K1-H7

Method BLASTN NCBI GI q3851004 135 BLAST score 7.0e-70 E value 343

Match length % identity

Zea mays pyruvate dehydrogenase E1 alpha subunit RNA, NCBI Description

nuclear gene encoding mitochondrial protein, complete cds

Seq. No.

295917

Seq. ID

LIB3079-024-Q1-K1-A1

Method BLASTN g829147 NCBI GI 99 BLAST score 9.0e-49 E value



```
115
Match length
                  97
% identity
NCBI Description Z.mays gene for cyclophilin
                  295918
Seq. No.
                  LIB3079-024-Q1-K1-C2
Seq. ID
                  {\tt BLASTX}
Method
                  g141600
NCBI GI
                  159
BLAST score
                  8.0e-11
E value
                  86
Match length
                   45
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
                  >gi 72315 pir_ ZIZMB1 19K zein precursor (clone cZ19B1) -
                  maize >gi 168674 (M12143) 19 kDa zein protein [Zea mays]
                   295919
Seq. No.
                  LIB3079-024-Q1-K1-C8
Seq. ID
                  BLASTX
Method
                   g567893
NCBI GI
                   181
BLAST score
                   2.0e-13
E value
                   83
Match length
                   46
% identity
NCBI Description (L37382) beta-galactosidase-complementation protein
                   [Cloning vector]
                   295920
Seq. No.
                   LIB3079-024-Q1-K1-G8
Seq. ID
                   BLASTX
Method
                   g2961178
NCBI GI
                   428
BLAST score
                   3.0e-42
E value
                   125
Match length
% identity
NCBI Description (AF050675) GTP-binding protein [Oryza sativa]
                 . 295921
Seq. No.
                   LIB3079-024-Q1-K1-H7
Seq. ID
                   BLASTX
Method
                   q3806098
NCBI GI
                   337
BLAST score
                   2.0e-31
E value
                   98
Match length
                   61
 % identity
                   (AF079100) arginine-tRNA-protein transferase 1; Atelp
NCBI Description
                    [Arabidopsis thaliana]
                   295922
 Seq. No.
                   LIB3079-025-Q1-K1-B11
 Seq. ID
```

BLASTX Method q141603 NCBI GI 244 BLAST score 2.0e-41 E value Match length 131 % identity

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)

Match length

86

Seq. No.



295923



>gi 72311_pir ZIZM2 19K zein precursor (clone A20) - maize

>gi 22529 emb CAA24723 (V01476) zein [Zea mays]

```
LIB3079-025-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g141617
                   203
BLAST score
                   6.0e-16
E value
Match length
                   36
% identity
                   100
                  ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                   >gi_100941_pir__S12140 zein Zc1 - maize
                   >gi_100945_pir__B29017 zein 2 - maize
                   >gi_22515_emb CAA37595_ (X53515) zein Zc1 [Zea mays]
                   >gi 168666 (M\overline{1}6460) 16-kDa zein protein [Zea mays]
Seq. No.
                   295924
                   LIB3079-025-Q1-K1-H3
Seq. ID
Method
                   BLASTX
                   q1076668
NCBI GI
BLAST score
                   207
                   7.0e-17
E value
                   64
Match length
% identity
                   NADH dehydrogenase (EC 1.6.99.3) - potato
NCBI Description
                   >gi 639834_emb_CAA58823_ (X83999) NADH dehydrogenase
                   [Solanum tuberosum]
                   295925
Seq. No.
                   LIB3079-025-Q1-K1-H5
Seq. ID
Method
                   BLASTN
                   q1037129
NCBI GI
                   210
BLAST score
                   1.0e-114
E value
                   425
Match length
% identity
                   88
                   (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                   Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                   295926
Seq. No.
                   LIB3079-026-Q1-K1-B3
Seq. ID
Method
                   BLASTX
                   g4028155
NCBI GI
                   253
BLAST score
                   9.0e-22
E value
                   112
Match length
% identity
                   44
                   (AF083221) YDR140w homolog [Fugu rubripes]
NCBI Description
                   295927
Seq. No.
                   LIB3079-026-Q1-K1-C12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2660669
                   275
BLAST score
                   2.0e-24
E value
```





```
% identity
                  (AC002342) human Mi-2 autoantigen-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  295928
Seq. No.
Seq. ID
                  LIB3079-026-Q1-K1-E2
Method
                  BLASTN
NCBI GI
                  q1037129
                  180
BLAST score
                  1.0e-96
E value
                  340
Match length
                  88
% identity
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
                  Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                  295929
Seq. No.
                  LIB3079-026-Q1-K1-G2
Seq. ID
                  BLASTX
Method
                  g3914467
NCBI GI
                  579
BLAST score
                  5.0e-60
E value
                  132
Match length
                  86
% identity
NCBI Description 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
                  >gi 1864003_dbj_BAA19252 (AB001422) 21D7 [Nicotiana
                  tabacum]
                  295930
Seq. No.
                  LIB3079-027-Q1-K1-D2
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1169782
BLAST score
                  142
                   6.0e-09
E value
Match length
                   45
% identity
NCBI Description FUSCA PROTEIN FUS6 >gi_432446 (L26498) FUS6 [Arabidopsis
                   thaliana]
                   295931
Seq. No.
Seq. ID
                   LIB3079-027-Q1-K1-F8
                   BLASTX
Method
NCBI GI
                   q4454452
BLAST score
                   465
E value
                   3.0e-48
                   119
Match length
% identity
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.
                   295932
                   LIB3079-028-Q1-K1-A8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2498329
BLAST score
                   210
E value
                   6.0e-17
                   95
Match length
                   47
 % identity
NCBI Description PATTERN FORMATION PROTEIN EMB30 >gi_2129665_pir__$65571
```





pattern-formation protein GNOM - Arabidopsis thaliana >gi 1209633 (U36433) GNOM gene product [Arabidopsis thaliana] >gi 1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi 1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana]

```
295933
Seq. No.
                   LIB3079-028-Q1-K1-C7
Seq. ID
                   BLASTX
Method
                   q3522956
NCBI GI
                   376
BLAST score
                   3.0e-36
E value
                   118
Match length
                   59
% identity
NCBI Description (AC004411) putative pectinacetylesterase precursor
                   [Arabidopsis thaliana]
                   295934
Seq. No.
                   LIB3079-028-Q1-K1-H3
Seq. ID
                   BLASTX
Method
                   q4115563
NCBI GI
                   207
BLAST score
                   2.0e-16
E value
                   115
Match length
                   39
% identity
                   (AB013598) UDP-glucose:anthocyanin 5-0-glucosyltransferase
NCBI Description
                   [Verbena x hybrida]
                   295935
Seq. No.
                   LIB3079-029-Q1-K1-A1
Seq. ID
                   BLASTX
Method
                   q141608
NCBI GI
                   198
BLAST score
                   8.0e-17
E value
                    104
Match length
% identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_
NCBI Description
                    zein, 19K - maize >gi_22446_emb_CAA3765\overline{1}_ (X53\overline{5}82)\overline{1}9 kDa
                    zein [Zea mays]
                    295936
Seq. No.
```

Seq. ID LIB3079-029-Q1-K1-C5
Method BLASTX
NCBI GI g3004950
BLAST score 305

BLAST score 305 E value 5.0e-28 Match length 92 % identity 64

NCBI Description (AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays]

Seq. No. 295937

Seq. ID LIB3079-029-Q1-K1-D10

Method BLASTN NCBI GI g799029 BLAST score 34



9.0e-10

Match length 79 % identity NCBI Description Z.mays BET1 mRNA

295938 Seq. No.

E value

LIB3079-029-Q1-K1-D5 Seq. ID

BLASTN Method q531031 NCBI GI 40 BLAST score 3.0e-13 E value 56 Match length 93 % identity

Pennisetum ciliare apomixis-associated mRNA NCBI Description

>gi_531481_emb_Z36544_PCAPOSPA1 P.ciliare (Higgins)

apospory associated mRNA, 1398bp

>gi_549983_gb_U13148_PCU13148 Pennisetum ciliare possible

apospory-associated mRNA clone pSUB C, complete cds

295939 Seq. No.

LIB3079-029-Q1-K1-D7 Seq. ID

BLASTX Method q3242753 NCBI GI 167 BLAST score 1.0e-11 E value 113 Match length 29 % identity

(AC005162) probable carboxypeptidase precursor; 64% similar NCBI Description

to P42660 (PID:g1718107) [Homo sapiens]

295940 Seq. No.

LIB3079-029-Q1-K1-D9 Seq. ID

BLASTX Method g1845197 NCBI GI 187 BLAST score 2.0e-16 E value 79 Match length 66 % identity

NCBI Description (Y08298) HMGc2 [Zea mays]

295941 Seq. No.

LIB3079-029-Q1-K1-F12 Seq. ID

BLASTX Method g1848225 NCBI GI BLAST score 188 3.0e-14E value 64 Match length 53 % identity

(U88090) nonspecific lipid transfer protein [Hordeum NCBI Description

vulgare]

295942 Seq. No.

LIB3079-029-Q1-K1-H1 Seq. ID

BLASTN Method NCBI GI q1657766 68 BLAST score 6.0e-30 E value



Match length 42 % identity

Zea mays retrotransposon Opie-2 5' LTR, primer binding NCBI Description site, gag gene, pol gene, complete cds, polypurine tract and 3' LTR

Seq. No.

295943

295944

295945

Seq. ID

LIB3079-029-Q1-K1-H6

Method BLASTX NCBI GI g1174783 BLAST score 247 4.0e-21 E value Match length 74

% identity 66

NCBI Description

TRYPTOPHAN SYNTHASE ALPHA CHAIN PRECURSOR

>gi_1362207_pir__S56665 tryptophan synthase (EC 4.2.1.20) alpha chain - maize >gi 440171 emb CAA54131 (X76713)

tryptophan synthase, alpha subunit [Zea mays]

Seq. No.

Seq. ID

LIB3079-030-Q1-K1-A7

Method BLASTX NCBI GI g2239179 BLAST score 209 E value 1.0e-16 Match length 61 % identity 62

(Z97208) hypothetical protein [Schizosaccharomyces pombe] NCBI Description

Seq. No.

Seq. ID

LIB3079-030-Q1-K1-B3

Method BLASTN NCBI GI g4416300 BLAST score 127 3.0e-65 E value Match length 262 % identity 87

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster

region, complete sequence

Seq. No.

295946

Seq. ID

LIB3079-030-Q1-K1-B5

Method BLASTX NCBI GI g417154 BLAST score 325 E value 3.0e-30 Match length 95 % identity 72

HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock NCBI Description

protein 82 - rice (strain Taichung Native One)

>gi_20256_emb_CAA77978 (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No.

295947

Seq. ID

LIB3079-030-Q1-K1-B6

Method NCBI GI BLASTX q417154



BLAST score 325 E value 3.0e-30 Match length 93 % identity 75

NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 295948

Seq. ID LIB3079-030-Q1-K1-C1

Method BLASTX
NCBI GI g4455202
BLAST score 164
E value 1.0e-11
Match length 47
% identity 68

NCBI Description (AL035440) putative APG protein [Arabidopsis thaliana]

Seq. No. 295949

Seq. ID LIB3079-030-Q1-K1-C5

Method BLASTX
NCBI GI g141604
BLAST score 277
E value 7.0e-25
Match length 79
% identity 77

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)

>gi_72310_pir__ZIZM91 19K zein precursor (clone cZ19C1) maize >gi_168678 (M12146) 19 kDa zein protein [Zea mays]

Seq. No. 295950

Seq. ID LIB3079-030-Q1-K1-E10

Method BLASTX
NCBI GI g168703
BLAST score 155
E value 3.0e-10
Match length 56
% identity 61

NCBI Description (M86591) 22 kDa zein protein [Zea mays]

Seq. No. 295951

Seq. ID LIB3079-030-Q1-K1-E6

Method BLASTN
NCBI GI g22524
BLAST score 51
E value 7.0e-20
Match length 139
% identity 84

NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)

Seq. No. 295952

Seq. ID LIB3079-030-Q1-K1-F3

Method BLASTX
NCBI GI g417333
BLAST score 151
E value 5.0e-10





```
Match length
% identity
                  MYB-RELATED PROTEIN B (B-MYB) >gi_283924_pir__S28050
NCBI Description
                  transforming protein (B-myb) - chicken
                  >gi_63099_emb_CAA47839_ (X67505) B-myb [Gallus gallus]
                  295953
Seq. No.
                  LIB3079-031-Q1-K1-B4
Seq. ID
                  BLASTX
Method
                  g3337350
NCBI GI
                  149
BLAST score
                   8.0e-10
E value
                   94
Match length
                   38
% identity
NCBI Description (AC004481) putative permease [Arabidopsis thaliana]
                   295954
Seq. No.
                   LIB3079-031-Q1-K1-C1
Seq. ID
Method
                   BLASTX
                   g531829
NCBI GI
                   148
BLAST score
E value
                   2.0e-09
                   70
Match length
                   44
% identity
                   (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                   pSport1]
                   295955
Seq. No.
                   LIB3079-031-Q1-K1-D7
Seq. ID
                   BLASTX
Method
                   g3273243
NCBI GI
                   168
BLAST score
                   2.0e-21
E value
                   83
Match length
 % identity
                   69
                   (AB004660) NLS receptor [Oryza sativa]
NCBI Description
                   >gi 3273245_dbj_BAA31166_ (AB004814) NLS receptor [Oryza
                   sativa]
                   295956
 Seq. No.
                   LIB3079-031-Q1-K1-D8
 Seq. ID
                   BLASTX
 Method
                   g576773
 NCBI GI
 BLAST score
                   176
                   3.0e-13
 E value
                   63
 Match length
                   11
 % identity
 NCBI Description (U16956) polyubiquitin [Filobasidiella neoformans]
                   295957
 Seq. No.
                   LIB3079-031-Q1-K1-F2
 Seq. ID
                   BLASTX
 Method
                   q2146741
 NCBI GI
 BLAST score
                    637
 E value
                    9.0e-67
                    132
 Match length
```

87

% identity





NCBI Description isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) - Arabidopsis thaliana >gi_1293565 (U49259) isopentenyl

diphosphate:dimethylally diphosphate isomerase [Arabidopsis thaliana]

Seq. No. 295958

Seq. ID LIB3079-031-Q1-K1-G5

Method BLASTX
NCBI GI g4309698
BLAST score 199
E value 2.0e-15
Match length 82
% identity 50

NCBI Description (AC006266) putative glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 295959

Seq. ID LIB3079-031-Q1-K1-H10

Method BLASTX
NCBI GI g136063
BLAST score 209
E value 5.0e-17
Match length 89
% identity 62

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)

>gi_68426_pir__ISZMT triose-phosphate isomerase (EC
5.3.1.1) - maize >gi_168647 (L00371) triosephosphate
isomerase 1 [Zea mays] >gi_217974_dbj_BAA00009_ (D00012)

triosephosphate isomerase [Zea mays]

Seq. No. 295960

Seq. ID LIB3079-032-Q1-K1-A8

Method BLASTX
NCBI GI g1835154
BLAST score 199
E value 3.0e-18
Match length 68
% identity 69

NCBI Description (Y10267) glutamine synthetase [Medicago truncatula]

Seq. No. 295961

Seq. ID LIB3079-032-Q1-K1-C2 Method BLASTN

NCBI GI g3821780 BLAST score 34 E value 1.0e-09 Match length 34

% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 295962

Seq. ID LIB3079-032-Q1-K1-D4

Method BLASTX
NCBI GI g3249081
BLAST score 205
E value 3.0e-16
Match length 110



```
% identity
                  (AC004473) Strong similarity to AROGP2 gene gb_1762634 from
NCBI Description
                  Lycopersicon esculentum. [Arabidopsis thaliana]
                  295963
Seq. No.
                  LIB3079-032-Q1-K1-F2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g224509
                  339
BLAST score
                   8.0e-32
E value
                  120
Match length
                   63
% identity
NCBI Description zein E19 [Zea mays]
                   295964
Seq. No.
                   LIB3079-032-Q1-K1-H5
Seq. ID
                   BLASTX
Method
                   g3294467
NCBI GI
BLAST score
                   183
                   8.0e-24
E value
                   80
Match length
                   78
% identity
NCBI Description (U89341) phosphoglucomutase 1 [Zea mays]
                   295965
Seq. No.
                   LIB3079-033-Q1-K1-B7
Seq. ID
                   BLASTX
Method
                   g2668742
NCBI GI
                   356
BLAST score
                   7.0e-34
E value
                   78
Match length
% identity
                   (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
Seq. No.
                   295966
                   LIB3079-033-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                   g3894214
NCBI GI
                   248
BLAST score
                   4.0e-21
E value
                   51
Match length
 % identity
                   (D83726) elongation factor 1 beta 2 [Oryza sativa]
NCBI Description
                   >gi 3894216_dbj_BAA34599_ (D83727) elongation factor 1 beta
                   2 [Oryza sativa]
                   295967
 Seq. No.
                   LIB3079-033-Q1-K1-F1
 Seq. ID
                   BLASTN
 Method
                   g22542
 NCBI GI
                    91
 BLAST score
                   7.0e-44
 E value
                   111
 Match length
                    95
 % identity
                   Maize gene for Mr 19000 alpha zein and 5'-flanking region
 NCBI Description
```

41431

295968

Seq. No.



LIB3079-033-Q1-K1-F4

Method BLASTN
NCBI GI g2832242
BLAST score 165
E value 7.0e-88
Match length 229
% identity 14

Seq. ID

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 295969

Seq. ID LIB3079-033-Q1-K1-F5

Method BLASTN
NCBI GI g643596
BLAST score 79
E value 9.0e-37
Match length 191
% identity 85

NCBI Description Corn mRNA for cysteine proteinase, clone CCP, complete cds

Seq. No. 295970

Seq. ID LIB3079-033-Q1-K1-F6

Method BLASTX
NCBI GI 94185513
BLAST score 144
E value 1.0e-09
Match length 72
% identity 42

NCBI Description (AF102823) actin depolymerizing factor 5 [Arabidopsis

thaliana] >gi 4185517 (AF102825) actin depolymerizing

factor 5 [Arabidopsis thaliana]

Seq. No. 295971

Seq. ID LIB3079-033-Q1-K1-G8

Method BLASTX
NCBI GI 94097579
BLAST score 208
E value 1.0e-16
Match length 90

% identity 51

NCBI Description (U64922) NTGP1 [Nicotiana tabacum]

Seq. No. 295972

Seq. ID LIB3079-033-Q1-K1-H2

Method BLASTX
NCBI GI g4467096
BLAST score 218
E value 9.0e-18
Match length 104
% identity 42

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 295973

Seq. ID LIB3079-034-Q1-K1-A4

Method BLASTX NCBI GI g3779021 BLAST score 184 E value 1.0e-13



```
Match length
% identity
                  (AC005171) putative reverse transcriptase [Arabidopsis
NCBI Description
                  thaliana]
                  295974
Seq. No.
Seq. ID
                  LIB3079-034-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  g3738297
BLAST score
                  277
                  2.0e-24
E value
                  138
Match length
% identity
                  24
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
                  295975
Seq. No.
Seq. ID
                  LIB3079-034-Q1-K1-C2
                  BLASTX
Method
NCBI GI
                  g1076813
BLAST score
                  494
E value
                  4.0e-50
Match length
                  122
% identity
                  83
NCBI Description initiator-binding protein - maize
                  295976
Seq. No.
Seq. ID
                  LIB3079-034-Q1-K1-C6
                  BLASTX
Method
NCBI GI
                  q4105719
BLAST score
                  348
E value
                  6.0e - 33
Match length
                  122
% identity
                  62
                  (AF050128) cell wall invertase Incw2; beta-fructosidase
NCBI Description
                   [Zea mays]
                  295977
Seq. No.
                  LIB3079-035-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1619602
                  158
BLAST score
                  1.0e-10
E value
Match length
                  72
                  42
% identity
NCBI Description
                  (Y08726) MtN3 [Medicago truncatula]
Seq. No.
                  295978
Seq. ID
                  LIB3079-035-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  g3510252
BLAST score
                  282
                  4.0e-25
E value
```

Match length 77 % identity 68

NCBI Description (AC005310) putative RNA-binding protein [Arabidopsis

thaliana]



LIB3079-035-Q1-K1-D5 Seq. ID Method BLASTX NCBI GI g1053059 BLAST score 228 E value 6.0e-19 98 Match length % identity 51

295980

NCBI Description (U38423) histone H3 [Triticum aestivum]

Seq. ID LIB3079-035-Q1-K1-F4 Method BLASTN NCBI GI g3819386 36 BLAST score 8.0e-11 E value

Match length 56 91 % identity

Seq. No.

Seq. No.

Hordeum vulgare genomic DNA fragment; clone MWG0872.rev NCBI Description

295981 Seq. No. Seq. ID LIB3079-035-Q1-K1-F9

Method BLASTX NCBI GI g4507223 BLAST score 450 9.0e-45 E value Match length 150 % identity 61

signal recognition particle receptor ('docking protein') NCBI Description >qi 134892 sp P08240 SRPR HUMAN SIGNAL RECOGNITION PARTICLE

RECEPTOR ALPHA SUBUNIT (SR-ALPHA) (DOCKING PROTEIN ALPHA)

(DP-ALPHA) >gi 88607 pir A29440 signal recognition

particle receptor - human >gi 30866 emb CAA29608 (X06272)

docking protein [Homo sapiens]

295982 Seq. No.

LIB3079-035-Q1-K1-H4 Seq. ID

Method BLASTX NCBI GI g1332579 BLAST score 192 5.0e-15 E value Match length 61 % identity

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 295983

Seq. ID LIB3079-035-Q1-K1-H6

Method BLASTX NCBI GI g3789942 BLAST score 311 5.0e-29 E value 64 Match length 20 % identity

(AF093505) polyubiquitin [Saccharum hybrid cultivar NCBI Description

H32-8560]

295984 Seq. No.

LIB3079-036-Q1-K1-A2 BLASTX q4115379 265 4.0e-23 88

% identity NCBI Description (AC005967) putative carbonyl reductase [Arabidopsis thaliana]

295985 Seq. No.

Seq. ID

Method

NCBI GI

E value Match length

BLAST score

Seq. ID LIB3079-036-Q1-K1-B12

BLASTX Method g730456 NCBI GI 285 BLAST score 2.0e-25 E value 113 Match length 55 % identity

NCBI Description 40S RIBOSOMAL PROTEIN S19

295986 Seq. No.

Seq. ID LIB3079-036-Q1-K1-C2

BLASTN Method NCBI GI g22149 BLAST score 70 4.0e-31 E value Match length 226 % identity 83

NCBI Description Z.mays mRNA for alpha-tubulin

295987 Seq. No.

LIB3079-036-Q1-K1-D4 Seq. ID

BLASTX Method g122022 NCBI GI 317 BLAST score 2.0e-29 E value 80 Match length % identity

NCBI Description HISTONE H2B >gi_283025_pir__S22323 histone H2B - wheat >gi_21801_emb_CAA42530_ (X $\overline{59}$ 873) histone H2B [Triticum

aestivum]

295988 Seq. No.

LIB3079-036-Q1-K1-E11 Seq. ID

BLASTX Method q3913426 NCBI GI BLAST score 178 6.0e-13 E value Match length 133 40 % identity

NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)

(SAMDC) >gi_1532048_emb_CAA69074_ (Y07766)

S-adenosylmethionine decarboxylase [Oryza sativa]

295989 Seq. No.

LIB3079-036-Q1-K1-F1 Seq. ID

BLASTN Method



NCBI GI g22540
BLAST score 100
E value 4.0e-49
Match length 220
% identity 87

NCBI Description Maize mRNA for 10kDa zein

Seq. No. 295990

Seq. ID LIB3079-036-Q1-K1-F10

Method BLASTX
NCBI GI g1644291
BLAST score 374
E value 7.0e-36
Match length 144
% identity 53

NCBI Description (Z73295) receptor-like protein kinase [Catharanthus roseus]

Seq. No. 295991

Seq. ID LIB3079-036-Q1-K1-F2

Method BLASTX
NCBI GI 94406816
BLAST score 204
E value 4.0e-17
Match length 66
% identity 77

NCBI Description (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No. 295992

Seq. ID LIB3079-036-Q1-K1-F7

Method BLASTX
NCBI GI g82654
BLAST score 207
E value 2.0e-16
Match length 63
% identity 68

NCBI Description 10K zein precursor - maize >gi_22541_emb_CAA30409_ (X07535)

10kDa zein (AA 1 - 150) [Zea mays]

Seq. No. 295993

Seq. ID LIB3079-036-Q1-K1-F9

Method BLASTN
NCBI GI g22455
BLAST score 58
E value 7.0e-24
Match length 82
% identity 95

NCBI Description Z.mays pollen specific mRNA C-terminal (clone 3A6)

Seq. No. 295994

Seq. ID LIB3079-036-Q1-K1-G7

Method BLASTX
NCBI GI g2088652
BLAST score 252
E value 1.0e-21
Match length 102

% identity 48 NCBI Description (AF002109) 26S proteasome regulatory subunit S12 isolog





[Arabidopsis thaliana] >gi_2351376 (U54561) translation initiation factor eIF2 p47 subunit homolog [Arabidopsis thaliana]

 Seq. No.
 295995

 Seq. ID
 LIB3079-037-Q1-K1-B1

 Method
 BLASTX

 NCBI GI
 g112994

BLAST score 383 E value 4.0e-37 Match length 80 % identity 96

NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN

>gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)

ABA-inducible gene protein [Zea mays]

>gi_226091_prf__1410284A abscisic acid inducible gene [Zea

mays]

Seq. No. 295996

Seq. ID LIB3079-037-Q1-K1-B8

Method BLASTX
NCBI GI g4115386
BLAST score 211
E value 5.0e-17
Match length 53
% identity 81

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 295997

Seq. ID LIB3079-037-Q1-K1-B9 Method BLASTX

Method BLASTX
NCBI GI g1169228
BLAST score 203
E value 7.0e-16
Match length 55
% identity 67

NCBI Description RNA HELICASE-LIKE PROTEIN DB10 >gi_1084413_pir__S42639

helicase-like protein - Wood tobacco

>gi_563986_dbj_BAA03763_ (D16247) RNA helicase like protein

DB10 [Nicotiana sylvestris]

Seq. No. 295998

Seq. ID LIB3079-037-Q1-K1-C2

Method BLASTX
NCBI GI g2244784
BLAST score 178
E value 4.0e-13
Match length 112
% identity 45

NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 295999

Seq. ID LIB3079-037-Q1-K1-G4

Method BLASTX
NCBI GI g4490747
BLAST score 276



```
1.0e-24
E value
Match length
                  87
% identity
                  (AL035708) DnaJ-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  296000
                  LIB3079-037-Q1-K1-H12
Seq. ID
                  BLASTX
Method
                  g1658313
NCBI GI
                  248
BLAST score
                  1.0e-21
E value
Match length
                  84
                  27
% identity
NCBI Description (Y08987) osr40g2 [Oryza sativa]
                  296001
Seq. No.
Seq. ID
                  LIB3079-038-Q1-K1-A12
                  BLASTX
Method
NCBI GI
                  g4204313
BLAST score
                  146
                   3.0e-09
E value
                  58
Match length
% identity
                  (AC003027) 1cl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   296002
Seq. No.
                  LIB3079-038-Q1-K1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2252851
                   187
BLAST score
                   5.0e-14
E value
Match length
                   62
% identity
NCBI Description (AF013294) No definition line found [Arabidopsis thaliana]
                   296003
Seq. No.
Seq. ID
                   LIB3079-038-Q1-K1-C4
Method
                   BLASTX
NCBI GI
                   q4220523
BLAST score
                   160
E value
                   6.0e-11
Match length
                   77
% identity
                  (AL035356) putative alliin lyase [Arabidopsis thaliana]
NCBI Description
                   296004
Seq. No.
Seq. ID
                   LIB3079-038-Q1-K1-D5
Method
                   BLASTX
NCBI GI
                   g135417
BLAST score
                   154
                   1.0e-10
E value
Match length
                   34
% identity
                   91
                   TUBULIN ALPHA-3 CHAIN >gi_100946_pir__JN0105 tubulin
NCBI Description
```

alpha-3 chain - maize >gi_22150_emb_CAA44861_

Alpha-tubulin #3 [Zea mays] $>gi_485\overline{3}77$ (M601 $\overline{7}1$) alpha-3

(X63176)

Seq. ID Method

NCBI GI



tubulin [Zea mays]

```
296005
Seq. No.
                  LIB3079-038-Q1-K1-E5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                  46
                  5.0e-17
E value
                  82
Match length
% identity
NCBI Description Cloning vector pSport1, complete cds
                  296006
Seq. No.
                  LIB3079-038-Q1-K1-E6
Seq. ID
                  BLASTX
Method
                  g1143864
NCBI GI
BLAST score
                  316
                  3.0e-29
E value
                  73
Match length
                  81
% identity
NCBI Description (U28047) beta glucosidase [Oryza sativa]
                   296007
Seq. No.
Seq. ID
                  LIB3079-038-Q1-K1-E8
                  BLASTX
Method
                   g22216
NCBI GI
BLAST score
                  154
                   2.0e-21
E value
                   91
Match length
                   67
% identity
NCBI Description (X55722) 22kD zein [Zea mays]
Seq. No.
                   296008
                   LIB3079-038-Q1-K1-F8
Seq. ID
Method
                   BLASTX
                   q2213882
NCBI GI
BLAST score
                   221
E value
                   3.0e-18
                   84
Match length
                   55
% identity
                  (AF004165) 2-isopropylmalate synthase [Lycopersicon
NCBI Description
                   pennellii]
Seq. No.
                   296009
                   LIB3079-038-Q1-K1-F9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4191785
BLAST score
                   328
E value
                   2.0e-30
Match length
                   146
% identity
                   49
                  (AC005917) putative hydrolase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   296010
```

41439

LIB3079-038-Q1-K1-G1

BLASTX

g2894534

```
BLAST score
                  7.0e-22
E value
Match length
                  65
% identity
                  75
NCBI Description (AJ224327) aquaporin [Oryza sativa]
Seq. No.
                  296011
                  LIB3079-038-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4079800
BLAST score
                  193
                  8.0e-15
E value
Match length
                  94
                  47
% identity
NCBI Description
                  (AF052503) S-phase-specific ribosomal protein [Oryza
Seq. No.
                  296012
                  LIB3079-039-Q1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1929056
BLAST score
                  169
E value
                  2.0e-12
                  65
Match length
                  57
% identity
NCBI Description (Y12090) putative 3,4-dihydroxy-2-butanone kinase
                  [Lycopersicon esculentum]
                  296013
                  LIB3079-039-Q1-K1-D11
                  BLASTX
                  g224508
                  498
                  2.0e-50
                  147
% identity
                  72
NCBI Description zein A20 [Zea mays]
```

Seq. No. Seq. ID Method NCBI GI BLAST score E value Match length

296014 Seq. No. LIB3079-039-Q1-K1-D12 Seq. ID Method BLASTN

NCBI GI g22528 BLAST score 41 7.0e-14 E value Match length 185 81 % identity

NCBI Description Zea mays mRNA encoding a zein (clone A20)

296015 Seq. No.

LIB3079-039-Q1-K1-D9 Seq. ID

BLASTN Method g3372517 NCBI GI BLAST score 34 4.0e-10 E value 70 Match length 87 % identity

NCBI Description Zea mays invertase mRNA, complete cds

Method

NCBI GI

BLASTN

g531828



```
296016
Seq. No.
Seq. ID
                  LIB3079-039-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  g2829918
BLAST score
                  191
E value
                  1.0e-14
Match length
                  88
% identity
                  53
NCBI Description
                   (AC002291) similar to "tub" protein gp_U82468_2072162
                   [Arabidopsis thaliana]
                  296017
Seq. No.
Seq. ID
                  LIB3079-039-Q1-K1-F9
Method
                  BLASTN
NCBI GI
                  q18058
BLAST score
                  68
E value
                  5.0e-30
Match length
                  144
% identity
                  87
NCBI Description Citrus limon cistron for 26S ribosomal RNA
Seq. No.
                  296018
Seq. ID
                  LIB3079-039-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g1332579
BLAST score
                  205
E value
                  1.0e-16
Match length
                  58
                  7
% identity
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
Seq. No.
                  296019
                  LIB3079-039-Q1-K1-H5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g625147
BLAST score
                  52
E value
                  1.0e-20
Match length
                  100
% identity
                  89
NCBI Description Zea mays protein disulfide isomerase (pdi) mRNA, complete
                  296020
Seq. No.
                  LIB3079-040-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3747111
BLAST score
                  147
E value
                  1.0e-09
Match length
                  54
% identity
                  52
NCBI Description (AF095641) MTN3 homolog [Arabidopsis thaliana]
                  296021
Seq. No.
Seq. ID
                  LIB3079-040-Q1-K1-E11
```



```
BLAST score
                  1.0e-14
E value
                  82
Match length
% identity
NCBI Description Cloning vector pSport1, complete cds
                  296022
Seq. No.
                  LIB3079-040-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4544454
BLAST score
                  270
E value
                  6.0e-24
                  99
Match length
% identity
                 (AC006592) putative DNAJ protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  296023
Seq. ID
                  LIB3079-040-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  g3913427
                  276
BLAST score
E value
                  1.0e-24
Match length
                  103
                  60
% identity
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                  (SAMDC) >gi_1532073_emb_CAA69075_ (Y07767)
                  S-adenosylmethionine decarboxylase [Zea mays]
                  296024
Seq. No.
Seq. ID
                  LIB3079-041-Q1-K1-C10
Method
                  BLASTN
NCBI GI
                  g22516
BLAST score
                  124
                  2.0e-63
E value
Match length
                  124
                  100
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.
                  296025
Seq. ID
                  LIB3079-041-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g122106
BLAST score
                  370
E value
                  2.0e-35
Match length
                  98
% identity
                  80
                  HISTONE H4 >gi 70771 pir HSZM4 histone H4 - maize
NCBI Description
                  >gi 81642 pir S06904 histone H4 - Arabidopsis thaliana
                  >gi 2119028 pir S60475 histone H4 - garden pea
                  >gi 21795 emb CAA24924 (X00043) histone H4 [Triticum
                  aestivum] >gi 166740 (M17132) histone H4 [Arabidopsis
                  thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis
                  thaliana] >gi 168499 (M36659) histone H4 (H4C13) [Zea mays]
                  >gi 168501 (M13370) histone H4 [Zea mays] >gi_168503
                  (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone
                  H4 homolog [Pisum sativum] >gi 1806285 emb CAB01914
                  (Z79638) histone H4 homologue [Sesbania rostrata]
```





>gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana]
>gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4
[Arabidopsis thaliana] >gi_225838_prf__1314298A histone H4
[Arabidopsis thaliana]

Seq. No. 296026

Seq. ID LIB3079-041-Q1-K1-D1

Method BLASTX
NCBI GI g1174853
BLAST score 342
E value 2.0e-32
Match length 94

% identity 66
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-18 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42)

>gi_481811_pir__S39483 ubiquitin-conjugating enzyme UBC2-1
- Arabidopsis thaliana >gi_22658_emb_CAA48378_ (X68306)
ubiquitin-conjugating enzyme [Arabidopsis thaliana]

Seq. No. 296027

Seq. ID LIB3079-041-Q1-K1-E5

Method BLASTX
NCBI GI g2190540
BLAST score 329
E value 1.0e-30
Match length 73
% identity 79

NCBI Description (AC001229) Similar to Arabidopsis TFL1 (gb U77674).

[Arabidopsis thaliana]

Seq. No. 296028

Seq. ID LIB3079-041-Q1-K1-E8

Method BLASTN
NCBI GI g3868757
BLAST score 42
E value 2.0e-14
Match length 62
% identity 92

NCBI Description Oryza sativa mRNA for elongation factor 1B gamma, complete

cds

Seq. No. 296029

Seq. ID LIB3079-041-Q1-K1-G9

Method BLASTX
NCBI GI g3695389
BLAST score 148
E value 5.0e-10
Match length 54
% identity 50

NCBI Description (AF096371) contains similarity to D-isomer specific

2-hydroxyacid dehydrogenases (Pfam: 2-Hacid DH.hmm, score:

19.11) [Arabidopsis thaliana]

Seq. No. 296030

Seq. ID LIB3079-041-Q1-K1-H6

Method BLASTX NCBI GI g4567260

Method

NCBI GI

BLASTN

g3821780





```
BLAST score
                   401
E value
                   3.0e-39
Match length
                   93
                   78
% identity
NCBI Description
                   (AC006841) putative NADPH dependent mannose 6-phosphate
                   reductase [Arabidopsis thaliana]
                   >gi_4582440_gb_AAD24825.1_AC007142_3 (AC007142) putative
                   NADPH-dependent mannose-6-phosphate reductase [Arabidopsis
                   thaliana]
Seq. No.
                   296031
Seq. ID
                  LIB3079-042-Q1-K1-A10
Method
                  BLASTN
NCBI GI
                   g22312
BLAST score
                  122
                   4.0e-62
E value
Match length
                  325
% identity
                  86
                  Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                  abscisic acid)
Seq. No.
                  296032
Seq. ID
                  LIB3079-042-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  g1619602
BLAST score
                  274
E value
                  3.0e-24
Match length
                  74
% identity
                  68
NCBI Description (Y08726) MtN3 [Medicago truncatula]
Seq. No.
                  296033
Seq. ID
                  LIB3079-042-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g3914557
BLAST score
                  309
E value
                  4.0e-28
Match length
                  168
                  46
% identity
NCBI Description RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED
                  PROTEIN) >gi_1155265 (U40219) possible apospory-associated
                  protein [Pennisetum ciliare]
Seq. No.
                  296034
Seq. ID
                  LIB3079-042-Q1-K1-E6
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                  35
E value
                  2.0e-10
Match length
                  83
% identity
                  86
NCBI Description Cloning vector pSport1, complete cds
                  296035
Seq. No.
Seq. ID
                  LIB3079-042-Q1-K1-F3
```





```
BLAST score
E value
                  6.0e-11
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  296036
Seq. No.
Seq. ID
                  LIB3079-042-Q1-K2-C9
Method
                  BLASTX
NCBI GI
                  g2668750
BLAST score
                  202
E value
                  2.0e-19
Match length
                  75
% identity
                  75
NCBI Description (AF034949) ribosomal protein L30 [Zea mays]
                  296037
Seq. No.
Seq. ID
                  LIB3079-042-Q1-K2-G11
Method
                  BLASTN
NCBI GI
                  g854644
BLAST score
                  39
                  1.0e-12
E value
Match length
                  47
% identity
                  96
NCBI Description Z.mays ZMM1 gene
                  296038
Seq. No.
                  LIB3079-043-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455364
BLAST score
                  260
E value
                  1.0e-22
Match length
                  92
% identity
                  57
NCBI Description
                  (AL035524) senescence-associated protein-like [Arabidopsis
                  thaliana]
Seq. No.
                  296039
Seq. ID
                  LIB3079-043-Q1-K1-C5
Method
                  BLASTN
NCBI GI
                  g1421729
BLAST score
                  116
E value
                  1.0e-58
Match length
                  120
% identity
                  99
NCBI Description
                  Zea mays T cytoplasm male sterility restorer factor 2 (rf2)
                  mRNA, complete cds
Seq. No.
                  296040
Seq. ID
                  LIB3079-043-Q1-K2-H8
Method
                  BLASTX
NCBI GI
                  q3861153
BLAST score
                  141
E value
                  1.0e-08
Match length
                  40
% identity
                  68
```

NCBI Description (AJ235272) CYANELLE 50S RIBOSOMAL PROTEIN L20 (rplT)





[Rickettsia prowazekii]

 Seq. No.
 296041

 Seq. ID
 LIB3079-045-Q1-K1-B7

 Method
 BLASTX

NCBI GI g3540186
BLAST score 160
E value 8.0e-11
Match length 56
% identity 61

NCBI Description (AC004122) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 296042

Seq. ID LIB3079-045-Q1-K1-D4

Method BLASTX
NCBI GI g118104
BLAST score 200
E value 8.0e-27
Match length 97
% identity 65

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)

>gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -

maize >gi_168461 (M55021) cyclophilin [Zea mays]

>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 296043

Seq. ID LIB3079-045-Q1-K1-E5

Method BLASTN
NCBI GI g1657766
BLAST score 89
E value 2.0e-42
Match length 165
% identity 88

NCBI Description Zea mays retrotransposon Opie-2 5' LTR, primer binding

site, gag gene, pol gene, complete cds, polypurine tract

and 3' LTR

Seq. No. 296044

Seq. ID LIB3079-045-Q1-K1-F11

Method BLASTX
NCBI GI g4314362
BLAST score 314
E value 8.0e-29
Match length 113
% identity 55

NCBI Description (AC006340) putative D-amino acid dehydrogenase [Arabidopsis

thaliana]

Seq. No. 296045

Seq. ID LIB3079-045-Q1-K1-F12

Method BLASTN
NCBI GI g2668739
BLAST score 77
E value 2.0e-35
Match length 113
% identity 92





NCBI Description Zea mays translation initiation factor GOS2 (TIF) mRNA, complete cds

Seq. No. 296046

Seq. ID LIB3079-045-Q1-K1-G11
Method BLASTX
NCBI GI g4033467
BLAST score 346
E value 1.0e-32
Match length 99
% identity 66

NCBI Description ARGININE/SERINE-RICH SPLICING FACTOR RSP31

>gi 1707366 emb CAA67798 (X99435) splicing factor

[Arabidopsis thaliana]

Seq. No. 296047

Seq. ID LIB3079-046-Q1-K1-A2

Method BLASTX
NCBI GI g730526
BLAST score 154
E value 3.0e-10
Match length 63
% identity 51

NCBI Description 60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)

>gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis
thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein

[Arabidopsis thaliana]

Seq. No. 296048

Seq. ID LIB3079-046-Q1-K1-A7

Method BLASTX
NCBI GI g497633
BLAST score 180
E value 1.0e-13
Match length 69
% identity 48

NCBI Description (D31731) ORF [Schizosaccharomyces pombe]

Seq. No. 296049

Seq. ID LIB3079-046-Q1-K1-C3

Method BLASTX
NCBI GI g1723388
BLAST score 162
E value 3.0e-11
Match length 46
% identity 65

NCBI Description HYPOTHETICAL 12.4 KD PROTEIN IN APCF-RPS4 INTERGENIC REGION

(ORF114) >gi_2147501_pir__S73138 hypothetical protein 114 - Porphyra purpurea chloroplast >gi_1276683 (U38804) ORF114

[Porphyra purpurea]

Seq. No. 296050

Seq. ID LIB3079-046-Q1-K1-C5

Method BLASTX
NCBI GI g4033424
BLAST score 197
E value 3.0e-21

% identity

57





```
Match length
% identity
                   56
NCBI Description
                  SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
                  PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic
                  pyrophosphatase [Zea mays]
Seq. No.
                  296051
Seq. ID
                  LIB3079-046-Q1-K1-D1
Method
                  BLASTN
NCBI GI
                  g1314400
BLAST score
                  47
E value
                  2.0e-17
Match length
                  103
% identity
                  86
NCBI Description Zea mays ssp. mays ITS1, 5.8S ribosomal RNA, ITS2
Seq. No.
                  296052
Seq. ID
                  LIB3079-046-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  g3182915
BLAST score
                  225 -
E value
                  9.0e-19
Match length
                  81
% identity
                  64
NCBI Description ADP-RIBOSYLATION FACTOR >gi 1842150 dbj BAA19225
                   (AB001051) ADP-ribosylation factor [Dugesia japonica]
Seq. No.
                  296053
Seq. ID
                  LIB3079-046-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g2191169
BLAST score
                  266
E value
                  7.0e-28
Match length
                  97
% identity
                  71
NCBI Description
                  (AF007270) Similar to shaggy related protein kinase.
                  Belongs to the CDC2/CDKX subfamily [Arabidopsis thaliana]
Seq. No.
                  296054
Seq. ID
                  LIB3079-046-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  q168586
BLAST score
                  295
E value
                  1.0e-26
Match length
                  71
% identity
                  83
NCBI Description
                  (M58656) pyruvate, orthophosphate dikinase [Zea mays]
                  296055
Seq. No.
Seq. ID
                  LIB3079-046-Q1-K1-F6
Method
                  BLASTX
                  g168586
NCBI GI
BLAST score
                  203
E value
                  5.0e-16
Match length
                  75
```

41448

NCBI Description (M58656) pyruvate, orthophosphate dikinase [Zea mays]





Seq. No. 296056 Seq. ID LIB3079-046-Q1-K1-G10 Method BLASTX NCBI GI q3176686 BLAST score 194 E value 2.0e-17 Match length 73 % identity 66 NCBI Description (AC003671) Similar to high affinity potassium transporter, HAK1 protein gb U22945 from Schwanniomyces occidentalis. [Arabidopsis thaliana] Seq. No. 296057 Seq. ID LIB3079-046-Q1-K1-G3 Method BLASTX NCBI GI g2641619 277

BLAST score E value 1.0e-24 Match length 60

% identity 87

NCBI Description (AF032468) ubiquitin-conjugating enzyme protein E2 [Zea

mays]

Seq. No. 296058

Seq. ID LIB3079-047-Q1-K1-A7

Method BLASTX NCBI GI g4587519 BLAST score 316 E value 4.0e-29 Match length 81 % identity 72

NCBI Description (AC007060) Strong similarity to F19I3.7 gi 3033380 putative

> coatomer epsilon subunit from Arabidopsis thaliana BAC gb AC004238. ESTs gb_Z17908, gb AA728673, gb_N96555, gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g

Seq. No. 296059

Seq. ID LIB3079-047-Q1-K1-B4

Method BLASTX g3617837 NCBI GI BLAST score 279 E value 9.0e-25 Match length 61 % identity 90

NCBI Description (AF035820) gibberellin action negative regulator SPY

[Hordeum vulgare]

Seq. No. 296060

Seq. ID LIB3079-047-Q1-K1-C1

Method BLASTN NCBI GI q1854375 BLAST score 51 E value 1.0e-19 Match length 97 % identity 89

NCBI Description Saccharum officinarum mRNA for Sucrose-Phosphate Synthase,



partial cds

```
Seq. No.
                  296061
Seq. ID
                  LIB3079-047-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g136640
BLAST score
                  167
E value
                  9.0e-12
Match length
                  56
% identity
                  59
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_170785 (M62720)
                  ubiquitin carrier protein [Triticum aestivum]
```

Seq. No. 296062

Seq. ID LIB3079-048-Q1-K1-C11

Method BLASTX
NCBI GI g629844
BLAST score 282
E value 9.0e-26
Match length 72
% identity 79

NCBI Description heat shock protein hsp70-5 - maize (fragment)

>gi_498775_emb_CAA55184 (X78415) heat shock protein 70 kDa

[Zea mays]

Seq. No. 296063

Seq. ID LIB3079-048-Q1-K1-D2

Method BLASTN
NCBI GI g1054795
BLAST score 51
E value 4.0e-20
Match length 82
% identity 90

NCBI Description H.vulgare mRNA for transmembrane protein

Seq. No. 296064

Seq. ID LIB3079-048-Q1-K1-E8

Method BLASTN
NCBI GI g309573
BLAST score 67
E value 8.0e-30
Match length 118
% identity 90

NCBI Description Corn ZAG1 mRNA, complete cds

Seq. No. 296065

Seq. ID LIB3079-048-Q1-K1-G7

Method BLASTN
NCBI GI g1658312
BLAST score 56
E value 3.0e-23
Match length 116
% identity 87

NCBI Description O.sativa osr40g2 gene

Seq. No. 296066



Seq. ID LIB3079-049-Q1-K1-A11

Method BLASTX
NCBI GI g1352088
BLAST score 309
E value 2.0e-28
Match length 101
% identity 59

NCBI Description CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR >gi_624676

(U19481) citrate synthase precursor [Citrus maxima]

Seq. No. 296067

Seq. ID LIB3079-049-Q1-K1-A12

Method BLASTX
NCBI GI g3913295
BLAST score 172
E value 9.0e-13
Match length 60
% identity 52

NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE

(S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID

3-O-METHYLTRANSFERASE) (COMT) >gi_602588_emb_CAA58218_ (X83217) caffeic O-methyltransferase [Prunus dulcis]

Seq. No. 296068

Seq. ID LIB3079-049-Q1-K1-C5

Method BLASTX
NCBI GI g2828280
BLAST score 272
E value 3.0e-24
Match length 57
% identity 89

NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

>gi_2832633_emb_CAA16762 (AL021711) putative protein

[Arabidopsis thaliana]

Seq. No. 296069

Seq. ID LIB3079-049-Q1-K1-E10

Method BLASTX
NCBI GI g1296955
BLAST score 158
E value 8.0e-11
Match length 28
% identity 45

NCBI Description (X95402) duplicated domain structure protein [Oryza sativa]

Seq. No. 296070

Seq. ID LIB3079-049-Q1-K1-F11

Method BLASTX
NCBI GI g3152556
BLAST score 227
E value 1.0e-18
Match length 92
% identity 50

NCBI Description (AC002986) Contains similarity to S. cerevisiae

hypothetical protein YOR197w, gb_Z75105. [Arabidopsis

thaliana]

Seq. No.

Seq. ID

296076

LIB3079-051-Q1-K1-C10





```
Seq. No.
                  296071
Seq. ID
                  LIB3079-049-Q1-K1-F5
Method
                  BLASTN
NCBI GI
                  g799029
BLAST score
                  68
                  5.0e-30
E value
Match length
                  168
                  85
% identity
NCBI Description Z.mays BET1 mRNA
                  296072
Seq. No.
Seq. ID
                  LIB3079-049-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  g421810
BLAST score
                  164
E value
                  2.0e-11
Match length
                  41
% identity
                  73
                  acetyl-CoA C-acyltransferase (EC 2.3.1.16) precursor -
NCBI Description
                  cucumber
Seq. No.
                  296073
Seq. ID
                  LIB3079-049-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g1172836
BLAST score
                  449
E value
                  4.0e-47
Match length
                  117
% identity
                  81
NCBI Description
                  GTP-BINDING NUCLEAR PROTEIN RAN-B1 >qi 496272 (L16787)
                  small ras-related protein [Nicotiana tabacum]
Seq. No.
                  296074
                  LIB3079-050-Q1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3282475
BLAST score
                  38
E value
                  1.0e-12
Match length
                  50
% identity
                  94
NCBI Description
                  Monachather paradoxus internal transcribed spacer 1, 5.8S
                  ribosomal RNA gene, and internal transcribed spacer 2,
                  complete sequence
                  296075
Seq. No.
Seq. ID
                  LIB3079-051-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  g2996096
BLAST score
                  229
                  2.0e-19
E value
Match length
                  50
% identity
                  90
NCBI Description
                  (AF030517) translation elongation factor-1 alpha; EF-1
                  alpha [Oryza sativa]
```





```
Method
                   BLASTX
NCBI GI
                   q168703
BLAST score
                   193
E value
                   6.0e-15
Match length
                   76
% identity
                   53
NCBI Description
                  (M86591) 22 kDa zein protein [Zea mays]
Seq. No.
                   296077
Seq. ID
                  LIB3079-051-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                   g2984709
BLAST score
                   481
E value
                   1.0e-48
Match length
                   109
% identity
                   83
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
NCBI Description
                   296078
Seq. No.
                  LIB3079-051-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3935167
BLAST score
                   317
E value
                  2.0e-29
Match length
                  79
% identity
                  76
NCBI Description
                  (AC004557) F17L21.10 [Arabidopsis thaliana]
Seq. No.
                  296079
                  LIB3079-051-Q1-K1-D9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2197121
BLAST score
                  86
E value
                  1.0e-40
Match length
                  140
% identity
                  90
NCBI Description Prunus armeniaca 26S ribosomal RNA gene, partial sequence
                  296080
Seq. No.
Seq. ID
                  LIB3079-051-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g2444148
BLAST score
                  141
E value
                  4.0e-09
Match length
                  32
% identity
                  88
NCBI Description
                  (U91620) alcohol dehydrogenase [Eragrostis japonica]
Seq. No.
                  296081
Seq. ID
                  LIB3079-052-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  g2668742
BLAST score
                  184
E value
                  3.0e-14
Match length
                  44
% identity
                  89
```

41453

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Method

BLASTX





```
Seq. No.
                   296082
Seq. ID
                   LIB3079-052-Q1-K1-B5
Method
                   BLASTX
NCBI GI
                   g2190540
BLAST score
                   365
E value
                   4.0e-35
Match length
                   96
% identity
                   67
NCBI Description
                  (AC001229) Similar to Arabidopsis TFL1 (gb_U77674).
                   [Arabidopsis thaliana]
Seq. No.
                   296083
Seq. ID
                   LIB3079-052-Q1-K1-C7
Method
                   BLASTX
NCBI GI
                   g1620753
BLAST score
                   227
E value
                   9.0e-19
Match length
                   60
% identity
                   65
NCBI Description
                  (U72942) proteinase inhibitor [Oryza sativa]
                   >gi_2829212_gb_AAC00503 (AF044059) proteinase inhibitor
                   [Oryza sativa]
Seq. No.
                   296084
Seq. ID
                  LIB3079-052-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                   g1050918
BLAST score
                  155
E value
                  2.0e-10
Match length
                  58
% identity
                  57
NCBI Description (X92648) lipid transfer protein [Helianthus annuus]
Seq. No.
                  296085
Seq. ID
                  LIB3079-052-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g3413700
BLAST score
                  172
E value
                  1.0e-12
Match length
                  74
% identity
                  47
NCBI Description (AC004747) putative YME1 protein [Arabidopsis thaliana]
Seq. No.
                  296086
Seq. ID
                  LIB3079-052-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g1616661
BLAST score
                  378
E value
                  2.0e-36
Match length
                  80
% identity
                  94
NCBI Description (U49388) adenylosuccinate synthetase [Zea mays]
Seq. No.
                  296087
Seq. ID
                  LIB3079-053-Q1-K1-H11
```



8

```
NCBI GI
                   q558367
BLAST score
                   308
E value
                   3.0e-28
Match length
                   113
% identity
                   61
NCBI Description
                 (X81830) cytochrome P450 [Zea mays]
Seq. No.
                  296088
Seq. ID
                  LIB3079-054-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g585202
BLAST score
                  338
E value
                   4.0e-33
Match length
                   80
% identity
                   90
NCBI Description
                  GLUTAMINE SYNTHETASE ROOT ISOZYME 2 (GLUTAMATE--AMMONIA
                  LIGASE) >gi_481807_pir__S39478 glutamate--ammonia ligase
                   (EC 6.3.1.2) 1-2, cytosolic - maize
                  >gi_434326_emb_CAA46720_ (X65927) glutamine synthetase [Zea
                  mays]
Seq. No.
                  296089
Seq. ID
                  LIB3079-054-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g3953471
BLAST score
                  201
E value
                  7.0e-16
Match length
                  103
% identity
                  46
NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]
Seq. No.
                  296090
Seq. ID
                  LIB3079-054-Q1-K1-H5
Method
                  BLASTN
NCBI GI
                  g3694806
BLAST score
                  34
E value
                  1.0e-09
Match length
                  98
% identity
                  84
NCBI Description Zea mays alanine aminotransferase (alt) gene, complete cds
Seq. No.
                  296091
Seq. ID
                  LIB3079-055-Q1-K1-A4
Method
                  BLASTN
NCBI GI
                  g3492855
BLAST score
                  70
E value
                  5.0e-31
Match length
                  158
% identity
                  86
NCBI Description
```

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No. 296092

Seq. ID LIB3079-055-Q1-K1-A7

Method BLASTX
NCBI GI g1931654
BLAST score 205





```
E value
                    2.0e-18
. Match length
                    99
  % identity
                    46
  NCBI Description
                     (U95973) BRCA1-associated RING domain protein isolog
                     [Arabidopsis thaliana]
  Seq. No.
                    296093
  Seq. ID
                    LIB3079-055-Q1-K1-E1
  Method
                    BLASTX
  NCBI GI
                    g1171991
  BLAST score
                    153
  E value
                    3.0e-10
  Match length
                    95
  % identity
                    37
  NCBI Description
                    PHENYLALANINE AMMONIA-LYASE 1 >gi 1076369 pir $52990
                    phenylalanine ammonia-lyase (EC 4.3.1.5) - Arabidopsis
                    thaliana >gi 497419 (L33677) phenylalanine ammonia lyase
                    [Arabidopsis thaliana]
  Seq. No.
                    296094
  Seq. ID
                    LIB3079-055-01-K1-E6
  Method
                    BLASTX
  NCBI GI
                    g2668744
  BLAST score
                    449
  E value
                    6.0e-45
  Match length
                    85
  % identity
  NCBI Description
                    (AF034946) ubiquitin conjugating enzyme [Zea mays]
  Seq. No.
                    296095
  Seq. ID
                    LIB3079-055-Q1-K1-H4
  Method
                    BLASTX
  NCBI GI
                    g1002379
  BLAST score
                    197
  E value
                    3.0e-15
  Match length
                    78
  % identity
                    45
  NCBI Description
                    (U24189) similar to product encoded by Drosophila
                    melanogaster Acrp gene, GenBank Accession Number L25314;
                    Method: conceptual conceptual translation supplied by
                    authors [Caenorhabditis elegans]
  Seq. No.
                    296096
  Seq. ID
                    LIB3079-056-Q1-K1-C1
  Method
                    BLASTX
  NCBI GI
                    g4263722
  BLAST score
                    254
                    4.0e-22
  E value
                    95
  Match length
                    65
  % identity
  NCBI Description
                    (AC006223) putative glucan synthase [Arabidopsis thaliana]
                    296097
  Seq. No.
  Seq. ID
                    LIB3079-056-Q1-K1-C2
```

NCBI GI g4263722

BLASTX

BLAST score 281

Method

Seq. No.

296103



8

```
E value
                   2.0e-25
Match length
                  74
% identity
                  77
NCBI Description
                  (AC006223) putative glucan synthase [Arabidopsis thaliana]
Seq. No.
                  296098
Seq. ID
                  LIB3079-056-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  g4204372
BLAST score
                  204
E value
                  3.0e-16
Match length
                  66
% identity
                  67
                  (U62748) acidic ribosomal protein P2a-2 [Zea mays]
NCBI Description
Seq. No.
                  296099
                  LIB3079-056-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2459412
BLAST score
                  410
E value
                  3.0e-40
Match length
                  126
% identity
                  57
                  (AC002332) putative G9a protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  296100
Seq. ID
                  LIB3079-058-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  q4585993
BLAST score
                  176
E value
                  6.0e-13
Match length
                  88
% identity
                  36
NCBI Description
                  (AC005287) Similar to serine/threonine kinases [Arabidopsis
                  thaliana]
Seq. No.
                  296101
Seq. ID
                  LIB3079-058-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g2078350
BLAST score
                  192
E value
                  2.0e-16
Match length
                  111
% identity
                  46
NCBI Description
                  (U95923) transaldolase [Solanum tuberosum]
Seq. No.
                  296102
                  LIB3079-058-Q1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3135543
BLAST score
                  279
E value
                  3.0e-25
Match length
                  77
                  73
% identity
NCBI Description (AF062393) aquaporin [Oryza sativa]
```



Seq. ID LIB3079-058-Q1-K1-H1

Method BLASTX
NCBI GI g1632822
BLAST score 275
E value 1.0e-24
Match length 55
% identity 93

NCBI Description (Y08962) transmembrane protein [Oryza sativa] >gi_1667594

(U77297) transmembrane protein [Oryza sativa]

Seq. No. 296104

Seq. ID LIB3079-058-Q1-K1-H7

Method BLASTX
NCBI GI g2119187
BLAST score 338
E value 9.0e-32
Match length 100
% identity 70

NCBI Description transmembrane protein, glucose starvation-induced - maize

>qi 575731 emb CAA57955 (X82633) transmembrane protein

[Zea mays]

Seq. No. 296105

Seq. ID LIB3079-059-Q1-K1-A1

Method BLASTX
NCBI GI g113621
BLAST score 162
E value 5.0e-15
Match length 69
% identity 62

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624 prf__1307278A

cytoplasmic aldolase [Zea mays]

Seq. No. 296106

Seq. ID LIB3079-059-Q1-K1-B2

Method BLASTX
NCBI GI g3928150
BLAST score 214
E value 3.0e-17
Match length 75
% identity 61

NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]

Seq. No. 296107

Seq. ID LIB3079-059-Q1-K1-C1

Method BLASTX
NCBI GI g4572671
BLAST score 219
E value 4.0e-18
Match length 58
% identity 69

NCBI Description (AC006954) putative cyclic nucleotide regulated ion channel

[Arabidopsis thaliana]

NCBI GI

BLAST score

g3122060

238





```
296108
Seq. No.
                  LIB3079-059-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076579
BLAST score
                  261
                  4.0e-23
E value
Match length
                  65
                  71
% identity
NCBI Description alcohol dehydrogenase homolog ADH3a - tomato
                  296109
Seq. No.
                  LIB3079-059-Q1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4587513
BLAST score
                  179
                  1.0e-13
E value
Match length
                  46
                  72
% identity
                  (AC007060) Contains eukaryotic protein kinase domain
NCBI Description
                  PF 00069. [Arabidopsis thaliana]
Seq. No.
                  296110
                  LIB3088-001-Q1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2213590
BLAST score
                  154
E value
                  3.0e-10
Match length
                  60
% identity
                  47
NCBI Description (AC000348) T7N9.10 [Arabidopsis thaliana]
                  296111
Seq. No.
                  LIB3088-001-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462759
BLAST score
                  235
E value
                  1.0e-19
Match length
                  55
% identity
                  71
NCBI Description (AC002292) Putative Cytochrome B5 [Arabidopsis thaliana]
                  296112
Seq. No.
                  LIB3088-001-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2668742
BLAST score
                  242
                  2.0e-20
E value
Match length
                  52
                  94
% identity
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]
                  296113
Seq. No.
                  LIB3088-001-Q1-K1-E1
Seq. ID
Method
                  BLASTX
```





```
E value
                  2.0e-20
Match length
                  90
% identity
                  61
NCBI Description
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                  >gi 2598657 emb CAA10847 (AJ222579) elongation factor
                  1-alpha (EF1-a) [Vicia faba]
Seq. No.
                  296114
                  LIB3088-001-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g113256
BLAST score
                  178
                  4.0e-13
E value
                  90
Match length
% identity
                  46
NCBI Description
                  ACTIN 3-SUB2 >qi 84085 pir D23412 actin 3-sub2 - slime
                  mold (Dictyostelium discoideum) >qi 7197 emb CAA27034
                  (X03284) actin A3-S2 (aa 1-380) [Dictyostelium discoideum]
Seq. No.
                  296115
Seq. ID
                  LIB3088-001-Q1-K1-H3
Method
                  BLASTN
NCBI GI
                  g4140643
BLAST score
                  35
E value
                  3.0e-10
Match length
                  39
% identity
                  97
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
                  complete sequence
                  296116
Seq. No.
Seq. ID
                  LIB3088-002-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g112994
BLAST score
                  432
E value
                  6.0e-43
Match length
                  88
% identity
                  97
NCBI Description
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
                  >gi 82685 pir S04536 embryonic abundant protein,
                  glycine-rich - maize >gi 22313 emb CAA31077 (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi 226091 prf 1410284A abscisic acid inducible gene [Zea
                  mays]
                  296117
Seq. No.
Seq. ID
                  LIB3088-002-Q1-K1-B10
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  37
E value
                  3.0e-11
Match length
                  49
% identity
                  67
NCBI Description Xenopus laevis cDNA clone 27A6-1
```

Seq. ID LIB3088-002-Q1-K1-C8

296118

Seq. No.

E value

3.0e-30





```
BLASTX
Method
                  g1899025
NCBI GI
BLAST score
                  405
                  2.0e-39
E value
                  129
Match length
                  64
% identity
                  (U28215) hexokinase 2 [Arabidopsis thaliana] >gi_3687232
NCBI Description
                  (AC005169) hexokinase [Arabidopsis thaliana]
Seq. No.
                  296119
                  LIB3088-002-Q1-K1-D12
Seq. ID
                  BLASTN
Method
                  g22468
NCBI GI
BLAST score
                  102
E value
                  1.0e-50
Match length
                  102
                  100
% identity
                  Z.mays mRNA for root-origin phosphoenolpyruvate carboxylase
NCBI Description
                  (PEPC)
Seq. No.
                  296120
                  LIB3088-002-Q1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244929
BLAST score
                  176
E value
                  1.0e-12
Match length
                  92
% identity
                  42
NCBI Description
                  (Z97339) unnamed protein product [Arabidopsis thaliana]
                  296121
Seq. No.
Seq. ID
                  LIB3088-002-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g729671
BLAST score
                  190
                  1.0e-14
E value
Match length
                  65
                  63
% identity
                  HISTONE H2A >gi 473603 (U08225) histone H2A [Zea mays]
NCBI Description
Seq. No.
                  296122
                  LIB3088-002-Q1-K1-H10
Seq. ID
Method
                  BLASTN
                  g1917018
NCBI GI
BLAST score
                  73
                  6.0e-33
E value
Match length
                  81
                  98
% identity
                  Zea mays ribosomal protein S6 RPS6-1 (rps6-1) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  296123
                  LIB3088-003-Q1-K1-A3
Seq. ID
Method
                  BLASTX
                  g122022
NCBI GI
BLAST score
                  323
```

E value

t

Match length

NCBI Description

% identity





```
Match length
                  96
% identity
                  HISTONE H2B >gi 283025_pir__S22323 histone H2B - wheat
NCBI Description
                  >gi 21801 emb CAA42530 (X59873) histone H2B [Triticum
                  aestivum]
Seq. No.
                  296124
                  LIB3088-003-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2980795
BLAST score
                  386
E value
                  2.0e-37
Match length
                  79
% identity
                  91
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]
Seq. No.
                  296125
                  LIB3088-003-Q1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2995380
BLAST score
                  242
E value
                  1.0e-20
Match length
                  76
% identity
                  61
NCBI Description (AJ001903) thioredoxin H [Triticum durum]
Seq. No.
                  296126
Seq. ID
                  LIB3088-003-Q1-K1-E1
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
E value
                  8.0e-11
Match length
                  48
% identity
                  67
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  296127
                  LIB3088-003-Q1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4099508
BLAST score
                  413
                  1.0e-40
E value
Match length
                  88
% identity
                  94
NCBI Description (U87949) proliferating cell nuclear antigen [Zea mays]
Seq. No.
                  296128
                  LIB3088-003-Q1-K1-H12
Seq. ID
Method
                  BLASTX
                  g2245095
NCBI GI
BLAST score
                  194
```

2.0e-15

thaliana]

48 75

(Z97343) formyltransferase purU homolog [Arabidopsis

Seq. No.

Seq. ID

296134

LIB3088-004-Q1-K1-E7



8

```
Seq. No.
                    296129
                    LIB3088-003-Q1-K1-H5
  Seq. ID
  Method
                    BLASTN
  NCBI GI
                    g22292
  BLAST score
                    87
                    2.0e-41
 E value

    Match length

                    174
  % identity
                    87
 NCBI Description Z.mays mRNA for glycine-rich protein
  Seq. No.
                    296130
                    LIB3088-004-Q1-K1-A4
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q4335773
  BLAST score
                    162
  E value
                    4.0e-11
  Match length
                    48
  % identity
                    85
                    (AC006284) unknown protein [Arabidopsis thaliana]
  NCBI Description
                    296131
  Seq. No.
  Seq. ID
                    LIB3088-004-01-K1-D10
  Method
                    BLASTX
  NCBI GI
                    g4539427
  BLAST score
                    226
                    2.0e-18
  E value
  Match length
                    72
                    57
  % identity
                    (AL049171) putative protein [Arabidopsis thaliana]
  NCBI Description
  Seq. No.
                    296132
  Seq. ID
                    LIB3088-004-Q1-K1-D7
  Method
                    BLASTX
  NCBI GI
                    q531829
  BLAST score
                    141
  E value
                    8.0e-09
  Match length
                    47
  % identity
                    55
                    (U12390) beta-galactosidase alpha peptide [cloning vector
  NCBI Description
                    pSport1]
                    296133
  Seq. No.
  Seq. ID
                    LIB3088-004-Q1-K1-E5
  Method
                    BLASTX
  NCBI GI
                    g113460
  BLAST score
                    457
                    8.0e-46
  E value
  Match length
                    97
  % identity
                    94
                    ADP, ATP CARRIER PROTEIN 2 PRECURSOR (ADP/ATP TRANSLOCASE 2)
  NCBI Description
                     (ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2)
                    >gi 100851 pir__S16568 ADP,ATP carrier protein precursor -
                    maize >gi 22164 emb CAA41812 (X59086) adenine nucleotide
                    translocator [Zea mays]
```

Seq. ID Method





```
Method
                  BLASTN
NCBI GI
                  q2624416
BLAST score
                  241
E value
                  1.0e-133
Match length
                  245
% identity
                  100
NCBI Description Zea mays mRNA for ubiquitin carrier protein UBC7
                  296135
Seq. No.
Seq. ID
                  LIB3088-004-Q1-K1-E8
Method
                  BLASTN
NCBI GI
                  g4096785
BLAST score
                  74
E value
                  2.0e-33
Match length
                  126
% identity
                  90
NCBI Description Zea mays NADP-malic enzyme root isoform mRNA, complete cds
                  296136
Seq. No.
Seq. ID
                  LIB3088-004-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  g3309170
BLAST score
                  295
E value
                  1.0e-26
Match length
                  135
                  47
% identity
NCBI Description (AF071314) COP9 complex subunit 4 [Mus musculus]
Seq. No.
                  296137
Seq. ID
                  LIB3088-004-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  g118104
BLAST score
                  267
E value
                  9.0e-24
Match length
                  69
% identity
                  78
NCBI Description
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
                  (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi 168461 (M55021) cyclophilin [Zea mays]
                  >gi 829148 emb CAA48638 (X68678) cyclophilin [Zea mays]
Seq. No.
                  296138
                  LIB3088-004-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g133867
BLAST score
                  159
E value
                  8.0e-11
Match length
                  38
                  82
% identity
                  40S RIBOSOMAL PROTEIN S11 >gi 82722 pir_ S16577 ribosomal
NCBI Description
                  protein S11 - maize >gi_22470_emb CAA39438 (X55967)
                  ribosomal protein S11 [Zea mays]
Seq. No.
                  296139
```

41464

LIB3088-004-Q1-K1-G10

BLASTN

BLAST score

E value

237

6.0e-31





```
NCBI GI
                  g2062705
BLAST score
                  38
E value
                  7.0e-12
Match length
                  42
% identity
                  98
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  296140
                  LIB3088-004-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1172995
BLAST score
                  210
E value
                  1.0e-16
Match length
                  96
% identity
                  52
NCBI Description
                  60S RIBOSOMAL PROTEIN L22 >gi 1083790 pir S52084 ribosomal
                  protein L22 - rat >gi 710295 emb CAA55204 (X78444)
                  ribosomal protein L22 [Rattus norvegicus]
                  >gi 1093952 prf 2105193A ribosomal protein L22 [Rattus
                  norvegicus]
Seq. No.
                  296141
Seq. ID
                  LIB3088-004-Q1-K1-G5
Method
                  BLASTN
NCBI GI
                  g168502
BLAST score
                  74
E value
                  1.0e-33
Match length
                  114
% identity
                  91
NCBI Description Maize (Zea mays) histone H4 gene (H4C7), complete cds
Seq. No.
                  296142
                  LIB3088-005-Q1-K1-A2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g902585
BLAST score
                  39
                  2.0e-12
E value
Match length
                  62
% identity
                  90
NCBI Description Zea mays clone MubG9 ubiquitin gene, complete cds
                  296143
Seq. No.
                  LIB3088-005-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2274993
BLAST score
                  406
E value
                  1.0e-39
Match length
                  99
                  73
% identity
NCBI Description (AJ000230) unnamed protein product [Hordeum vulgare]
                  296144
Seq. No.
Seq. ID
                  LIB3088-005-Q1-K1-B12
Method
                  BLASTX
                  g2911073
NCBI GI
```





```
Match length
% identity
                  69
NCBI Description
                  (AL021960) putative protein [Arabidopsis thaliana]
Seq. No.
                  296145
                  LIB3088-005-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g128191
BLAST score
                  162
E value
                  2.0e-12
Match length
                  96
% identity
                  55
NCBI Description
                  NITRATE REDUCTASE (NAD(P)H) >gi 66210 pir RDBHNP nitrate
                  reductase (NAD(P)H) (EC 1.6.6.2) - barley
                  >gi_19065_emb_CAA42739 (X60173) nitrate reductase
                  (NAD(P)H) [Hordeum vulgare]
Seq. No.
                  296146
                  LIB3088-005-Q1-K1-D3
                  BLASTX
                  g960289
```

Seq. ID Method NCBI GI BLAST score 170 E value 3.0e-12 Match length 66 % identity 58

NCBI Description (L34343) anthranilate synthase alpha subunit [Ruta

graveolens]

296147 Seq. No. Seq. ID LIB3088-005-Q1-K1-D6 Method BLASTX NCBI GI g310587

BLAST score 221 E value 6.0e-18 Match length 84 % identity 55

NCBI Description (L20864) ascorbate peroxidase [Spinacia oleracea]

>gi_1384110_dbj_BAA12890_ (D85864) cytosolic ascorbate

peroxidase [Spinacia oleracea]

296148 Seq. No.

Seq. ID LIB3088-005-Q1-K1-E11

Method BLASTN NCBI GI q2062691 BLAST score 34 E value 1.0e-09 Match length 34 % identity 100

NCBI Description Human sodium phosphate transporter (NPT4) mRNA, complete

Seq. No. 296149

Seq. ID LIB3088-005-Q1-K1-E4

Method BLASTX NCBI GI q2853081 BLAST score 201 E value 1.0e-15





```
Match length
% identity
                   55
                  (ALO21768) ATP binding protein-like [Arabidopsis thaliana]
NCBI Description
                  296150
Seq. No.
                  LIB3088-005-Q1-K1-H10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
                  100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  296151
                  LIB3088-006-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q542200
BLAST score
                  248
E value
                  3.0e-21
Match length
                  132
% identity
                  41
NCBI Description
                  hypothetical protein - garden asparagus
                  >gi 452714 emb CAA54526 (X77320) unknown [Asparagus
                  officinalis]
Seq. No.
                  296152
Seq. ID
                  LIB3088-006-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g2191175
BLAST score
                  159
E value
                  8.0e-11
Match length
                  56
                  55
% identity
                  (AF007270) A_IG002P16.24 gene product [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  296153
                  LIB3088-006-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3056601
BLAST score
                  149
E value
                  1.0e-09
Match length
                  48
                  54
% identity
NCBI Description
                  (AC004255) T1F9.22 [Arabidopsis thaliana]
                  296154
Seq. No.
                  LIB3088-006-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g462243
BLAST score
                  215
E value
                  2.0e-17
Match length
```

% identity 68 NCBI Description HISTONE H4 >gi_421921_pir__S32769 histone H4 - tomato >gi 297150 emb CAA48923 (X69179) histone H4 [Lycopersicon





esculentum] >gi 297152 emb CAA48924 (X69180) histone H4 [Lycopersicon esculentum] >gi 2746721 (AF038387) histone H4 [Capsicum annuum]

Seq. No. 296155

LIB3088-006-Q1-K1-E10 Seq. ID

Method BLASTX NCBI GI q1699024 BLAST score 155 E value 7.0e-11 Match length 67 % identity 46

(U78866) gene1000 [Arabidopsis thaliana] >gi_1699057 NCBI Description

(U78870) unknown [Arabidopsis thaliana]

Seq. No. 296156

LIB3088-006-Q1-K1-E4 Seq. ID

Method BLASTN g531832 NCBI GI BLAST score 34 1.0e-09 E value Match length 74 % identity 86

NCBI Description Cloning vector pSport2, complete sequence

Seq. No. 296157

LIB3088-006-Q1-K1-G5 Seq. ID

Method BLASTX NCBI GI g3142300 BLAST score 150 9.0e-10 E value Match length 75 % identity 45

(AC002411) Contains similarity to pre-mRNA processing NCBI Description

protein PRP39 gb L29224 from S. cerevisiae. ESTs gb R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this

gene. [Arabidopsis thaliana]

Seq. No. 296158

LIB3088-006-Q1-K1-H11 Seq. ID

Method BLASTX g2429087 NCBI GI BLAST score 140 3.0e-16 E value 99 Match length 56 % identity

NCBI Description (L37358) lipoxygenase 2 [Hordeum vulgare]

Seq. No.

296159

Seq. ID LIB3088-007-Q1-K1-C10

Method BLASTX g134613 NCBI GI BLAST score 282 3.0e-25 E value Match length 114 % identity

NCBI Description SUPEROXIDE DISMUTASE-2 (CU-ZN) >gi_82727_pir__A29077





superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 2 - maize >gi_168620 (M54936) superoxide dismutase 2 [Zea mays] >gi_168622 (M15175) SOD2 protein [Zea mays]

Seq. No. 296160

LIB3088-007-Q1-K1-C3 Seq. ID

Method BLASTX NCBI GI g2335096 BLAST score 145 4.0e-09 E value Match length 134 28 % identity

NCBI Description (AC002339) hypothetical protein [Arabidopsis thaliana]

296161 Seq. No.

Seq. ID LIB3088-007-Q1-K1-C9

Method BLASTN NCBI GI q168502 BLAST score 288 1.0e-161 E value 344 Match length % identity 97

NCBI Description Maize (Zea mays) histone H4 gene (H4C7), complete cds

296162 Seq. No.

LIB3088-007-Q1-K1-E2 Seq. ID

Method BLASTN NCBI GI g602252 BLAST score 57 2.0e-23 E value Match length 61 98 % identity

Zea mays enolase (eno2) mRNA, complete cds NCBI Description

296163 Seq. No.

LIB3088-007-Q1-K1-F9 Seq. ID

Method BLASTN NCBI GI g2345153 BLAST score 78 7.0e-36 E value Match length 142 89 % identity

Zea mays ribsomal protein S4 (rps4) mRNA, complete cds NCBI Description

296164 Seq. No.

LIB3088-007-Q1-K1-G2 Seq. ID

BLASTX Method g121964 NCBI GI BLAST score 161 5.0e-11 E value 41 Match length % identity 80

HISTONE H2A.1 >gi_70708_pir__HSTE91 histone H2A.1 -NCBI Description Tetrahymena pyriformis (SGC5) >gi 351324 prf 0906228A

histone H2A(1) [Tetrahymena pyriformis]

Seq. No. 296165



8

```
LIB3088-007-Q1-K1-H5
Seq. ID
Method
                  BLASTX
                  g3413473
NCBI GI
BLAST score
                  140
                  9.0e-09
E value
                  85
Match length
% identity
                  38
                  (AJ006308) tyrosine phosphatase 1 [Glycine max]
NCBI Description
Seq. No.
                  296166
                  LIB3088-008-Q1-K1-B9
Seq. ID
                  BLASTN
Method
                  g531828
NCBI GI
BLAST score
                  33
E value
                  4.0e-09
Match length
                  45
% identity
                  93
NCBI Description Cloning vector pSport1, complete cds
                  296167
Seq. No.
Seq. ID
                  LIB3088-008-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g2440160
BLAST score
                  176
                  1.0e-12
E value
Match length
                  79
% identity
                  48
                  (Y14836) beta-galactosidase [Phagemid cloning vector
NCBI Description
                  pTZ19U]
                  296168
Seq. No.
                  LIB3088-008-Q1-K1-H5
Seq. ID
                  BLASTX
Method
                  g2109457
NCBI GI
                  198
BLAST score
                  2.0e-15
E value
Match length
                  69
                  59
% identity
NCBI Description (AF001501) chitinase [Oryza sativa]
                  296169
Seq. No.
                  LIB3088-009-Q1-K1-A12
Seq. ID
                  BLASTN
Method
                  g1777719
NCBI GI
BLAST score
                  43
E value
                  5.0e-15
Match length
                  65
                  91
% identity
                  Saxifraga mertensiana 18S ribosomal RNA gene, partial
NCBI Description
                   sequence
Seq. No.
                   296170
                  LIB3088-009-Q1-K1-B11
Seq. ID
Method
                  BLASTX
                  q126066
NCBI GI
BLAST score
                   483
```

41470

8.0e - 49

E value





```
Match length
% identity
                  88
                  L-LACTATE DEHYDROGENASE (LDH) >gi 82704 pir S22492
NCBI Description
                  L-lactate dehydrogenase (EC 1.1.1.27) chain Ldh1 - maize
                  >gi 22353 emb CAA77808 (Z11754) lactate dehydrogenase [Zea
                  mays]
                  296171
Seq. No.
                  LIB3088-009-Q1-K1-C9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g58207
BLAST score
                  34
                  1.0e-09
E value
Match length
                  42
% identity
                  95
NCBI Description
                  Cloning vector pGEM-4Z
                  296172
Seq. No.
                  LIB3088-009-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2981475
BLAST score
                  147
                  1.0e-09
E value
Match length
                  61
% identity
                  52
NCBI Description
                  (AF053084) putative cinnamyl alcohol dehydrogenase [Malus
                  domestica]
Seq. No.
                  296173
Seq. ID
                  LIB3088-009-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  q531829
BLAST score
                  179
                  4.0e-13
E value
Match length
                  77
% identity
                  49
NCBI Description
                  (U12390) beta-galactosidase alpha peptide [cloning vector
                  pSport1]
                  296174
Seq. No.
Seq. ID
                  LIB3088-009-Q1-K1-E7
Method
                  BLASTX
                  g114682
NCBI GI
BLAST score
                  251
E value
                  1.0e-21
Match length
                  101
% identity
                  51
NCBI Description
                  ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR
                  (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)
                  >gi_100471_pir__A35227 H+-transporting ATP synthase (EC
```

>gi_100471_pir__A35227 H+-transporting ATP synthase (EC
3.6.1.34) gamma chain precursor, mitochondrial - sweet
potato >gi_168270 (J05397) F-1-ATPase delta subunit

precursor (EC 3.6.1.3) [Ipomoea batatas]

Seq. No. 296175

Seq. ID LIB3088-009-Q1-K1-G8

Method BLASTX



NCBI GI



```
g121982
BLAST score
                    185
                    5.0e-14
  E value
                    40
  Match length
  % identity
                    93
  NCBI Description HISTONE H2A.2.2
  Seq. No.
                    296176
                    LIB3088-009-Q1-K1-H8
  Seq. ID
  Method
                    BLASTN
  NCBI GI
                    g22157
  BLAST score
                    41
  E value
                    7.0e-14
  Match length
                    41
                    100
  % identity
  NCBI Description Z.mays mRNA for alpha-tubulin
                    296177
  Seq. No.
                    LIB3088-010-Q1-K1-A10
  Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4539454
 BLAST score
                    183
                    1.0e-13
  E value
 Match length
                    74
  % identity
                    50
  NCBI Description (AL049500) contains EST gb:AA728416 [Arabidopsis thaliana]
                    296178
  Seq. No.
                    LIB3088-010-Q1-K1-A4
  Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g309573
 BLAST score
                    236
 E value
                    1.0e-130
 Match length
                    394
  % identity
                    93
  NCBI Description Corn ZAG1 mRNA, complete cds
  Seq. No.
                    296179
  Seq. ID
                    LIB3088-010-Q1-K1-B8
  Method
                    BLASTX
                    g951172
  NCBI GI
  BLAST score
                    200
                    5.0e-16
  E value
                    55
  Match length
  % identity
                    73
  NCBI Description
                   (U31521) MADS box protein [Zea mays]
                    >gi_1001934_emb_CAA56504_ (X80206) ZAG2 [Zea mays]
  Seq. No.
                    296180
                    LIB3088-010-Q1-K1-E10
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q3551954
  BLAST score
                    465
  E value
                    1.0e-46
  Match length
                    138
  % identity
                    62
  NCBI Description (AF082030) senescence-associated protein 5 [Hemerocallis
```





hybrid cultivar]

```
296181
Seq. No.
Seq. ID
                   LIB3088-010-Q1-K1-H9
Method
                   BLASTX
NCBI GI
                   q531829
BLAST score
                   191
E value
                   1.0e-14
Match length
                   79
% identity
                   49
NCBI Description
                   (U12390) beta-galactosidase alpha peptide [cloning vector
                   pSport1]
Seq. No.
                   296182
Seq. ID
                   LIB3088-011-Q1-K1-D5
Method
                   BLASTX
NCBI GI
                   g70753
BLAST score
                   362
E value
                   9.0e-35
Match length
                   88
% identity
                   85
NCBI Description
                  histone H3 - garden pea >gi_82610 pir_ S00373 histone H3 -
                   wheat
                   296183
Seq. No.
Seq. ID
                   LIB3088-011-Q1-K1-F5
Method
                   BLASTX
NCBI GI
                   g1684913
BLAST score
                   451
                   5.0e-45
E value
Match length
                   126
% identity
                   69
                  (U77888) receptor-like protein kinase [Ipomoea nil]
NCBI Description
Seq. No.
                   296184
Seq. ID
                   LIB3088-011-Q1-K1-H8
Method
                   BLASTX
NCBI GI
                   g1707868
BLAST score
                   172
E value
                   3.0e-12
Match length
                   70
% identity
                   54
NCBI Description
                  (Y09636) 40S ribosomal subunit protein S21 [Zea mays]
Seq. No.
                  296185
Seq. ID
                  LIB3088-012-Q1-K1-A4
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                  53
E value
                  4.0e-21
Match length
                  169
% identity
                  83
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  296186
Seq. ID
                  LIB3088-012-Q1-K1-D3
Method
                  BLASTN
```

Method

NCBI GI

BLASTX

g464707





```
NCBI GI
                  g2062691
BLAST score
                  35
E value
                  2.0e-10
Match length
                  35
                  100
% identity
                  Human sodium phosphate transporter (NPT4) mRNA, complete
NCBI Description
                  cds
Seq. No.
                  296187
                  LIB3088-012-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3033397
BLAST score
                  549
E value
                  2.0e-56
Match length
                  119
% identity
                  84
NCBI Description (AC004238) unknown protein [Arabidopsis thaliana]
                  296188
Seq. No.
Seq. ID
                  LIB3088-012-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  g3386546
BLAST score
                  154
                  4.0e-10
E value
Match length
                  91
% identity
                  48
NCBI Description (AF079503) H-protein promoter binding factor-2a
                  [Arabidopsis thaliana]
Seq. No.
                  296189
                  LIB3088-013-Q1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1001111
BLAST score
                  146
E value
                  4.0e-09
Match length
                  119
% identity
                  34
NCBI Description (D64001) hypothetical protein [Synechocystis sp.]
Seq. No.
                  296190
Seq. ID
                  LIB3088-013-Q1-K1-C4
Method
                  BLASTX
                  g1351791
NCBI GI
BLAST score
                  481
E value
                  2.0e-48
Match length
                  123
% identity
                  33
NCBI Description
                  HYPOTHETICAL 57.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN
                  CPR4-SSK22 INTERGENIC REGION >gi 83249 pir S19487
                  hypothetical protein YCR072c - yeast (Saccharomyces
                  cerevisiae) >gi_1907211_emb_CAA42270_ (X59720) YCR072c,
                  len:515 [Saccharomyces cerevisiae]
Seq. No.
                  296191
Seq. ID
                  LIB3088-013-Q1-K1-F2
```





BLAST score 153
E value 2.0e-14
Match length 67
% identity 60
NCBI Description 40S RIB

40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana

>gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
[Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)

S18 ribosomal protein [Arabidopsis thaliana]

>gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal

protein [Arabidopsis thaliana]

Seq. No. 296192

Seq. ID LIB3088-014-Q1-K1-A10

Method BLASTX
NCBI GI g4558564
BLAST score 219
E value 1.0e-17
Match length 114
% identity 44

NCBI Description (AC007138) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 296193

Seq. ID LIB3088-014-Q1-K1-D5

Method BLASTX
NCBI GI g585963
BLAST score 176
E value 8.0e-13
Match length 58
% identity 67

NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT

Seq. No. 296194

Seq. ID LIB3088-014-Q1-K1-G11

Method BLASTX
NCBI GI g112994
BLAST score 333
E value 3.0e-31
Match length 78
% identity 86

NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN

>gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi 22313 emb CAA31077 (X12564)

ABA-inducible gene protein [Zea mays]

>gi 226091 prf 1410284A abscisic acid inducible gene [Zea

mays]

Seq. No. 296195

E value

Match length

5.0e-24

104





```
LIB3088-014-Q1-K1-G9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  34
E value
                  6.0e-10
Match length
                  34
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  296196
Seq. No.
                  LIB3088-019-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076678
BLAST score
                  333
                  3.0e-31
E value
Match length
                  102
% identity
                  70
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)
Seq. No.
                  296197
                  LIB3088-019-Q1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2224914
BLAST score
                  38
E value
                  6.0e-12
Match length
                  94
% identity
                  85
NCBI Description Oryza sativa beta-expansin mRNA, complete cds
                  296198
Seq. No.
Seq. ID
                  LIB3088-019-Q1-K1-E1
Method
                  BLASTN
NCBI GI
                  q1870202
BLAST score
                  66
E value
                  9.0e-29
Match length
                  162
% identity
                  86
NCBI Description Z.mays cyp71c3 gene
                  296199
Seq. No.
Seq. ID
                  LIB3088-019-Q1-K1-E2
Method
                  BLASTN
NCBI GI
                  g2062691
BLAST score
                  33
E value
                  5.0e-09
Match length
                  33
                  100
% identity
NCBI Description Human sodium phosphate transporter (NPT4) mRNA, complete
                  cds
Seq. No.
                  296200
Seq. ID
                  LIB3088-019-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g2245066
BLAST score
                  272
```

Seq. No.

296206





```
% identity
NCBI Description
                  (Z97342) Beta-Amylase [Arabidopsis thaliana]
Seq. No.
                  296201
Seq. ID
                  LIB3088-019-Q1-K1-F6
Method
                  BLASTN
                  g1089800
NCBI GI
BLAST score
                  89
                  3.0e-42
E value
Match length
                  145
% identity
                  90
                  Rice mitochondrial atp9 gene for ATPase subunt 9, partial
NCBI Description
                  sequence
Seq. No.
                  296202
Seq. ID
                  LIB3088-019-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  g1666173
BLAST score
                  332
E value
                  4.0e-31
Match length
                  77
% identity
                  87
NCBI Description
                  (Y09106) transcription factor [Nicotiana plumbaginifolia]
Seq. No.
                  296203
Seq. ID
                  LIB3088-019-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g1705667
BLAST score
                  572
E value
                  4.0e-59
Match length
                  126
% identity
                  83
NCBI Description
                  SERINE CARBOXYPEPTIDASE-LIKE PRECURSOR
                  >gi 409582 dbj BAA04511 (D17587) serine
                  carboxypeptidase-like protein [Oryza sativa]
Seq. No.
                  296204
Seq. ID
                  LIB3088-020-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  g899610
BLAST score
                  253
E value
                  6.0e-22
Match length
                  58
% identity
                  91
NCBI Description (U29383) acidic ribosomal protein P2 [Zea mays]
Seq. No.
                  296205
Seq. ID
                  LIB3088-020-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  g2149640
BLAST score
                  302
E value
                  3.0e-37
Match length
                  88
% identity
NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]
```

Method

NCBI GI

BLASTX

g1708107





```
Seq. ID
                  LIB3088-020-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  q3176965
                  193
BLAST score
                  1.0e-14
E value
Match length
                  41
% identity
                  88
NCBI Description
                  (AF067967) pyrroline-5-carboxylate synthetase
                   [Mesembryanthemum crystallinum]
Seq. No.
                  296207
Seq. ID
                  LIB3088-020-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                  g4538975
BLAST score
                  245
                  4.0e-21
E value
Match length
                  57
                  77
% identity
NCBI Description (AL049487) putative protein [Arabidopsis thaliana]
Seq. No.
                  296208
Seq. ID
                  LIB3088-020-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g131773
BLAST score
                  198
E value
                  1.0e-17
Match length
                  50
% identity
                  88
NCBI Description
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
                  >gi_82724_pir B30097 ribosomal protein S14 (clone MCH2) -
                  maize
                  296209
Seq. No.
Seq. ID
                  LIB3088-021-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  g3334112
BLAST score
                  230
E value
                  2.0e-19
Match length
                  61
% identity
                  72
NCBI Description ACYL-COA-BINDING PROTEIN (ACBP) >gi_1938236 emb CAA70200
                  (Y08996) acyl-CoA-binding protein [Ricinus communis]
Seq. No.
                  296210
Seq. ID
                  LIB3088-021-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g1498053
BLAST score
                  403
E value
                  2.0e-39
Match length
                  107
% identity
                  77
NCBI Description (U64436) ribosomal protein S8 [Zea mays]
Seq. No.
                  296211
Seq. ID
                  LIB3088-021-Q1-K1-B8
```





```
BLAST score
                   171
E value
                   3.0e-12
Match length
                   65
% identity
                   58
NCBI Description
                  HISTONE H2B >gi 473605 (U08226) histone H2B [Zea mays]
Seq. No.
                   296212
Seq. ID
                   LIB3088-021-Q1-K1-G4
Method
                   BLASTX
NCBI GI
                   g3513736
BLAST score
                   208
E value
                   2.0e-16
Match length
                   63
% identity
                   62
NCBI Description
                   (AF080118) No definition line found [Arabidopsis thaliana]
                   >gi_4539367_emb_CAB40061.1 (AL049525) putative protein
                   [Arabidopsis thaliana]
                   296213
Seq. No.
Seq. ID
                   LIB3088-021-Q1-K1-H4
Method
                   BLASTX
NCBI GI
                   q4249382
BLAST score
                   161
E value
                   2.0e-16
Match length
                   64
% identity
                   67
NCBI Description
                   (AC005966) Strong similarity to gi_3337350 F13P17.3
                   putative permease from Arabidopsis thaliana BAC
                   gb_AC004481. [Arabidopsis thaliana]
Seq. No.
                   296214
Seq. ID
                  LIB3088-022-Q1-K1-B2
Method
                  BLASTN
NCBI GI
                   g2911365
BLAST score
                   59
E value
                  1.0e-24
Match length
                  118
% identity
                   89
NCBI Description
                  Zea mays NADPH HC toxin reductase (hm2) gene, hm2-B73
                  allele, partial cds
                  296215
Seq. No.
Seq. ID
                  LIB3088-022-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  g2130090
BLAST score
                  142
E value
                  1.0e-09
Match length
                  101
% identity
                  42
NCBI Description
                  2-oxoglutarate/malate translocator (clone OMT134),
                  mitochondrial membrane - proso millet
                  >gi_1100739_dbj_BAA08103 (D45073) 2-oxoglutarate/malate
                  translocator [Panicum miliaceum] >gi_1100741_dbj_BAA08104_
                   (D45074) 2-oxoglutarate/malate trans\overline{\text{locator}} \overline{\text{[Panicum]}}
                  miliaceum]
```

Seq. No. 296216

NCBI GI

BLAST score





```
LIB3088-022-Q1-K1-G2
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g2130107
  BLAST score
                    188
  E value
                    4.0e-14
  Match length
                    136
                    38
  % identity
NCBI Description porin (clone Tavdac1) - wheat
  Seq. No.
                    296217
                    LIB3088-023-Q1-K1-E4
  Seq. ID
  Method
                    BLASTN
  NCBI GI
                    g3821780
  BLAST score
                    36
  E value
                    8.0e-11
  Match length
                    36
  % identity
                    100
  NCBI Description Xenopus laevis cDNA clone 27A6-1
                    296218
  Seq. No.
  Seq. ID
                    LIB3088-023-Q1-K1-H11
  Method
                    BLASTX
  NCBI GI
                    g3914431
 BLAST score
                    262
  E value
                    4.0e-23
 Match length
                    82
  % identity
                    63
  NCBI Description
                    PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8)
                    (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8)
                    >gi 2285802 dbj BAA21651 (D78173) 26S proteasome alpha
                    subunit [Spinacia oleracea]
  Seq. No.
                    296219
  Seq. ID
                    LIB3088-024-Q1-K1-A8
  Method
                    BLASTX
  NCBI GI
                    g4539677
  BLAST score
                    311
  E value
                    1.0e-28
 Match length
                    91
  % identity
                    77
  NCBI Description (AF061282) patatin-like protein [Sorghum bicolor]
                    296220
  Seq. No.
  Seq. ID
                    LIB3088-024-Q1-K1-E11
  Method
                    BLASTX
  NCBI GI
                    g3136336
  BLAST score
                    201
 E value
                    6.0e-16
 Match length
                    74
  % identity
                    62
  NCBI Description (AF064552) calmodulin; Cam [Apium graveolens]
                    296221
  Seq. No.
  Seq. ID
                    LIB3088-024-Q1-K1-F4
  Method
                    BLASTX
```

41480

g3004950



E value

3.0e-15



```
Match length
                  46
% identity
                  87
                  (AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays]
NCBI Description
                  296222
Seq. No.
                  LIB3088-024-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                  g1399450
NCBI GI
BLAST score
                  528
E value
                  4.0e-54
Match length
                  101
% identity
                  97
                  (U47660) beta-tubulin 2 [Lupinus albus]
NCBI Description
Seq. No.
                  296223
Seq. ID
                  LIB3088-025-Q1-K1-A7
Method
                  BLASTN
NCBI GI
                  g311238
BLAST score
                  38
                  4.0e-12
E value
Match length
                  130
% identity
                  82
NCBI Description Z.mays cat1 gene for catalase
                  296224
Seq. No.
Seq. ID
                  LIB3088-025-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  q2130042
BLAST score
                  432
E value
                  9.0e-43
Match length
                  96
% identity
                  91
                  Mq-chelatase chain Xantha-f - barley >qi 861199 (U26916)
NCBI Description
                  protoporphyrin IX Mg-chelatase subunit precursor [Hordeum
                  vulgare]
                  296225
Seq. No.
                  LIB3088-025-Q1-K1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1185553
BLAST score
                  40
                  4.0e-13
E value
                  100
Match length
% identity
                  85
                  Zea mays qlyceraldehyde-3-phosphate dehydrogenase (gpc2)
NCBI Description
                  gene, complete cds
                  296226
Seq. No.
                  LIB3088-025-Q1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q417154
BLAST score
                  236
                  6.0e-20
E value
Match length
                  96
                  53
% identity
NCBI Description HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock
```





protein 82 - rice (strain Taichung Native One) >gi 20256 emb CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

296227 Seq. No.

LIB3088-025-Q1-K1-E4 Seq. ID

Method BLASTX g1708110 NCBI GI BLAST score 150 6.0e-10 E value Match length 77 44 % identity

HISTONE H4 >gi 2119025 pir S59586 histone H4 (clone NCBI Description

> CH-III) - Chlamydomonas reinhardtii >gi 2119027_pir_ S59124 histone H4 - Chlamydomonas reinhardtii >gi_571471 (U16724) histone H4 [Chlamydomonas reinhardtii] >gi_571476 (U16725) histone H4 [Chlamydomonas reinhardtii] >gi_576634 (U16825) histone H4 [Chlamydomonas reinhardtii] >gi 790701 (L41841)

histone H4 [Chlamydomonas reinhardtii]

296228 Seq. No.

LIB3088-025-Q1-K1-E9 Seq. ID

Method BLASTX NCBI GI g4325282 BLAST score 146 E value 2.0e-09 Match length 39 69 % identity

(AF123310) NAC domain protein NAM [Arabidopsis thaliana] NCBI Description

>gi 4325286 gb AAD17314 (AF123311) NAC domain protein NAM

[Arabidopsis thaliana]

296229 Seq. No.

LIB3088-025-Q1-K1-F2 Seq. ID

Method BLASTN NCBI GI g22161 BLAST score 55 3.0e-22 E value Match length 151 % identity

Z.mays MANT1 mRNA for adenine nucleotide translocator (also NCBI Description

called ADP/ATP translocase)

296230 Seq. No.

Seq. ID LIB3088-026-Q1-K1-A12

Method BLASTX NCBI GI q266567 BLAST score 150 E value 9.0e-10 Match length 111 % identity 36

NCBI Description MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR

(ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II) >gi_421956_pir__S23558 mitochondrial processing peptidase
(EC 3.4.99.41) alpha chain precursor - potato

>gi 21493 emb CAA46990 (X66284) mitochondrial processing

peptidase [Solanum tuberosum]





```
Seq. No.
                  296231
Seq. ID
                  LIB3088-026-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  g1362015
BLAST score
                  146
                  2.0e-09
E value
Match length
                  38
% identity
                  66
NCBI Description
                  zinc finger protein 1 - Arabidopsis thaliana
                  >gi 2129779 pir S71240 zinc finger protein 1 - Arabidopsis
                  thaliana >gi 790673 (L39644) zinc finger protein
                  [Arabidopsis thaliana] >gi 1297186 (U53501) zinc finger
                  protein 1 [Arabidopsis thaliana]
Seq. No.
                  296232
Seq. ID
                  LIB3088-027-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  q2833378
BLAST score
                  159
                  1.0e-10
E value
Match length
                  112
% identity
                  37
NCBI Description
                  HEXOKINASE >gi 619928 (U18754) hexokinase [Arabidopsis
                  thaliana] >gi 1582383 prf 2118367A hexokinase [Arabidopsis
                  thaliana]
                  296233
Seq. No.
Seq. ID
                  LIB3088-027-Q1-K1-B7
Method
                  BLASTX
                  g3193292
NCBI GI
BLAST score
                  305
E value
                  7.0e-28
Match length
                  101
% identity
                  59
NCBI Description
                  (AF069298) similar to ATPases associated with various
                  cellular activites (Pfam: AAA.hmm, score: 230.91)
                  [Arabidopsis thaliana]
Seq. No.
                  296234
Seq. ID
                  LIB3088-027-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g730512
BLAST score
                  238
E value
                  4.0e-20
Match length
                  84
% identity
                  61
NCBI Description
                  RAS-RELATED PROTEIN RIC2 >gi_481506_pir_ S38741 GTP-binding
                  protein ric2 - rice >gi_218228_dbj_BAA02904_ (D13758)
                  ras-related GTP binding protein [Oryza sativa]
```

Seq. No. 296235

Seq. ID LIB3088-029-Q1-K1-C11

Method BLASTN NCBI GI g1944204 BLAST score 37 3.0e-11E value





```
Match length
                  89
% identity
NCBI Description Oryza sativa mRNA for RicMT, complete cds
                  296236
Seq. No.
                  LIB3088-029-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3608133
BLAST score
                  149
                  2.0e-09
E value
Match length
                  57
                  56
% identity
NCBI Description (AC005314) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  296237
                  LIB3088-029-Q1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2809262
BLAST score
                  155
E value
                  2.0e-10
Match length
                  93
% identity
                  43
NCBI Description (AC002560) F21B7.31 [Arabidopsis thaliana]
Seq. No.
                  296238
                  LIB3088-029-Q1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2058273
BLAST score
                  382
E value
                  7.0e-37
Match length
                  88
% identity
                  88
NCBI Description (D83527) YK426 [Oryza sativa]
Seq. No.
                  296239
Seq. ID
                  LIB3088-029-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g2911068
BLAST score
                  205
E value
                  1.0e-32
Match length
                  131
                  56
% identity
NCBI Description (AL021960) G10-like protein [Arabidopsis thaliana]
Seq. No.
                  296240
                  LIB3088-029-Q1-K1-F11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22292
BLAST score
                  35
E value
                  2.0e-10
Match length
                  55
% identity
                  91
NCBI Description Z.mays mRNA for glycine-rich protein
```

Seq. No. 296241

Seq. ID LIB3088-029-Q1-K1-G11

Method BLASTX





```
NCBI GI
                  g1172977
                  199
BLAST score
                  2.0e-15
E value
Match length
                  124
% identity
                  40
                  60S RIBOSOMAL PROTEIN L18 >qi 606970 (U15741) cytoplasmic
NCBI Description
                  ribosomal protein L18 [Arabidopsis thaliana]
Seq. No.
                  296242
                  LIB3088-029-Q1-K1-G2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3980378
BLAST score
                  178
                  6.0e-13
E value
Match length
                  114
% identity
                  40
                  (AC004561) putative RNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  296243
Seq. ID
                  LIB3088-029-Q1-K1-H1
                  BLASTN
Method
                  g397395
NCBI GI
BLAST score
                  97
                  3.0e-47
E value
Match length
                  167
                  98
% identity
NCBI Description Z.mays MNB1b mRNA for DNA-binding protein
                  296244
Seq. No.
               LIB3088-030-Q1-K1-C3
Seq. ID
                  BLASTX
Method
                  g4371282
NCBI GI
                  181
BLAST score
E value
                  3.0e-13
                  44
Match length
                  80
% identity
                  (AC006260) putative 60S ribosomal protein L12 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  296245
                  LIB3088-030-Q1-K1-F3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q532622
BLAST score
                  104
E value
                  2.0e-51
Match length
                  213
                  95
% identity
NCBI Description Zea mays lipase (LIP) mRNA, complete cds
```

Seq. No. 296246

Seq. ID LIB3088-030-Q1-K1-G3

Method BLASTX
NCBI GI g4468792
BLAST score 428
E value 2.0e-42
Match length 88

% identity

53





```
% identity
NCBI Description
                  (AJ010295) Glutathione transferase III(a) [Zea mays]
                  296247
Seq. No.
                  LIB3088-030-Q1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3201632
BLAST score
                  200
                  7.0e-16
E value
Match length
                  75
                  55
% identity
NCBI Description (AC004669) putative 2A6 protein [Arabidopsis thaliana]
Seq. No.
                  296248
                  LIB3088-031-Q1-K1-B3
Seq. ID
Method
                  BLASTX
                  g4455364
NCBI GI
BLAST score
                  180
                  2.0e-13
E value
Match length
                  70
                  49
% identity
                  (AL035524) senescence-associated protein-like [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  296249
                  LIB3088-031-Q1-K1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4388782
BLAST score
                  44
E value
                  1.0e-15
                  104
Match length
                  87
% identity
NCBI Description Zea mays 40S ribosomal protein S27 homolog mRNA, complete
                  296250
Seq. No.
Seq. ID
                  LIB3088-031-Q1-K1-C7
Method
                  BLASTX
                  g118104
NCBI GI
BLAST score
                  412
E value
                  2.0e-40
Match length
                  98
% identity
                  81
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                  (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi_168461 (M55021) cyclophilin [Zea mays]
                  >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]
Seq. No.
                  296251
Seq. ID
                  LIB3088-031-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  q3953458
BLAST score
                  195
E value
                  3.0e-15
Match length
                  74
```

% identity





```
NCBI Description
                     (AC002328) F20N2.3 [Arabidopsis thaliana]
                     296252
   Seq. No.
   Seq. ID
                     LIB3088-031-Q1-K1-H2
   Method
                     BLASTN
   NCBI GI
                     q2065239
   BLAST score
                     34
E value
                     1.0e-09
   Match length
                     38
                     97
   % identity
   NCBI Description
                     M.musculus mRNA for coxsackie and adenovirus receptor
                     homologue
   Seq. No.
                     296253
   Seq. ID
                     LIB3088-032-Q1-K1-G5
   Method
                     BLASTN
   NCBI GI
                     g435678
   BLAST score
                     39
                     1.0e-12
   E value
   Match length
                     59
   % identity
                     92
                     L.esculentum Mill (cv. Rutgers) mRNA for ribosomal protein
   NCBI Description
                     S25
   Seq. No.
                     296254
                     LIB3088-033-Q1-K1-A7
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                     g3915842
   BLAST score
                     394
                     2.0e-38
   E value
   Match length
                     93
                     84
   % identity
   NCBI Description RAS-RELATED PROTEIN RAB11A >qi 2598229 emb CAA70112
                     (Y08904) Rab11 protein [Arabidopsis thaliana]
   Seq. No.
                     296255
                     LIB3088-033-Q1-K1-B7
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                     g118104
   BLAST score
                     531
   E value
                     2.0e-54
   Match length
                     114
   % identity
                     89
   NCBI Description
                     PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
                     (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                     >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                     maize >gi_168461 (M55021) cyclophilin [Zea mays]
                     >gi_829148 emb_CAA48638 (X68678) cyclophilin [Zea mays]
   Seq. No.
                     296256
                     LIB3088-033-Q1-K1-C11
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                     g586076
   BLAST score
                     583
   E value
                     2.0e-60
   Match length
                     120
```





```
NCBI Description
                   TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta
                   chain - white lupine >gi 402636 emb CAA49736 (X70184) Beta
                   tubulin 1 [Lupinus albus]
 Seq. No.
                   296257
 Seq. ID
                   LIB3088-033-Q1-K1-G1
Method
                   BLASTN
NCBI GI
                   g22646
BLAST score
                   181
E value
                   2.0e-97
Match length
                   200
 % identity
                   98
NCBI Description Z.mays MFS18 mRNA
                   296258
 Seq. No.
                   LIB3088-033-Q1-K1-H10
 Seq. ID
Method
                   BLASTN
                   g3821780
NCBI GI
BLAST score
                   34
                   1.0e-09
E value
Match length
                   34
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   296259
Seq. No.
Seq. ID
                   LIB3088-033-Q1-K1-H8
Method
                   BLASTX
NCBI GI
                   q133414
BLAST score
                   429
E value
                   1.0e-42
Match length
                   90
                   94
% identity
                   DNA-DIRECTED RNA POLYMERASE BETA CHAIN >gi_66971_pir__RNZMB
NCBI Description
                   DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - maize
                   chloroplast >gi_12480_emb_CAA35195_ (X17318) RNA polymerase
                   beta subunit (AA 1-1075) [Zea mays]
                   >gi_902212_emb_CAA60276_ (X86563) RNA polymerase beta
                   subunit [Zea mays]
Seq. No.
                   296260
Seq. ID
                   LIB3088-034-Q1-K1-E7
Method
                   BLASTN
                   g22091
NCBI GI
BLAST score
                   253
E value
                   1.0e-140
Match length
                   322
% identity
NCBI Description
                   Z.diploperennis gene for hydroxyproline-rich glycoprotein
```

Seq. No.

296261

Seq. ID LIB3088-034-Q1-K1-G2

Method BLASTN
NCBI GI g577824
BLAST score 137
E value 6.0e-71
Match length 304
% identity 87





```
NCBI Description Z.mays gene for H2B histone (gH2B3)

Seq. No. 296262
Seq. ID LIB3088-035-Q1-K1-A10
Method BLASTX

NCBI GI g1085621
BLAST score 505
```

NCBI GI g1085621
BLAST score 505
E value 2.0e-51
Match length 102
% identity 92
NCBI Description algebal

NCBI Description alcohol dehydrogenase (EC 1.1.1.1) 1CN - Phaseolus acutifolius >gi 452767 emb CAA80692 (Z23171) alcohol

dehydrogenase-1CN [Phaseolus acutifolius]

Seq. No. 296263

Seq. ID LIB3088-035-Q1-K1-B10

Method BLASTX
NCBI GI g3309269
BLAST score 306
E value 5.0e-28
Match length 90
% identity 73

NCBI Description (AF074940) ferric leghemoglobin reductase-2 precursor

[Glycine max]

Seq. No. 296264

Seq. ID LIB3088-035-Q1-K1-B11

Method BLASTX
NCBI GI g585338
BLAST score 346
E value 1.0e-32
Match length 90
% identity 79

NCBI Description ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)

>gi_391879_dbj_BAA01181_ (D10335) adenylate kinase-b [Oryza

sativa]

Seq. No. 296265

Seq. ID LIB3088-035-Q1-K1-B2

Method BLASTX
NCBI GI g629844
BLAST score 160
E value 9.0e-11
Match length 35
% identity 89

NCBI Description heat shock protein hsp70-5 - maize (fragment)

>gi_498775_emb_CAA55184_ (X78415) heat shock protein 70 kDa

[Zea mays]

Seq. No. 296266

Seq. ID LIB3088-035-Q1-K1-C1

Method BLASTX
NCBI GI g3885336
BLAST score 234
E value 1.0e-19
Match length 98
% identity 50

NCBI Description





```
NCBI Description
                  (AC005623) receptor-like protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  296267
                  LIB3088-035-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g585338
BLAST score
                  397
                  9.0e-39
E value
Match length
                  88
                  88
% identity
                  ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)
NCBI Description
                  >gi_391879 dbj BAA01181 (D10335) adenylate kinase-b [Oryza
                  sativa]
                  296268
Seq. No.
                  LIB3088-035-Q1-K1-D10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g18569
BLAST score
                  60
                  5.0e-25
E value
Match length
                  148
% identity
                  86
NCBI Description G.max coxII gene for cytochrome oxidase subunit
                  296269
Seq. No.
                  LIB3088-035-Q1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3342800
BLAST score
                  196
E value
                  7.0e-16
                  68
Match length
% identity
                  76
NCBI Description
                  (AF061837) putative cytosolic 6-phosphogluconate
                  dehydrogenase [Zea mays]
Seq. No.
                  296270
Seq. ID
                  LIB3088-035-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  q1171577
BLAST score
                  232
                  2.0e-19
E value
                  90
Match length
% identity
                  53
NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]
Seq. No.
                  296271
Seq. ID
                  LIB3088-035-Q1-K1-F2
Method
                  BLASTN
NCBI GI
                  g4140643
BLAST score
                  129
E value
                  3.0e-66
Match length
                  258
% identity
                  90
```

41490

complete sequence

Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

BLAST score

E value

192

1.0e-16





```
Seq. No.
                   296272
Seq. ID
                  LIB3088-035-Q1-K1-F9
Method
                  BLASTN
NCBI GI
                   g18569
BLAST score
                   155
E value
                   8.0e-82
Match length
                   167
                   98
% identity
NCBI Description G.max coxII gene for cytochrome oxidase subunit
                   296273
Seq. No.
                  LIB3088-035-Q1-K1-H7
Seq. ID
Method
                  BLASTN
NCBI GI
                   q2446997
BLAST score
                   133
                   1.0e-68
E value
                   189
Match length
                   93
% identity
NCBI Description Zea mays FAD7 gene for fatty acid desaturase, complete cds
                   296274
Seq. No.
                   LIB3088-036-Q1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2613143
BLAST score
                   244
E value
                   5.0e-21
Match length
                   68
% identity
                  74
                  (AF030548) tubulin [Oryza sativa]
NCBI Description
                   296275
Seq. No.
                   LIB3088-036-Q1-K1-B2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g22350
BLAST score
                   37
E value
                   8.0e-12
Match length
                   57
% identity
                   91
NCBI Description Z.mays Knotted-1 (Kn-1) gene
                   296276
Seq. No.
Seq. ID
                  LIB3088-036-Q1-K1-C4
Method
                  BLASTN
NCBI GI
                   q294844
BLAST score
                   82
E value
                   1.0e-38
Match length
                   154
% identity
                   90
NCBI Description
                  Saccharum hybrid cultivar H65-7052 membrane protein mRNA,
                   complete cds
                   296277
Seq. No.
Seq. ID
                  LIB3088-036-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                   q4128133
```

% identity

66





```
Match length
% identity
                  53
                  (AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]
NCBI Description
Seq. No.
                  296278
                  LIB3088-036-Q1-K1-H8
Seq. ID
Method
                  BLASTX
                  q399853
NCBI GI
BLAST score
                  168
E value
                  6.0e-12
Match length
                  41
% identity
                  88
                  HISTONE H2B.1 >gi 283041 pir S28048 histone H2B - maize
NCBI Description
                  >gi 22323 emb CAA40564 (X57312) H2B histone [Zea mays]
Seq. No.
                  296279
                  LIB3088-037-Q1-K1-B4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2984708
BLAST score
                  71
E value
                  1.0e-31
Match length
                  119
% identity
                  91
                  Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
NCBI Description
                  296280
Seq. No.
                  LIB3088-037-Q1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2244797
BLAST score
                  190
                  2.0e-14
E value
Match length
                  78
% identity
                  50
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
                  296281
Seq. No.
                  LIB3088-037-Q1-K1-H2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  6.0e-11
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  296282
Seq. No.
                  LIB3088-038-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q137460
BLAST score
                  292
                  1.0e-26
E value
Match length
                  94
```

NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_67952_pir_PXPZV9 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 69K chain - carrot >gi_167560 (J03769)





vacular H+-ATPase [Daucus carota] Seq. No. 296283 Seq. ID LIB3088-038-Q1-K1-E1 Method BLASTX NCBI GI q3915826 BLAST score 399 E value 6.0e-39 Match length 97 % identity 79 NCBI Description 60S RIBOSOMAL PROTEIN L5 Seq. No. 296284 Seq. ID LIB3088-038-Q1-K1-F7 Method BLASTX NCBI GI q303750 BLAST score 422 E value 2.0e-41 Match length 86 % identity 95 NCBI Description (D12548) GTP-binding protein [Pisum sativum] >gi 738940 prf 2001457H GTP-binding protein [Pisum sativum] Seq. No. 296285 Seq. ID LIB3088-038-Q1-K1-G9 Method BLASTN NCBI GI q1244652 BLAST score 61 E value 1.0e-25 Match length 116 % identity 88 NCBI Description Zea mays copia-type retroelement PREM-2 gag gene, complete Seq. No. 296286 ·LIB3088-038-Q1-K1-H10 Seq. ID Method BLASTX NCBI GI g464621 BLAST score 244 E value 7.0e-21 Match length 81 % identity 65 NCBI Description ribosomal protein ML16 - common ice plant

60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >qi 280374 pir S28586

>gi 19539 emb CAA49175 (X69378) ribosomal protein YL16

[Mesembryanthemum crystallinum]

296287 Seq. No.

Seq. ID LIB3088-039-Q1-K1-A3

Method BLASTN g2668741 NCBI GI BLAST score 38 E value 2.0e-12 Match length 80 86 % identity

NCBI Description Zea mays glycine-rich RNA binding protein (GRP) mRNA,





complete cds

```
Seq. No.
                  296288
Seq. ID
                  LIB3088-039-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g3549666
BLAST score
                  160
                   4.0e-12
E value
Match length
                  84
% identity
                  57
NCBI Description
                  (AL031394) putative protein [Arabidopsis thaliana]
                  296289
Seq. No.
                  LIB3088-039-Q1-K1-G12
Seq. ID
```

Method BLASTX NCBI GI g3482979 BLAST score 158 E value 3.0e-11 Match length 67 % identity 48

NCBI Description (AL031369) putative protein [Arabidopsis thaliana] >gi 4567258 gb AAD23672.1 AC007070 21 (AC007070)

hypothetical protein [Arabidopsis thaliana]

Seq. No. 296290

Seq. ID LIB3088-040-Q1-K1-E10

Method BLASTN NCBI GI g22149 BLAST score 35 E value 3.0e-10 Match length 63 % identity 89

NCBI Description Z.mays mRNA for alpha-tubulin

296291 Seq. No.

LIB3088-040-Q1-K1-E12 Seq. ID

Method BLASTX NCBI GI g2668742 BLAST score 414 1.0e-40 E value Match length 86 % identity 95

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 296292

Seq. ID LIB3088-040-Q1-K1-F9

Method BLASTX NCBI GI g451193 BLAST score 261 E value 1.0e-22 Match length 91 % identity 59

NCBI Description (L28008) wali7 [Triticum aestivum]

>gi 1090845 prf 2019486B wali7 gene [Triticum aestivum]

Seq. No. 296293

Seq. ID LIB3088-040-Q1-K1-H10





```
Method
                  BLASTX
NCBI GI
                  g4586449
BLAST score
                  169
                  6.0e-12
E value
Match length
                  64
% identity
                  52
                  (AB025187) cytochrome c oxidase subunit 6b-1 [Oryza sativa]
NCBI Description
Seq. No.
                  296294
                  LIB3088-041-Q1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2781347
BLAST score
                  487
E value
                  3.0e-49
Match length
                  116
% identity
                  79
NCBI Description
                  (AC003113) F2401.3 [Arabidopsis thaliana]
Seq. No.
                  296295
                  LIB3088-041-Q1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2446994
BLAST score
                  777
                  4.0e-83
E value
Match length
                  145
% identity
                  95
                  (D63952) fatty acid desaturase [Zea mays]
NCBI Description
Seq. No.
                  296296
                  LIB3088-042-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2668742
BLAST score
                  151
E value
                  3.0e-10
Match length
                  69
% identity
                  51
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]
                  296297
Seq. No.
                  LIB3088-042-Q1-K1-A4
Seq. ID
Method
                  BLASTN
                  g2062705
NCBI GI
BLAST score
                  36
E value
                  8.0e-11
Match length
                  36
% identity
                  100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  296298
Seq. ID
                  LIB3088-042-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  g115525
BLAST score
                  338
E value
                  1.0e-31
Match length
                  69
% identity
                  50
NCBI Description CALMODULIN >gi 71685 pir MCSP calmodulin - spinach
```



8

Seq. No. 296299

Seq. ID LIB3088-042-Q1-K1-B9

Method BLASTX
NCBI GI g417103
BLAST score 426
E value 2.0e-44
Match length 121
% identity 83

NCBI Description HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi_488563
(U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460)
histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone
H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2

[Medicago sativa] >gi $4885\overline{7}7$ (U09465) histone H3.2

[Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi $1\overline{4}351\overline{5}7$ emb CAA58445 (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum]

>gi_2558944 (AF024716) histone 3 [Gossypium hirsutum]

>gi_3273350_dbj_BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa]

>gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >qi_4490755 emb_CAB38917.1

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 296300

Seq. ID LIB3088-042-Q1-K1-E7

Method BLASTX
NCBI GI g2959360
BLAST score 496
E value 3.0e-50
Match length 98
% identity 97

NCBI Description (AJ222588) poly(ADP-ribose) polymerase [Zea mays]

Seq. No. 296301

Seq. ID LIB3088-042-Q1-K1-G6

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 7.0e-11
Match length 48
% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 296302

Seq. ID LIB3088-043-Q1-K1-A10

Method BLASTX
NCBI GI g118104
BLAST score 331
E value 5.0e-31
Match length 96
% identity 68

```
NCBI Description
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
                  (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi 68408 pir CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi 168461 (M55021) cyclophilin [Zea mays]
                  >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]
                  296303
Seq. No.
Seq. ID
                  LIB3088-043-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  a82263
BLAST score
                  334
                  3.0e-31
E value
                  90
Match length
% identity
                  74
NCBI Description
                  ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
                  cl precursor (clone pC(1)3II) - potato
Seq. No.
                  296304
                  LIB3088-043-Q1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4531441
BLAST score
                  343
E value
                  2.0e-32
                  103
Match length
% identity
                  63
NCBI Description (AC006224) putative pectinesterase [Arabidopsis thaliana]
Seq. No.
                  296305
                  LIB3088-043-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g531829
BLAST score
                  153
E value
                  3.0e-10
Match length
                  59
                  53
% identity
NCBI Description
                  (U12390) beta-galactosidase alpha peptide [cloning vector
                  pSport1]
Seq. No.
                  296306
Seq. ID
                  LIB3088-043-Q1-K1-E2
Method
                  BLASTN
NCBI GI
                  q3420038
BLAST score
                  79
E value
                  1.0e-36
Match length
                  208
% identity
                  43
NCBI Description
                  Zea mays gypsy/Ty3-type retrotransposon Tekay, complete
                  sequence
Seq. No.
                  296307
Seq. ID
                  LIB3088-043-Q1-K1-F10
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
                  1.0e-10
E value
Match length
                  36
                  100
% identity
```

```
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  296308
Seq. No.
                  LIB3088-043-Q1-K1-H7
Seq. ID
                  BLASTN
Method
                  g1185555
NCBI GI
                  38
BLAST score
                  2.0e-12
E value
                  117
Match length
% identity
                  84
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc4)
NCBI Description
                  gene, partial cds
                  296309
Seq. No.
                  LIB3088-043-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g629844
                  283
BLAST score
                  2.0e-25
E value
                  89
Match length
                  70
% identity
                  heat shock protein hsp70-5 - maize (fragment)
NCBI Description
                  >gi 498775 emb CAA55184 (X78415) heat shock protein 70 kDa
                  [Zea mays]
                  296310
Seq. No.
                  LIB3088-044-Q1-K1-A11
Seq. ID
Method
                  BLASTX
                  g2668742
NCBI GI
                  244
BLAST score
                  1.0e-20
E value
                  55
Match length
% identity
                  89
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                  296311
Seq. No.
Seq. ID
                  LIB3088-044-Q1-K1-B10
                  BLASTX
Method
                  g399854
NCBI GI
                  207
BLAST score
                  1.0e-21
E value
                  116
Match length
                   54
% identity
                  HISTONE H2B.2 >gi 283042 pir S28049 histone H2B - maize
NCBI Description
                  >gi 22325 emb CAA40565 (X57313) H2B histone [Zea mays]
                  296312
Seq. No.
Seq. ID
                  LIB3088-044-Q1-K1-B4
                  BLASTX
Method
NCBI GI
                   q4587572
BLAST score
                   209
                   1.0e-16
E value
                   88
Match length
                   49
% identity
                  (AC006550) Similar to gb_U70015 lysosomal trafficking
NCBI Description
                   regulator from Mus musculus and contains 2 PF 00400 WD40,
                   G-beta repeats. ESTs gb_T43386 and gb_AA395236 come from
```

```
this gene. [Arabidopsis thaliana]
                 296313
Seq. No.
                 LIB3088-044-Q1-K1-C5
Seq. ID
                 BLASTN
Method
                 g3821780
NCBI GI
BLAST score
                  36
E value
                 1.0e-10
                  36
Match length
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  296314
Seq. No.
                  LIB3088-044-Q1-K1-D1
Seq. ID
                  BLASTN
Method
                  g2257755
NCBI GI
                  105
BLAST score
                  6.0e-52
E value
                  133
Match length
                  95
% identity
NCBI Description Zea mays nucleolar histone deacetylase HD2-p39 mRNA,
                  complete cds
                  296315
Seq. No.
                  LIB3088-044-Q1-K1-D11
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
                  36
BLAST score
                  1.0e-10
E value
                  48
Match length
                  67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  296316
Seq. No.
                  LIB3088-044-Q1-K1-D2
Seq. ID
                  BLASTX
Method
                  g729671
NCBI GI
BLAST score
                  303
                  1.0e-27
E value
                  107
Match length
% identity
                  65
NCBI Description HISTONE H2A >gi_473603 (U08225) histone H2A [Zea mays]
                  296317
Seq. No.
                  LIB3088-044-Q1-K1-E12
Seq. ID
Method
                  BLASTX
                  g595768
NCBI GI
                  173
BLAST score
                  2.0e-12
E value
Match length
                  51
% identity
                  61
NCBI Description (U13866) non-functional lacZ alpha peptide [Cloning vector]
                  296318
Seq. No.
                  LIB3088-044-Q1-K1-E8
Seq. ID
Method
                  BLASTX
```

g2979552

NCBI GI

```
BLAST score
                  171
                  2.0e-22
E value
Match length
                  118
                  47
% identity
NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]
                  296319
Seq. No.
                  LIB3088-044-Q1-K1-G7
Seq. ID
Method
                  BLASTX
                  g531829
NCBI GI
BLAST score
                  160
                  6.0e-11
E value
Match length
                  67
% identity
                  49
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
                   296320
Seq. No.
                  LIB3088-044-Q1-K1-H2
Seq. ID
                  BLASTX
Method
                   g544437
NCBI GI
                   345
BLAST score
                   1.0e-32
E value
                   78
Match length
% identity
                   83
                  GLUTATHIONE PEROXIDASE HOMOLOG (SALT-ASSOCIATED PROTEIN)
NCBI Description
                   >gi_296358_emb_CAA47018_ (X66377) CIT-SAP [Citrus sinensis]
                   296321
Seq. No.
                   LIB3088-044-Q1-K1-H3
Seq. ID
                   BLASTX
Method
                   q4371280
NCBI GI
                   277
BLAST score
                   2.0e-24
E value
Match length
                   63
                   87
% identity
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]
                   296322
Seq. No.
                   LIB3088-045-Q1-K1-B9
Seq. ID
                   BLASTX
Method
                   q1711618
NCBI GI
                   234
BLAST score
                   2.0e~19
E value
Match length
                   78
                   47
% identity
NCBI Description LOW AFFINITY SULPHATE TRANSPORTER 3 >gi_1085993_pir__S51765
                   low affinity sulphate transporter - Stylosanthes hamata
                   >gi_607188_emb_CAA57831_ (X82454) low affinity sulphate
                   transporter [Stylosanthes hamata]
                   296323
Seq. No.
                   LIB3088-045-Q1-K1-E7
 Seq. ID
                   BLASTX
Method
                   g4455367
NCBI GI
BLAST score
                   210
                   1.0e-16
E value
```



```
Match length
                  45
% identity
                  (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                  296324
Seq. No.
                  LIB3088-045-Q1-K1-H6
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
                  36
BLAST score
                  7.0e-11
E value
Match length
                  48
                  67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  296325
Seq. No.
Seq. ID
                  LIB3088-046-Q1-K1-A7
Method
                  BLASTN
NCBI GI
                  g531828
                  41
BLAST score
                   8.0e-14
E value
                  73
Match length
                   89
% identity
NCBI Description Cloning vector pSport1, complete cds
                   296326
Seq. No.
                   LIB3088-046-Q1-K1-B1
Seq. ID
Method
                   BLASTN
                   g13904
NCBI GI
                   73
BLAST score
E value
                   3.0e - 33
                   165
Match length
                   87
% identity
NCBI Description Maize mitochondrial cytochrome b gene
                   296327
Seq. No.
                   LIB3088-046-Q1-K1-C11
Seq. ID
Method
                   BLASTN
                   g3925236
NCBI GI
BLAST score
                   84
                   1.0e-39
E value
Match length
                   136
                   94
% identity
NCBI Description Zea mays 6-phosphogluconate dehydrogenase gene, partial cds
                   296328
Seq. No.
                   LIB3088-046-Q1-K1-E8
Seq. ID
                   BLASTX
Method
                   g3152605
NCBI GI
BLAST score
                   202
                   8.0e-20
E value
Match length
                   76
```

% identity 64

NCBI Description (AC004482) hypothetical protein [Arabidopsis thaliana]

296329 Seq. No.

LIB3088-046-Q1-K1-F11 Seq. ID

Method BLASTX

E value

Match length

57

```
q2842493
NCBI GI
BLAST score
                  155
                  3.0e-10
E value
                  51
Match length
% identity
NCBI Description (AL021749) predicted protein [Arabidopsis thaliana]
                  296330
Seq. No.
                  LIB3088-046-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2062405
BLAST score
                  180
                   3.0e-13
E value
                  74
Match length
                   47
% identity
                  (U79011) cytochrome b5 [Borago officinalis]
NCBI Description
                   296331
Seq. No.
                  LIB3088-046-Q1-K1-F9
Seq. ID
                   BLASTN
Method
                   q397395
NCBI GI
BLAST score
                   152
                   3.0e-80
E value
                   164
Match length
% identity
                   98
                  Z.mays MNB1b mRNA for DNA-binding protein
NCBI Description
                   296332
Seq. No.
                   LIB3088-046-Q1-K1-G5
Seq. ID
Method
                   BLASTX
                   q2736147
NCBI GI
BLAST score
                   150
E value
                   8.0e-10
Match length
                   39
                   79
% identity
                   (AF021804) fatty acid hydroxylase Fahlp [Arabidopsis
NCBI Description
                   thaliana] >gi 3132481 (AC003096) fatty acid hydroxylase,
                   FAH1 [Arabidopsis thaliana]
                   296333
Seq. No.
                   LIB3088-046-Q1-K1-H10
Seq. ID
                   BLASTX
Method
                   q2245036
NCBI GI
                   272
BLAST score
                   6.0e-24
E value
                   111
Match length
                   60
% identity
                   (Z97342) triacylglycerol lipase homolog [Arabidopsis
NCBI Description
                   thaliana]
                   296334
Seq. No.
                   LIB3088-047-Q1-K1-D2
Seq. ID
                   BLASTX
Method
                   g1574938
NCBI GI
                   235
BLAST score
                   1.0e-19
```

```
% identity
                  (U34726) superoxide dismutase 4 [Zea mays]
NCBI Description
                  296335
Seq. No.
                  LIB3088-047-Q1-K1-D5
Seq. ID
Method
                  BLASTX
                  q927577
NCBI GI
                  154
BLAST score
                  3.0e-10
E value
                  75
Match length
% identity
NCBI Description (U12927) alpha-galactosidase [Phaseolus vulgaris]
                  296336
Seq. No.
                  LIB3088-047-Q1-K1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3785995
BLAST score
                  510
                  7.0e-52
E value
                  114
Match length
% identity
                  (AC005499) unknown protein [Arabidopsis thaliana]
NCBI Description
                  296337
Seq. No.
                  LIB3088-047-Q1-K1-F3
Seq. ID
                  BLASTX
Method
                  g2632105
NCBI GI
                   405
BLAST score
E value
                   1.0e-39
Match length
                   96
% identity
                   78
                   (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]
NCBI Description
                   >gi 4539426 emb CAB38959.1 (AL049171) arginyl-tRNA
                   synthetase [Arabidopsis thaliana]
Seq. No.
                   296338
                   LIB3088-047-Q1-K1-H9
Seq. ID
```

```
      Seq. No.
      296338

      Seq. ID
      LIB3088-047-Q1-K1-H9

      Method
      BLASTX

      NCBI GI
      g2827139

      BLAST score
      191

      E value
      6.0e-15

      Match length
      71
```

% identity 56
NCBI Description (AF027172) cellulose synthase catalytic subunit

[Arabidopsis thaliana] >gi_4049343_emb_CAA22568_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis

thaliana]

Seq. No. 296339

Seq. ID LIB3088-049-Q1-K1-C2

Method BLASTX
NCBI GI g2632252
BLAST score 176
E value 1.0e-12
Match length 52
% identity 63

NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor]

% identity

70

```
296340
Seq. No.
                  LIB3088-049-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3927831
BLAST score
                  203
E value
                   8.0e-16
Match length
                  108
% identity
NCBI Description
                  (AC005727) similar to mouse ankyrin 3 [Arabidopsis
                  thaliana]
Seq. No.
                  296341
Seq. ID
                  LIB3088-049-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  g1705585
BLAST score
                  305
E value
                   5.0e-28
                  96
Match length
% identity
                   69
NCBI Description PHOSPHOENOLPYRUVATE CARBOXYLASE 2 (PEPCASE)
                  >gi_82710_pir__JH0667 phosphoenolpyruvate carboxylase (EC
                   4.1.1.31) C3-form - maize >gi 429149 emb CAA43709 (X61489)
                  phosphoenolpyruvate carboxylase [Zea mays]
Seq. No.
                   296342
                  LIB3088-049-Q1-K1-F7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2668741
BLAST score
                  151
                  1.0e-79
E value
Match length
                   227
% identity
                   92
NCBI Description Zea mays glycine-rich RNA binding protein (GRP) mRNA,
                  complete cds
Seq. No.
                   296343
Seq. ID
                   LIB3088-050-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                   g3309086
BLAST score
                   298
                   4.0e-27
E value
                   93
Match length
% identity
                   67
NCBI Description
                  (AF076253) calcineurin B-like protein 3 [Arabidopsis
                   thaliana]
Seq. No.
                   296344
Seq. ID
                  LIB3088-050-Q1-K1-C2
Method
                   BLASTX
NCBI GI
                   g729671
BLAST score
                   200
                   7.0e-16
E value
                   66
Match length
```

NCBI Description HISTONE H2A >gi 473603 (U08225) histone H2A [Zea mays]

```
296345
Seq. No.
                  LIB3088-050-Q1-K1-F4
Seq. ID
                  BLASTN
Method
                  g22484
NCBI GI
                  73
BLAST score
                  7.0e-33
E value
                  213
Match length
                  84
% identity
NCBI Description Z.mays RNA for superoxide dismutase Sod4A
                  29.6346
Seq. No.
                  LIB3088-050-Q1-K1-F5
Seq. ID
                  BLASTX
Method
                   g538607
NCBI GI
BLAST score
                   164
                   3.0e-14
E value
                   70
Match length
                   67
% identity
                   superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 4A - maize
NCBI Description
                   >gi_1885354 (U34727) superoxide dismutase 4A [Zea mays]
                   296347
Seq. No.
                   LIB3088-050-Q1-K1-F6
Seq. ID
                   BLASTX
Method
                   g4586265
NCBI GI
BLAST score
                   160
                   6.0e-11
E value
                   105
Match length
                   34
% identity
                   (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
                   296348
Seq. No.
                   LIB3088-050-Q1-K1-G10
Seq. ID
                   BLASTX
Method
                   g663070
NCBI GI
                   330
BLAST score
                   8.0e-31
E value
                   96
Match length
                   76
 % identity
                   (X77806) histone H4 [Pyrenomonas salina]
NCBI Description
                   296349
 Seq. No.
                   LIB3088-058-Q1-K1-A2
 Seq. ID
                   BLASTN
 Method
                   g22356
 NCBI GI
                   86
 BLAST score
                   1.0e-40
 E value
```

186 Match length 87 % identity

Maize mRNA for light-harvesting chlorophyll a/b binding NCBI Description

protein LHCP

296350 Seq. No.

LIB3088-058-Q1-K1-B4 Seq. ID

BLASTX Method NCBI GI g1346809 258 BLAST score



E value 1.0e-22 Match length 75 % identity 65

NCBI Description PATHOGEN-RELATED PROTEIN >gi_499074_emb_CAA34641_ (X16648)

pathogenesis related protein [Hordeum vulgare]

Seq. No. 296351

Seq. ID LIB3088-058-Q1-K1-B6

Method BLASTX
NCBI GI g3128209
BLAST score 228
E value 2.0e-19
Match length 117
% identity 54

NCBI Description (AC004077) unknown protein [Arabidopsis thaliana]

Seq. No. 296352

Seq. ID LIB3115-001-Q1-K1-B8

Method BLASTX
NCBI GI g461999
BLAST score 156
E value 3.0e-10
Match length 39
% identity 79

NCBI Description ELONGATION FACTOR G, CHLOROPLAST PRECURSOR (EF-G)

Seq. No. 296353

Seq. ID LIB3115-001-Q1-K1-C8

Method BLASTX
NCBI GI 94504771
BLAST score 318
E value 2.0e-29
Match length 85
% identity 66

NCBI Description integrin beta 4 binding protein

>gi_3122258_sp_P56537_IF6_HUMAN EUKARYOTIC TRANSLATION
INITIATION FACTOR 6 (EIF-6) (B4 INTEGRIN INTERACTOR) (CAB)
>gi_2809383 (AF022229) translation initiation factor 6
[Homo sapiens] >gi_2910997_emb_CAA72243_ (Y11435) b4
integrin interactor [Homo sapiens] >gi_3335506 (AF047433)

b(2)gcn homolog [Homo sapiens]

Seq. No. 296354

Seq. ID LIB3115-001-Q1-K1-D7

Method BLASTN
NCBI GI g531828
BLAST score 43
E value 5.0e-15
Match length 79
% identity 89

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 296355

Seq. ID LIB3115-001-Q1-K1-E3

Method BLASTX NCBI GI g2827704 BLAST score 200

```
E value
                  63
Match length
                  57
% identity
NCBI Description (AL021684) LRR-like protein [Arabidopsis thaliana]
                  296356
Seq. No.
                  LIB3115-001-Q1-K1-E6
Seq. ID
                  BLASTX
Method
                  q141597
NCBI GI
                  285
BLAST score
                   3.0e - 36
E value
                   150
Match length
                   62
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
                   296357
Seq. No.
                   LIB3115-001-Q1-K1-G9
Seq. ID
                   BLASTX
Method
                   g217909
NCBI GI
                   272
BLAST score
                   4.0e-24
E value
                   107
Match length
                   56
% identity
NCBI Description (D14044) glycolate oxidase [Cucurbita sp.]
                   296358
Seq. No.
Seq. ID
                   LIB3115-002-Q1-K1-A2
                   BLASTX
Method
NCBI GI
                   q2911076
BLAST score
                   151
                   1.0e-09
E value
                   45
Match length
% identity
                   (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                   296359
 Seq. No.
Seq. ID
                   LIB3115-002-Q1-K1-B1
                   BLASTN
Method
NCBI GI
                   q2665839
BLAST score
                   92
                   3.0e-44
E value
Match length
                   367
                   82
 % identity
                   Zea mays putative histone deacetylase RPD3 mRNA, complete
 NCBI Description
                   296360
 Seq. No.
                   LIB3115-002-Q1-K1-B9
 Seq. ID
                   BLASTX
 Method
                   g3386621
 NCBI GI
 BLAST score
                   241
                   2.0e-20
 E value
                   62
 Match length
                   71
 % identity
```

```
(AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
                  296361
Seq. No.
                  LIB3115-002-Q1-K1-F8
Seq. ID
Method
                  BLASTX
                  q2511574
NCBI GI
                  181
BLAST score
                  3.0e-13
E value
                  108
Match length
% identity
                   47
                   (Y13176) multicatalytic endopeptidase [Arabidopsis
NCBI Description
                   thaliana] >gi_3421075 (AF043520) 20S proteasome subunit
                   PAB1 [Arabidopsis thaliana]
                   296362
Seq. No.
                   LIB3115-002-Q1-K1-G2
```

Seq. ID LIB3115-002
Method BLASTN
NCBI GI g3043528
BLAST score 292
E value 1.0e-163
Match length 353
% identity 98

NCBI Description Zea mays mRNA for flavin containing polyamine oxidase (PAO)

296363 Seq. No. LIB3115-003-Q1-K1-F9 Seq. ID BLASTX Method q445612 NCBI GI 234 BLAST score E value 8.0e-20 90 Match length 53 % identity

NCBI Description ribosomal protein S19 [Solanum tuberosum]

 Seq. No.
 296364

 Seq. ID
 LIB3115-003-Q1-K1-G10

 Method
 BLASTX

 NCBI GI
 g3928150

 BLAST score
 222

 E value
 4.0e-18

E value 4.0eMatch length 66
% identity 61
NCBI Description (All)

NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]

Seq. No. 296365

Seq. ID LIB3115-005-Q1-K1-D12

Method BLASTX
NCBI GI g4185740
BLAST score 444
E value 4.0e-44
Match length 150
% identity 62

NCBI Description (AF079999) putative glutamate receptor [Arabidopsis

thaliana]

Seq. No. 296366

Seq. ID LIB3115-005-Q1-K1-F2

Match length

64

```
Method
                   q1122315
NCBI GI
BLAST score
                   200
                   8.0e-16
E value
Match length
                   97
% identity
                   51
                  (X94191) heat shock protein 17.0 [Pennisetum glaucum]
NCBI Description
                  296367
Seq. No.
                   LIB3115-005-Q1-K1-F9
Seq. ID
Method
                   BLASTN
                   q2623247
NCBI GI
                   81
BLAST score
E value
                   1.0e-37
                   157
Match length
                   98
% identity
NCBI Description Zea mays SU1 isoamylase (sugary1) gene, complete cds
                   296368
Seq. No.
                   LIB3115-005-Q1-K1-H11
Seq. ID
                   BLASTN
Method
NCBI GI
                   q22292
                   50
BLAST score
                   2.0e-19
E value
                   82
Match length
                   90
% identity
                   Z.mays mRNA for glycine-rich protein
NCBI Description
                   296369
Seq. No.
                   LIB3115-005-Q1-K1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2668742
BLAST score
                   422
                   2.0e-41
E value
Match length
                   86
                   95
% identity
                   (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                   296370
Seq. No.
                   LIB3115-006-Q1-K1-C10
Seq. ID
Method
                   BLASTX
                   g2088647
NCBI GI
                   195
BLAST score
                   6.0e-20
E value
                   98
Match length
                   54
% identity
                   (AF002109) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3158394 (AF036340) LRR-containing F-box protein
                   [Arabidopsis thaliana]
                   296371
Seq. No.
                   LIB3115-006-Q1-K1-C2
Seq. ID
                   BLASTX
Method
                   g730588
NCBI GI
BLAST score
                   187
E value
                   1.0e-14
```



```
% identity
NCBI Description MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L5
                  296372
Seq. No.
                  LIB3115-006-Q1-K1-C4
Seq. ID
                  BLASTX
Method
                  g4510385
NCBI GI
BLAST score
                  280
                  7.0e-25
E value
Match length
                  129
                  48
% identity
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
                  296373
Seq. No.
                  LIB3115-006-Q1-K1-D2
Seq. ID
Method
                  BLASTX
                  g4510385
NCBI GI
                  271
BLAST score
                  7.0e-24
E value
                  94
Match length
% identity
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
                  296374
Seq. No.
                  LIB3115-006-Q1-K1-E1
Seq. ID
Method
                  BLASTX
                  g4512651 <sup>25</sup>
NCBI GI
BLAST score
                  261
                   1.0e-22
E value
                   110
Match length
% identity
                   43
                  (AC007048) putative tyrosine transaminase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   296375
                   LIB3115-006-Q1-K1-F1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q1403523
BLAST score
                   42
E value
                   7.0e-15
Match length
                   66
                   91
% identity
NCBI Description Plasmid pIJ2581 tsr & glkA genes
                   296376
Seq. No.
                   LIB3115-006-Q1-K1-G3
Seq. ID
                   BLASTN
Method
                   q22537
NCBI GI
```

NCBI GI g22537
BLAST score 86
E value 9.0e-41
Match length 229
% identity 88

NCBI Description Maize mRNA for zein polypeptide (clone M6)

Seq. No. 296377

Seq. ID LIB3115-006-Q1-K1-H3

Method BLASTN

est.



```
q22445
NCBI GI
                  109
BLAST score
                  2.0e-54
E value
                  232
Match length
                  88
% identity
NCBI Description Zea mays ZMPMS1 gene for 19 kDa zein protein
                  296378
Seq. No.
                  LIB3115-007-Q1-K1-A3
Seq. ID
                  BLASTX
Method
                  q4490706
NCBI GI
                  320
BLAST score
                  9.0e-30
E value
                  81
Match length
% identity
NCBI Description (AL035680) putative protein [Arabidopsis thaliana]
                   296379
Seq. No.
                  LIB3115-007-Q1-K1-G5
Seq. ID
                  BLASTX
Method
                   g4455190
NCBI GI
                   143
BLAST score
                   5.0e-09
E value
                   90
Match length
% identity
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
                   296380
Seq. No.
                   LIB3115-007-Q1-K1-H5
Seq. ID
                   BLASTN
Method
                   g1944204
NCBI GI
                   40
BLAST score
E value
                   3.0e-13
Match length
                   56
                   93
% identity
NCBI Description Oryza sativa mRNA for RicMT, complete cds
                   296381
Seq. No.
Seq. ID
                   LIB3115-008-Q1-K1-A9
                   BLASTX
Method
                   g3860020
NCBI GI
 BLAST score
                   245
 E value
                   6.0e-21
 Match length
                   113
 % identity
                   (AF091091) unknown [Homo sapiens]
 NCBI Description
                   296382
 Seq. No.
                   LIB3115-008-Q1-K1-C8
 Seq. ID
                   BLASTN
 Method
                   g1377914
 NCBI GI
                   35
 BLAST score
 E value
                   9.0e-11
 Match length
                   59
 % identity
                   90
                   Cloning vector pEGFP-C1, complete sequence, enhanced green
 NCBI Description
                   fluorescent protein (egfp) and neomycin phosphotransferase
```

NCBI Description

```
genes, complete cds
```

```
296383
Seq. No.
                  LIB3115-008-Q1-K1-D10
Seq. ID
Method
                  BLASTX
                  g3298540
NCBI GI
BLAST score
                  167
                  4.0e-12
E value
                  64
Match length
% identity
NCBI Description (AC004681) unknown protein [Arabidopsis thaliana]
                  296384
Seq. No.
                  LIB3115-008-Q1-K1-D2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q82696
BLAST score
                  238
E value
                   3.0e-20
                   51
Match length
                   88
% identity
                  glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
                   296385
Seq. No.
                   LIB3115-008-Q1-K1-G7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1345881
                   280
BLAST score
                   5.0e-25
E value
Match length
                   98
                   56
% identity
                   CYTOCHROME B5 >gi_1076743_pir__S46307 cytochrome b5 - rice
NCBI Description
                   >qi 414705 emb CAA53366 (X75670) cytochrome b5 [Oryza
                   sativa]
                   296386
Seq. No.
                   LIB3115-008-Q1-K1-H9
Seq. ID
Method
                   BLASTX
                   g168701
NCBI GI
                   150
BLAST score
E value
                   1.0e-20
Match length
                   68
% identity
                   82
                   (M60837) zein [Zea mays]
NCBI Description
                   296387
Seq. No.
                   LIB3115-009-Q1-K1-B2
Seq. ID
Method
                   BLASTX
                   g517500
NCBI GI
                   154
BLAST score
                   2.0e-10
E value
                   75
Match length
% identity
                   56
```

OE17 protein [Pisum sativum]

(M87435) precursor of the oxygen evolving complex 17 kDa

protein [Zea mays] >gi_444338_prf__1906386A photosystem II

BLAST score

E value Match length 1.0e-10

78

```
296388
Seq. No.
Seq. ID
                  LIB3115-009-Q1-K1-B7
                  BLASTX
Method
                  g4539002
NCBI GI
                  200
BLAST score
                  1.0e-15
E value
Match length
                  75
% identity
NCBI Description (AL049481) putative protein [Arabidopsis thaliana]
                  296389
Seq. No.
                  LIB3115-009-Q1-K1-D3
Seq. ID
                  BLASTN
Method
                   g559535
NCBI GI
                   207
BLAST score
                   1.0e-113
E value
                   307
Match length
                   92
% identity
NCBI Description Z.mays mRNA for metallothionein
                   296390
Seq. No.
                   LIB3115-009-Q1-K1-E12
Seq. ID
                   BLASTN
Method
NCBI GI
                   g168704
                   72
BLAST score
                   1.0e-32
E value
                   128
Match length
                   89
% identity
NCBI Description Zea mays zein protein gene, complete cds
                   296391
Seq. No.
                   LIB3115-009-Q1-K1-F1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2832243
                   222
BLAST score
                   4.0e-18
E value
                   106
Match length
                   55
% identity
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
                   296392
Seq. No.
                   LIB3115-009-Q1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q520570
                   438
BLAST score
                   2.0e-43
E value
                   119
Match length
                   71
 % identity
                   (U12315) peroxidase [Cenchrus ciliaris]
 NCBI Description
                   296393
 Seq. No.
                   LIB3115-009-Q1-K1-G4
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g531829
                   158
```



```
% identity
NCBI Description
                  (U12390) beta-galactosidase alpha peptide [cloning vector
                  pSport1]
Seq. No.
                  296394
Seq. ID
                  LIB3115-010-Q1-K1-A1
Method
                  BLASTN
NCBI GI
                  q397395
BLAST score
                  97
E value
                  2.0e-47
Match length
                  157
% identity
                  90
                  Z.mays MNB1b mRNA for DNA-binding protein
NCBI Description
Seq. No.
                  296395
Seq. ID
                  LIB3115-010-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  q1173275
BLAST score
                  204
                  1.0e-18
E value
Match length
                  88
% identity
                  64
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S7
NCBI Description
                  >gi 2119068 pir S58630 ribosomal protein S7 - maize
                  chloroplast >gi_902274_emb_CAA60339_ (X86563) ribosomal
                  protein S7 [Zea mays] >gi_902298_emb_CAA60362_ (X86563)
                  ribosomal protein S7 [Zea mays]
Seq. No.
                  296396
                  LIB3115-010-Q1-K1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q998429
BLAST score
                  51
E value
                  3.0e-20
Match length
                  67
% identity
                  94
                  GRF1=general regulatory factor [Zea mays, XL80, Genomic,
NCBI Description
                  5348 nt]
                  296397
Seq. No.
Seq. ID
                  LIB3115-010-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g2668742
BLAST score
                  284
                  1.0e-25
E value
Match length
                  81
% identity
NCBI Description
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
```

Seq. No. 296398

Seq. ID LIB3115-010-Q1-K1-E12

Method BLASTN NCBI GI q998429 BLAST score 79 E value 1.0e-36 Match length 244 % identity 83



NCBI Description GRF1=general regulatory factor [Zea mays, XL80, Genomic, 5348 nt]

Seq. No. 296399

Seq. ID LIB3115-010-Q1-K1-F4

Method BLASTX
NCBI GI g82733
BLAST score 330
E value 8.0e-31
Match length 102
% identity 70

NCBI Description ubiquitin fusion protein UBF9 - maize >gi_168651 (M68937)

ubiquitin fusion protein [Zea mays] >gi_902527 (U29161)

ubiquitin fusion protein [Zea mays]

>gi_1589388_prf__2211240B ubiquitin fusion protein [Zea

mays]

Seq. No. 296400

Seq. ID LIB3115-010-Q1-K1-G1

Method BLASTN
NCBI GI 9454880
BLAST score 62
E value 3.0e-26
Match length 92
% identity 92

NCBI Description Rice mRNA for WSI724 protein induced by water stress,

complete cds

Seq. No. 296401

Seq. ID LIB3115-010-Q1-K1-G12

Method BLASTX
NCBI GI g2947070
BLAST score 155
E value 9.0e-11
Match length 55
% identity 58

NCBI Description (AC002521) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 296402

Seq. ID LIB3115-010-Q1-K1-H11

Method BLASTN
NCBI GI g1673455
BLAST score 40
E value 1.0e-13
Match length 56
% identity 93

NCBI Description Z.mays rubisco small subunit gene

Seq. No. 296403

Seq. ID LIB3115-010-Q1-K1-H3

Method BLASTX
NCBI GI g141603
BLAST score 269
E value 9.0e-24
Match length 80
% identity 70

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20) NCBI Description >gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize >gi 22529 emb CAA24723 (V01476) zein [Zea mays] Seq. No. 296404 Seq. ID LIB3115-011-Q1-K1-C7 Method BLASTN NCBI GI q168579 BLAST score 219 E value 1.0e-120 Match length 275 95 % identity NCBI Description Maize pyruvate, orthophosphate dikinase mRNA, complete cds Seq. No. 296405 LIB3115-011-Q1-K1-E3 Seq. ID Method BLASTX NCBI GI q551047 BLAST score 413 8.0e-41 E value Match length 97 % identity 80 (X79277) type II LHCI [Lolium temulentum] NCBI Description Seq. No. 296406 LIB3115-011-Q1-K1-H3 Seq. ID Method BLASTX g1778141 NCBI GI BLAST score 275 1.0e-24 E value 99 Match length 55 % identity (U66321) phosphate/phosphoenolpyruvate translocator NCBI Description precursor; PPT [Arabidopsis thaliana] 296407 Seq. No. LIB3115-012-Q1-K1-C3 Seq. ID Method BLASTX NCBI GI g1237250 BLAST score 222 2.0e-18 E value Match length 82 % identity 50 NCBI Description (X96784) cytochrome P450 [Nicotiana tabacum] 296408 Seq. No.

Seq. ID LIB3115-012-Q1-K1-C6

Method BLASTX
NCBI GI g2738248
BLAST score 298
E value 4.0e-27
Match length 95
% identity 63

NCBI Description (U97200) cobalamin-independent methionine synthase

[Arabidopsis thaliana]

Seq. No. 296409

```
LIB3115-012-Q1-K1-D10
Seq. ID
                  BLASTN
Method
                  g3355716
NCBI GI
BLAST score
                  154
                  3.0e-81
E value
                  191
Match length
                  95
% identity
NCBI Description Zea mays mRNA for seryl-tRNA synthetase
                  296410
Seq. No.
                  LIB3115-012-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                  g629862
NCBI GI
BLAST score
                  260
                  1.0e-22
E value
Match length
                  121
% identity
                   51
                  zein Zd1, 19K - maize >gi_535021_emb_CAA47640_ (X67203)
NCBI Description
                   zein Zd1 (19 kDa zein) [Zea mays]
                   296411
Seq. No.
                   LIB3115-013-P1-K1-A4
Seq. ID
                  BLASTX
Method
                   g2832247
NCBI GI
BLAST score
                   179
                   3.0e-13
E value
Match length
                   82
                   51
% identity
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]
                   296412
Seq. No.
                   LIB3115-013-P1-K1-C11
Seq. ID
                   BLASTX
Method
                   g2564920
NCBI GI
                   178
BLAST score
                   4.0e-13
E value
                   50
Match length
                   70
% identity
NCBI Description (AF025951) heat-shock cognate protein 70; Hsc70
                   [Dictyostelium discoideum]
                   296413
```

Seq. No.

LIB3115-013-P1-K1-D9 Seq. ID

BLASTX Method g4098880 NCBI GI 312 BLAST score 8.0e-29 E value 72 Match length 85 % identity

(U80970) heat shock protein 70B/SSB1 [Pneumocystis carinii NCBI Description

f. sp. hominis]

296414 Seq. No.

LIB3115-013-P1-K1-E5 Seq. ID

BLASTX Method g168586 NCBI GI BLAST score 226

```
E value 3.0e-19
Match length 56
% identity 80
```

NCBI Description (M58656) pyruvate, orthophosphate dikinase [Zea mays]

Seq. No. 296415

Seq. ID LIB3115-013-P1-K1-E9

Method BLASTX
NCBI GI g1723506
BLAST score 242
E value 2.0e-20
Match length 121
% identity 40

NCBI Description HYPOTHETICAL PROTEIN C19G10.16 IN CHROMOSOME I

>gi 1216256_emb_CAA93798_ (Z69909) hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 296416

Seq. ID LIB3115-013-P1-K1-F7

Method BLASTX
NCBI GI g4206306
BLAST score 590
E value 2.0e-61
Match length 119
% identity 94

NCBI Description (AF049110) prpol [Zea mays]

Seq. No. 296417

Seq. ID LIB3115-013-P1-K1-F8

Method BLASTX
NCBI GI g82660
BLAST score 211
E value 2.0e-17
Match length 62
% identity 68

NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment) >gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 296418

Seq. ID LIB3115-013-P1-K1-F9

Method BLASTX
NCBI GI g2506443
BLAST score 338
E value 1.0e-31
Match length 78
% identity 87

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,

CHLOROPLAST >gi 2117520 pir JQ1285

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde

3-phosphate dehydrogenase [Arabidopsis thaliana]

>gi 1402885 emb CAA66816 (X98130)

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) [Arabidopsis thaliana]

Seq. No. 296419



```
Seq. ID
                  LIB3115-014-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g115779
BLAST score
                  293
E value
                  4.0e-27
Match length
                  99
% identity
                  67
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB) (LHCP) >gi_81772_pir__JA0179 chlorophyll a/b-binding
                  protein precursor - soybean (fragment) >gi 169933 (M21396)
                  chlorophyll a/b-binding protein precursor [Glycine max]
                  296420
Seq. No.
Seq. ID
                  LIB3115-014-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  q2832246
BLAST score
                  218
E value
                  1.0e-17
Match length
                  103
% identity
                  50
NCBI Description
                  (AF031569) 22-kDa alpha zein 8 [Zea mays]
                  296421
Seq. No.
                  LIB3115-014-P1-K1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g236729
BLAST score
                  54
                  1.0e-21
E value
Match length
                  70
% identity
                  94
NCBI Description metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]
                  296422
Seq. No.
Seq. ID
                  LIB3115-014-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g20733
BLAST score
                  226
E value
                  3.0e-19
Match length
                  66
                  73
% identity
                  (X15188) precursor C-terminal fragment (AA -80 to 367)
NCBI Description
                  [Pisum sativum]
Seq. No.
                  296423
                  LIB3115-014-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4106577
BLAST score
                  206
E value
                  4.0e-16
Match length
                  76
% identity
                  (AL031866) ORF10, len: 268 aa, hutG, highly similar to
NCBI Description
```

Seq. No. 296424

in 260 aa overlap [Yersinia pestis]

N-formylglutamate amidohydrolase, from Pseudomonas putida AF032970 3, Fasta scores: opt: 1057, E(): 0, 59.6% identity



```
Seq. ID
                  LIB3115-014-P1-K1-D10
Method
                  BLASTN
NCBI GI
                  g2645165
BLAST score
                  49
E value
                  1.0e-18
Match length
                  73
% identity
                  92
NCBI Description Oryza sativa mRNA, similar to ribosomal protein
                  296425
Seq. No.
Seq. ID
                  LIB3115-014-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g1723177
BLAST score
                  215
E value
                  2.0e-17
Match length
                  82
% identity
                  50
                  HYPOTHETICAL 13.8 KD PROTEIN SLR0709
NCBI Description
                  >gi 1361332 pir S56682 hypothetical protein 2 -
                  Synechocystis sp >gi 1006602 dbj BAA10755 (D64005)
                  hypothetical protein [Synechocystis sp.]
                  >gi 1006750 emb CAA54600 (X77454) ORF2 [Synechocystis sp.]
Seq. No.
                  296426
                  LIB3115-014-P1-K1-E5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3819345
BLAST score
                  62
E value
                  3.0e-26
Match length
                  218
% identity
NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG0803
Seq. No.
                  296427
Seq. ID
                  LIB3115-015-P1-K1-C4
Method
                  BLASTN
NCBI GI
                  g532622
BLAST score
                  38
E value
                  6.0e-12
Match length
                  165
                  91
% identity
NCBI Description Zea mays lipase (LIP) mRNA, complete cds
Seq. No.
                  296428
                  LIB3115-015-P1-K1-F11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q22548
BLAST score
                  54
                  4.0e-22
E value
Match length
                  58
% identity
                  98
NCBI Description
                 Maize chimeric zein/beta-phaseolin gene 3'end region
```

Seq. No. 296429

Seq. ID LIB3115-015-P1-K1-F4

Method BLASTX NCBI GI g2262105

Seq. ID Method



```
BLAST score
                  6.0e-15
E value
Match length
                  61
                  61
% identity
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
                  296430
Seq. No.
                  LIB3115-015-P1-K1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g542176
                  252
BLAST score
                  1.0e-21
E value
                  111
Match length
                   51
% identity
NCBI Description probable finger protein WZF1 - wheat
                   >gi_485814_dbj_BAA03901_ (D16415) WZF1 [Triticum aestivum]
                   >gi_485816_dbj_BAA03902_ (D16416) WZF1 [Triticum aestivum]
                   296431
Seq. No.
                   LIB3115-015-P1-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g112994
BLAST score
                   212
                   1.0e-17
E value
                   46
Match length
                   91
% identity
                   GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                   >gi_82685_pir__S04536 embryonic abundant protein,
                   glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                   ABA-inducible gene protein [Zea mays]
                   >gi 226091 prf 1410284A abscisic acid inducible gene [Zea
                   mays]
                   296432
Seq. No.
                   LIB3115-016-P1-K1-B4
Seq. ID
                   BLASTX
Method
                   g4455232
NCBI GI
                   236
BLAST score
                   3.0e-21
E value
                   88
Match length
% identity
                   (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
                   296433
Seq. No.
                   LIB3115-016-P1-K1-D12
Seq. ID
                   BLASTX
Method
                   g2145477
NCBI GI
                   229
BLAST score
                   1.0e-26
E value
                   123
Match length
                   58
 % identity
                   (X91406) phosphoenolpyruvate carboxylase [Tillandsia
NCBI Description
                   usneoides]
                   296434
 Seq. No.
```

41521

LIB3115-016-P1-K1-F5

BLASTX

```
g2612826
NCBI GI
                  181
BLAST score
                  2.0e-13
E value
                  57
Match length
                  68
% identity
                  (AJ002731) ribosomal protein s30 [Schizosaccharomyces
NCBI Description
                  pombe] >gi 4581509 emb_CAA17057.2_ (AL021839) ribosomal
                  protein s30 [Schizosaccharomyces pombe]
                  296435
Seq. No.
                  LIB3115-017-P1-K1-A8
Seq. ID
                  BLASTN
Method
                  g168436
NCBI GI
                  56
BLAST score
                  6.0e-23
E value
Match length
                  60
                  98
% identity
NCBI Description Zea mays catalase (Cat3) gene, complete cds
                  296436
Seq. No.
                  LIB3115-017-P1-K1-C1
Seq. ID
                  BLASTX
Method
                  g1710752
NCBI GI
                  217
BLAST score
                  1.0e-17
E value
                  102
Match length
% identity
                   45
                  PROBABLE 40S RIBOSOMAL PROTEIN S25 >gi 1118105 (U41558)
NCBI Description
                   coded for by C. elegans cDNA CEMSA31R; coded for by C.
                   elegans cDNA yk116e4.5; coded for by C. elegans cDNA
                   yk94b11.5; coded for by C. elegans cDNA yk90d1.5; coded for
                   by C. elegans cDNA CEESK93F; coded for by C. elegans cDNA
                   yk94b1
                   296437
Seq. No.
                   LIB3115-017-P1-K1-D3
Seq. ID
                   BLASTX
Method
                   g4582468
NCBI GI
                   188
BLAST score
                   3.0e-14
E value
Match length
                   65
                   58
% identity
                   (AC007071) putative 40S ribosomal protein; contains
NCBI Description
                   C-terminal domain [Arabidopsis thaliana]
                   296438
Seq. No.
                   LIB3115-017-P1-K1-E11
Seq. ID
                   BLASTN
Method
                   q3550984
NCBI GI
                   71
BLAST score
E value
                   1.0e-31
                   151
Match length
                   87
 % identity
```

LIB3115-017-P1-K1-E4 Seq. ID

NCBI Description Oryza sativa mRNA for OsS5a, complete cds



```
BLASTX
Method
                   g1835731
NCBI GI
                   195
BLAST score
E value
                   6.0e-15
Match length
                   72
                   56
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                   296440
Seq. No.
                   LIB3115-017-P1-K1-E5
Seq. ID
                   BLASTX
Method
                   q1709619
NCBI GI
BLAST score
                   214
                   3.0e-17
E value
Match length
                   75
% identity
                   64
                   PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) /
NCBI Description
                   DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE
                   (GLYCOSYLATION SITE-BINDING CHAIN) (GSBP)
                   >gi_2146814_pir__S69181 protein disulfide isomerase (EC
                   5.3.4.1) precursor - maize >gi_625148 (L39014) protein
                   disulfide isomerase [Zea mays]
                   296441
Seq. No.
                   LIB3115-018-P1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3522929
BLAST score
                   438
                   1.0e-43
E value
Match length
                   97
% identity
                    (AC002535) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                    [Arabidopsis thaliana] >gi 3738279 (AC005309) putative
                   dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
                    296442
Seq. No.
                   LIB3115-018-P1-K1-A7
Seq. ID
                   BLASTX
Method
                   g3522929
NCBI GI
                    165
BLAST score
                    1.0e-11
E value
Match length
                    46
                    72
% identity
                    (AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative
NCBI Description
                    dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
                    296443
Seq. No.
                    LIB3115-018-P1-K1-B7
Seq. ID
                    BLASTX
Method
                    g2827992
NCBI GI
BLAST score
                    273
                    4.0e-24
E value
                    89
Match length
                    54
% identity
                   (AF034743) UDP-glucuronosyltransferase [Pisum sativum]
NCBI Description
```

```
296444
Seq. No.
                  LIB3115-018-P1-K1-F10
Seq. ID
Method
                  BLASTN
                  g3450892
NCBI GI
BLAST score
                  55
                  3.0e-22
E value
                  75
Match length
                  93
% identity
NCBI Description Avena fatua ras-like small monomeric GTP-binding protein
                  (SAR1) mRNA, complete cds
                  296445
Seq. No.
                  LIB3115-018-P1-K1-G8
Seq. ID
                  BLASTX
Method
                  q4455254
NCBI GI
BLAST score
                  154
E value
                   3.0e-10
                  72
Match length
% identity
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]
                   296446
Seq. No.
                   LIB3115-019-P1-K1-C8
Seq. ID
                   BLASTX
Method
                   g1750404
NCBI GI
                   169
BLAST score
E value
                   6.0e-12
                   60
Match length
% identity
                   (U80953) Similar to 40S ribosomal protein S29; coded for by
NCBI Description
                   C. elegans cDNA cm10c2; coded for by C. elegans cDNA
                   yk61d8.5; coded for by C. elegans cDNA yk107e8.5; coded for
                   by C. elegans cDNA CEESF55F; coded for by C. elegans cDNA
                   yk107e8.3;
                   296447
Seq. No.
                   LIB3115-020-P1-K1-A2
Seq. ID
                   BLASTX
Method
                   g551047
NCBI GI
                   215
BLAST score
                   8.0e-18
E value
Match length
                   58
                   72
 % identity
                   (X79277) type II LHCI [Lolium temulentum]
NCBI Description
                   296448
Seq. No.
                   LIB3115-020-P1-K1-B7
 Seq. ID
                   BLASTX
Method
                   g2149640
NCBI GI
                   210
BLAST score
                   3.0e-17
E value
 Match length
                   65
                   63
```

% identity

NCBI Description

LIB3115-020-P1-K1-B8 Seq. ID

(U91995) Argonaute protein [Arabidopsis thaliana]



```
Method
                  BLASTX
NCBI GI
                  q730536
BLAST score
                  164
                  2.0e-11
E value
                  76
Match length
% identity
                  46
                  60S RIBOSOMAL PROTEIN L23 >gi 310933 (L18915) 60S ribosomal
NCBI Description
                  protein subunit L17 [Nicotiana tabacum]
Seq. No.
                  296450
Seq. ID
                  LIB3115-020-P1-K1-D5
                  BLASTX
Method
NCBI GI
                  g2494417
BLAST score
                  254
                  4.0e-22
E value
                  75
Match length
                  72
% identity
                  FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC
NCBI Description
                  (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi 1364071 pir S57717 fructose-1, 6-bisphosphatase (EC
                  3.1.3.11) - sugarcane hybrid H65-7052
                  >gi 895909 emb CAA61409.1 (X89006) fructose-1,
                  6-bisphosphatase [Saccharum hybrid cultivar H65-7052]
Seq. No.
                  296451
Seq. ID
                  LIB3115-020-P1-K1-E5
Method
                  BLASTN
NCBI GI
                  q2431766
BLAST score
                  115
                  7.0e-58
E value
Match length
                  190
                  92
% identity
                  Zea mays acidic ribosomal protein P3a (rpp3a) mRNA,
NCBI Description
                  complete cds
                  296452
Seq. No.
Seq. ID
                  LIB3115-021-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g266578
BLAST score
                  241
E value
                  2.0e-20
Match length
                  56
                  77
% identity
NCBI Description
                  METALLOTHIONEIN-LIKE PROTEIN 1 >gi 100898 pir S17560
                  metallothionein-like protein - maize >gi 236730 bbs 57629
                  (S57628) metallothionein homologue [Zea mays, Peptide, 76
                  aa] [Zea mays] >gi 559536 emb CAA57676 (X82186)
                  metallothionein- like protein [Zea mays]
                  >gi 228095 prf 1717215A metallothionein-like protein [Zea
                  mays]
                  296453
```

LIB3115-021-P1-K1-D9 Seq. ID

Method BLASTX NCBI GI q3080425 BLAST score 287 E value 6.0e-26



```
Match length 71
% identity 83
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 296454
Seq. ID LIB3115-021-P1-K1-G9
Method BLASTX
NCBI GI g3914465
BLAST score 187
```

NCBI GI g3914465
BLAST score 187
E value 3.0e-14
Match length 83
% identity 54

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)

>gi 2981207 (AF052076) photosystem I complex PsaH subunit

precursor [Zea mays]

Seq. No. 296455 Seq. ID LIB3115-021-P1-K1-H1

Method BLASTX
NCBI GI g115786
BLAST score 231
E value 2.0e-19
Match length 61
% identity 79

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB) (LHCP) >gi_82680_pir__A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea

mays]

Seq. No. 296456

Seq. ID LIB3115-021-P1-K1-H3

Method BLASTX
NCBI GI g2827548
BLAST score 409
E value 4.0e-40
Match length 131
% identity 56

NCBI Description (AL021635) cytochrome P450 - like protein [Arabidopsis

thaliana]

Seq. No. 296457

Seq. ID LIB3115-022-P1-K1-C2

Method BLASTX
NCBI GI g2911043
BLAST score 176
E value 8.0e-13
Match length 75
% identity 43

NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 296458

Seq. ID LIB3115-022-P1-K1-E9

Method BLASTX
NCBI GI g166410
BLAST score 379
E value 1.0e-36

41526



```
Match length
% identity
                    66
                   (L07291) Alfin-1 [Medicago sativa]
NCBI Description
Seq. No.
                    296459
                    LIB3115-023-P1-K1-B8
Seq. ID
                    BLASTX
Method
                    q485518
NCBI GI
                    312
BLAST score
                    6.0e-29
E value
Match length
                    60
                    100
% identity
                    ubiquitin / ribosomal protein CEP52 - rice
NCBI Description
                    >gi_303857_dbj_BAA02154_ (D12629) ubiquitin/ribosomal
                    polyprotein [Oryza sativa]
                    296460
Seq. No.
                    LIB3115-023-P1-K1-E10
Seq. ID
                    BLASTX
Method
                    q4115913
NCBI GI
BLAST score
                    150
                    3.0e-10
E value
                    61
Match length
                    43
% identity
                    (AF118222) contains similarity to Iron/Ascorbate family of
NCBI Description
                    oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88, N=1) [Arabidopsis thaliana] >gi_4539409_emb_CAB40042.1_
                     (AL049524) putative flavanone 3-beta-hydroxylase
                     [Arabidopsis thaliana]
                    296461
Sea. No.
                    LIB3115-023-P1-K1-G2
Seq. ID
                    BLASTN
Method
                    g168436
NCBI GI
                     61
 BLAST score
                     7.0e-26
 E value
 Match length
                     111
                     90
 % identity
 NCBI Description Zea mays catalase (Cat3) gene, complete cds
                     296462
 Seq. No.
                     LIB3115-023-P1-K1-H10
 Seq. ID
                     BLASTX
 Method
                     q4506621
 NCBI GI
                     157
 BLAST score
                     4.0e-11
 E value
                     49
 Match length
                     63
 % identity
                     ribosomal protein L26 >gi_400990_sp_Q02877_RL26_HUMAN 60S
 NCBI Description
                     RIBOSOMAL PROTEIN L26 >gi 423068 pir S33713 ribosomal protein L26 - human >gi 1071990 pir S48864 gene L26
                     protein - mouse >gi_36115_emb_CAA49189_ (X69392) ribosomal
                     protein L26 [Homo sapiens] >gi_565624_emb_CAA56716_
```

Seq. ID LIB3115-024-P1-K1-A11

(X80699) L26 [Mus musculus]



```
BLASTX
Method
                  q3256035
NCBI GI
BLAST score
                  151
                  8.0e-10
E value
Match length
                  53
                  51
% identity
NCBI Description (Y14274) putative serine/threonine protein kinase [Sorghum
                  bicolor]
                  296464
Seq. No.
                  LIB3115-024-P1-K1-A9
Seq. ID
                  BLASTX
Method
                  q3327033
NCBI GI
                  284
BLAST score
E value
                  2.0e-25
Match length
                  79
% identity
                  71
NCBI Description (Z68198) 40S ribosomal protein [Schizosaccharomyces pombe]
                   296465
Seq. No.
                  LIB3115-024-P1-K1-E10
Seq. ID
Method
                   BLASTX
                   g544421
NCBI GI
                   159
BLAST score
                   1.0e-10
E value
                   39
Match length
% identity
                   GLYCINE-RICH RNA-BINDING PROTEIN 1 >gi_485420_pir__S12311
NCBI Description
                   glycine-rich RNA-binding protein (clone S1) - sorghum
                   (fragment) >gi_21623_emb_CAA40863_ (X57663) glycine-rich
                   RNA-binding protein [Sorghum bicolor]
                   296466
Seq. No.
                   LIB3115-025-P1-K1-B12
Seq. ID
                   BLASTX
Method
                   g4559358
NCBI GI
 BLAST score
                   176
                   1.0e-12
 E value
                   50
 Match length
                   68
 % identity
                   (AC006585) putative steroid binding protein [Arabidopsis
 NCBI Description
                   thaliana]
                   296467
 Seq. No.
                   LIB3115-025-P1-K1-B3
 Seq. ID
                   BLASTN
 Method
                   g1272684
 NCBI GI
                   50
 BLAST score
                   4.0e-19
 E value
                   62
 Match length
                   97
 % identity
 NCBI Description Z.mays mRNA for acetyl CoA carboxylase (partial)
                   296468
 Seq. No.
                   LIB3115-025-P1-K1-B6
 Seq. ID
                   BLASTX
 Method
```

41528

g4574320

NCBI GI



BLAST score 164 E value 3.0e-11 Match length 67 % identity 57

NCBI Description (AF117224) wound-induced protein WI12 [Mesembryanthemum

crystallinum]

Seq. No. 296469

Seq. ID LIB3115-025-P1-K1-C8

Method BLASTX
NCBI GI g3122625
BLAST score 260
E value 6.0e-23
Match length 90
% identity 59

NCBI Description PROBABLE 26S PROTEASE REGULATORY SUBUNIT S10B >gi_2394434

(AF024493) strong similarity to the AAA family of ATPases

[Caenorhabditis elegans]

Seq. No. 296470

Seq. ID LIB3115-025-P1-K1-F6

Method BLASTX
NCBI GI g466172
BLAST score 173
E value 2.0e-12
Match length 34
% identity 100

NCBI Description GTP-BINDING PROTEIN YPTM2 >gi_283056_pir_B38202 ypt family

- maize >gi_287835_emb_CAA44919_ (X63278) yptm2 [Zea mays]

Seq. No. 296471

Seq. ID LIB3115-026-P1-K1-A11

Method BLASTX
NCBI GI g1352681
BLAST score 473
E value 1.0e-47
Match length 113
% identity 80

NCBI Description PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir__S55457

phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis

thaliana >gi_633028_dbj_BAA07287_ (D38109) protein

phosphatase 2C [Arabidopsis thaliana]

Seq. No. 296472

Seq. ID LIB3115-026-P1-K1-A2

Method BLASTN
NCBI GI g1935910
BLAST score 175
E value 8.0e-94
Match length 247
% identity 93

NCBI Description Zea mays lethal leaf-spot 1 (lls1) gene, partial cds

Seq. No. 296473

Seq. ID LIB3115-026-P1-K1-H2

Method BLASTN NCBI GI g170784

41529

```
BLAST score
                  4.0e-10
E value
                  59
Match length
% identity
                  90
NCBI Description Wheat ubiquitin carrier protein (UBC1) mRNA, complete cds
                  296474
Seq. No.
                  LIB3115-026-P1-K1-H3
Seq. ID
                  BLASTX
Method
                  g548603
NCBI GI
BLAST score
                  345
                  1.0e-32
E value
                   106
Match length
                   70
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                   >gi 478404 pir JQ2247 photosystem I chain D precursor -
                  barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
                   296475
Seq. No.
                   LIB3115-028-P1-K1-A6
Seq. ID
                   BLASTN
Method
NCBI GI
                   g22312
                   117
BLAST score
                   3.0e-59
E value
                   177
Match length
                   92
% identity
                   Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                   abscisic acid)
                   296476
Seq. No.
                   LIB3115-028-P1-K1-B10
```

Seq. ID

Method BLASTX g4099090 NCBI GI BLAST score 219 3.0e-18 E value Match length 63 % identity 63

(U83178) unknown [Arabidopsis thaliana] NCBI Description

296477 Seq. No.

LIB3115-028-P1-K1-B4 Seq. ID

Method BLASTX g4335745 NCBI GI 275 BLAST score 2.0e-24 E value 133 Match length % identity 41

(AC006284) putative hydrolase (contains an NCBI Description

esterase/lipase/thioesterase active site serine domain

(prosite: PS50187) [Arabidopsis thaliana]

296478 Seq. No.

LIB3115-028-P1-K1-D8 Seq. ID

BLASTX Method g1173071 NCBI GI 303 BLAST score



```
1.0e-27
E value
                                                                             40
                   113
Match length
                   60
% identity
                   60S ACIDIC RIBOSOMAL PROTEIN P2 (MINOR ALLERGEN ALT A 6)
NCBI Description
                   (ALT A VI) >gi_1085614_pir__S43109 acidic ribosomal protein
                  P2 - Alternaria alternata >gi_467617_emb_CAA55066_ (X78222)
                  minor allergen, ribosomal protein [Alternaria alternata]
                   296479
Seq. No.
                   LIB3115-028-P1-K1-E3
Seq. ID
Method
                   BLASTX
                   g2245138
NCBI GI
                   542
BLAST score
                   1.0e-55
E value
                   136
Match length
% identity
                   71
NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]
                   296480
Seq. No.
                   LIB3115-028-P1-K1-F12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2507443
                   221
BLAST score
                   2.0e-18
E value
                   72
Match length
                   62
% identity
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) (23
NCBI Description
                   KD CALLUS PROTEIN) (P23) >gi_1675196 (L47968) callus
                   protein P23 [Pisum sativum]
                   296481
Seq. No.
                   LIB3115-028-P1-K1-G3
Seq. ID
                   BLASTN
Method
                   g2331140
NCBI GI
BLAST score
                   43
                   5.0e-15
E value
                   109
Match length
                   85
 % identity
                   Oryza sativa water-stress inducible protein (WSI) mRNA,
NCBI Description
                   complete cds
                    296482
 Seq. No.
                   LIB3115-028-P1-K1-H8
 Seq. ID
                   BLASTX
 Method
                    g141608
 NCBI GI
                    293
 BLAST score
                    1.0e-26
 E value
                    94
Match length
                    67
 % identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655
 NCBI Description
                    zein, 19K - maize >gi_22446_emb_CAA3765\overline{1}_ (X53\overline{5}82) \overline{1}9 kDa
                    zein [Zea mays]
```

Seq. ID LIB3115-029-P1-K1-F7

Method BLASTX NCBI GI g2459430

41531

NCBI Description



```
BLAST score
                  2.0e-18
E value
                  91
Match length
                   48
% identity
NCBI Description (AC002332) putative CUC2 protein [Arabidopsis thaliana]
                  296484
Seq. No.
                  LIB3115-030-P1-K1-A10
Seq. ID
                  BLASTX
Method
                   g4204265
NCBI GI
                   168
BLAST score
                   1.0e-11
E value
Match length
                   66
                   47
% identity
NCBI Description (AC005223) 45643 [Arabidopsis thaliana]
                   296485
Seq. No.
                   LIB3115-030-P1-K1-A12
Seq. ID
                   BLASTX
Method
                   q2245066
NCBI GI
BLAST score
                   166
                   8.0e-12
E value
                   80
Match length
                   45
% identity
NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]
                   296486
Seq. No.
                   LIB3115-030-P1-K1-A4
Seq. ID
Method
                   BLASTX
                   g2982297
NCBI GI
                   209
BLAST score
                   1.0e-16
E value
                   69
Match length
                   62
% identity
NCBI Description (AF051233) KIAA0107-like protein [Picea mariana]
                   296487
 Seq. No.
                   LIB3115-030-P1-K1-B12
 Seq. ID
                   BLASTN
 Method
                   g2668739
 NCBI GI
                   64
 BLAST score
                   2.0e-27
 E value
                   152
 Match length
                   86
 % identity
                   Zea mays translation initiation factor GOS2 (TIF) mRNA,
 NCBI Description
                   complete cds
                   296488
 Seq. No.
                   LIB3115-030-P1-K1-B4
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                    g2245066
                    203
 BLAST score
 E value
                    3.0e-16
                    85
 Match length
 % identity
                   (Z97342) Beta-Amylase [Arabidopsis thaliana]
```

Match length

% identity

105 72



```
Seq. No.
Seq. ID
                   LIB3115-030-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   q2781345
BLAST score
                   245
E value
                   5.0e-21
Match length
                   80
% identity
                   55
                   (AC003113) F2401.2 [Arabidopsis thaliana]
NCBI Description
                   296490
Seq. No.
                   LIB3115-030-P1-K1-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g445612
BLAST score
                   192
E value
                   1.0e-14
Match length
                   73
% identity
                   53
                  ribosomal protein S19 [Solanum tuberosum]
NCBI Description
                   296491
Seq. No.
                   LIB3115-030-P1-K1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g120657_
BLAST score
                   155
                   3.0e-10
E value
Match length
                   67
% identity
                   51
NCBI Description
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
                   CHLOROPLAST >gi_66024_pir__DEZMG3 glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                   (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                   maize >gi_168479 (M18976) glyceraldehyde-3-phosphate
                   dehydrogenase [Zea mays] >gi_763035_emb_CAA33455_ (X15408)
                   glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
Seq. No.
                   296492
Seq. ID
                   LIB3115-030-P1-K1-F10
                   BLASTX
Method
NCBI GI
                   g548774
BLAST score
                   220
E value
                   8.0e-18
Match length
                   118
% identity
                   65
                   60S RIBOSOMAL PROTEIN L7A >qi 542158 pir S38360 ribosomal
NCBI Description
                   protein L7a - rice >gi 303855 dbj BAA02156 (D12631)
                   ribosomal protein L7A [Oryza sativa]
Seq. No.
                   296493
                   LIB3115-030-P1-K1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g68029
                   390
BLAST score
                   1.0e-37
E value
```

NCBI Description phosphoenolpyruvate carboxylase (EC 4.1.1.31) - maize

>gi_22408_emb_CAA33317_ (X15239) PEP carboxylase [Zea mays]
>gi_228619_prf__1807332A phosphoenolpyruvate carboxylase
[Zea mays]

 Seq. No.
 296494

 Seq. ID
 LIB3115-030-P1-K1-H7

 Method
 BLASTX

 NCBI GI
 32267595

NCBI GI g2267595
BLAST score 181
E value 3.0e-13
Match length 52
% identity 65

NCBI Description (AF009412) plastocyanin precursor [Oryza sativa]

Seq. No. 296495

Seq. ID LIB3115-031-P1-K1-A12

Method BLASTX
NCBI GI g2944417
BLAST score 304
E value 1.0e-27
Match length 88
% identity 64

% identity 64 NCBI Description (AF049881) peroxidase FLXPER4 [Linum usitatissimum]

Seq. No. 296496

Seq. ID LIB3115-031-P1-K1-G2

Method BLASTX
NCBI GI g1171866
BLAST score 158
E value 9.0e-11
Match length 54
% identity 57

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (COMPLEX I-20KD) (CI-20KD) >gi 629601_pir__S48826 NADH

(COMPLEX I-20KD) (CI-20KD) >g1_629601_p1r___S48826 NADA dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild cabbage >gi_562282_emb_CAA57725_ (X82274) PSST subunit of

NADH: ubiquinone oxidoreductase [Brassica oleracea]

Seq. No. 296497

Seq. ID LIB3115-031-P1-K1-G3

Method BLASTX
NCBI GI g3059131
BLAST score 259
E value 2.0e-22
Match length 94
% identity 50

NCBI Description (AJ000478) cytochrome P450 [Helianthus tuberosus]

Seq. No. 296498

Seq. ID LIB3115-032-P1-K1-D11

Method BLASTN
NCBI GI g2326946
BLAST score 65
E value 5.0e-28
Match length 125
% identity 88

NCBI Description Z.mays mRNA for chlorophyll a/b-binding protein CP29

Method

NCBI GI

BLASTX

g3928519



```
296499
Seq. No.
                  LIB3115-032-P1-K1-D5
Seq. ID
Method
                  BLASTX
                  q4220594
NCBI GI
BLAST score
                  229
                  6.0e-19
E value
                  96
Match length
                  47
% identity
                  (AB011264) nicochianamine synthase 3 [Hordeum vulgare]
NCBI Description
                  296500
Seq. No.
                  LIB3115-034-P1-K2-A1
Seq. ID
Method
                  BLASTX
                  g168701
NCBI GI
BLAST score
                  369
E value
                  2.0e-35
Match length
                  100
% identity
                  80
NCBI Description
                  (M60837) zein [Zea mays]
                  296501
Seq. No.
                  LIB3115-034-P1-K2-A2
Seq. ID
Method
                  BLASTN
                  g168700
NCBI GI
BLAST score
                  62
E value
                  2.0e-26
Match length
                  152
% identity
                  85
NCBI Description Z.mays zein mRNA, complete cds
Seq. No.
                  296502
Seq. ID
                  LIB3115-034-P1-K2-C5
                  BLASTN
Method
NCBI GI
                  g168521
BLAST score
                  44
E value
                  1.0e-15
Match length
                  84
                  88
% identity
                  Maize glyceraldehyde-3-phosphate dehydrogenase, 3' end
NCBI Description
                  296503
Seq. No.
Seq. ID
                  LIB3115-034-P1-K2-D5
Method
                  BLASTX
NCBI GI
                  q100907
BLAST score
                  285
                  1.0e-25
E value
Match length
                  91
% identity
                  63
                  pathogenesis-related protein 1 - maize
NCBI Description
                  >gi 228409 prf 1803521A pathogenesis-related protein 1
                  [Zea mays]
                  296504
Seq. No.
                  LIB3115-034-P1-K2-D7
Seq. ID
```

41535

```
BLAST score
                  1.0e-10
E value
                  45
Match length
                  69
% identity
                 (AB011670) wpk4 protein kinase [Triticum aestivum]
NCBI Description
Seq. No.
                  296505
Seq. ID
                  LIB3115-034-P1-K2-E4
                  BLASTN
Method
NCBI GI
                  g248336
BLAST score
                  99
                  2.0e-48
E value
                  247
Match length
% identity
                  89
NCBI Description polyubiquitin [maize, Genomic, 3841 nt]
                  296506
Seq. No.
                  LIB3115-034-P1-K2-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1350930
BLAST score
                  375
                  3.0e-36
E value
Match length
                  96
% identity
                  74
NCBI Description 40S RIBOSOMAL PROTEIN S13
                  296507
Seq. No.
                  LIB3115-036-P1-K2-B3
Seq. ID
Method
                  BLASTX
                  g2708745
NCBI GI
```

Method BLASTX
NCBI GI g2708745
BLAST score 458
E value 6.0e-46
Match length 114
% identity 79

NCBI Description (AC003952) putative calcium-dependent ser/thr protein

kinase [Arabidopsis thaliana]

Seq. No. 296508

Seq. ID LIB3115-036-P1-K2-C1

Method BLASTX
NCBI GI g3820648
BLAST score 143
E value 2.0e-09
Match length 56
% identity 55

NCBI Description (Y12636) allene oxide synthase [Arabidopsis thaliana]

Seq. No. 296509

Seq. ID LIB3115-036-P1-K2-C12

Method BLASTN
NCBI GI g606814
BLAST score 195
E value 1.0e-105
Match length 319
% identity 91

NCBI Description Zea mays Golden Bantam carbonic anhydrase mRNA, complete

cds



```
Seq. No.
                     296510
  Seq. ID
                     LIB3115-038-P1-K2-G5
  Method
                     BLASTX
  NCBI GI
                     g2739387
                     202
  BLAST score
  E value
                     8.0e-16
  Match length
                     125
                     36
  % identity
  NCBI Description (AC002505) hypothetical protein [Arabidopsis thaliana]
                     296511
  Seq. No.
                     LIB3115-038-P1-K2-H10
  Seq. ID
                     BLASTX
  Method
  NCBI GI
                     q131147
  BLAST score
                     337
  E value
                     8.0e-32
  Match length
                     99
  % identity
                     PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2
  NCBI Description
                     >qi 72675 pir A2LVP7 photosystem I P700 apoprotein A2 -
                     liverwort (Marchantia polymorpha) chloroplast
                     >gi_11671_emb_CAA28084_ (X04465) psaB [Marchantia
                     polymorpha]
                     296512
  Seq. No.
                     LIB3115-039-P1-K2-B1
  Seq. ID
  Method
                     BLASTX
                     g1076653
  NCBI GI
  BLAST score
                     144
  E value
                     5.0e-09
  Match length
                     62
  % identity
                     45
                     water-stress-inducible protein DS2 - Chaco potato
  NCBI Description
                     >gi 607905 (U12439) abscisic stress ripening protein
                     [Solanum chacoense]
Seq. No.
                     296513
  Seq. ID
                     LIB3115-039-P1-K2-D5
                     BLASTN
  Method
  NCBI GI
                     q2331300
  BLAST score
                     105
  E value
                     3.0e-52
  Match length
                     177
                     92
  % identity
                     Zea mays ribosomal protein S4 type I (rps4) mRNA, complete
  NCBI Description
                     cds
  Seq. No.
                     296514
  Seq. ID
                     LIB3115-039-P1-K2-G11
  Method
                     BLASTN
  NCBI GI
                     q12429
  BLAST score
                     299
  E value
                     1.0e-167
                     363
  Match length
```

96

NCBI Description Maize chloroplast ORF170 and psaA gene

% identity

% identity

36



```
Seq. No.
                  296515
Seq. ID
                  LIB3116-001-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  g729304
BLAST score
                  149
                  6.0e-22
E value
Match length
                  87
                  58
% identity
                  PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC)
NCBI Description
                  >gi 479730 pir S35258 pyruvate decarboxylase (EC 4.1.1.1)
                  2 - maize (fragment) >gi 22763 emb CAA79818 (Z21721)
                  pyruvate decarboxylase [Zea mays] >gi 217970 dbj BAA03353_
                  (D14456) Pyruvate Decarboxylase [Zea mays]
Seq. No.
                  296516
                  LIB3116-001-Q1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1850968
BLAST score
                  165
E value
                  1.0e-11
Match length
                  101
% identity
                  38
                 (U79733) Hs1pro-1 [Beta procumbens]
NCBI Description
                  296517
Seq. No.
                  LIB3116-001-Q1-K1-G1
Seq. ID
Method
                  BLASTN
                  g4538990
NCBI GI
BLAST score
                  55
E value
                  3.0e-22
Match length
                  83
% identity
                  92
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19
                  (ESSA project)
Seq. No.
                  296518
Seq. ID
                  LIB3116-001-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  g3334376
BLAST score
                  401
E value
                  4.0e-39
Match length
                  121
% identity
                  67
                  THIOREDOXIN M-TYPE PRECURSOR (TRX-M) >gi 725276 (L40957)
NCBI Description
                  thioredoxin M [Zea mays]
Seq. No.
                  296519
Seq. ID
                  LIB3116-001-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  g4455232
BLAST score
                  184
E value
                  1.0e-13
Match length
                  142
```

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]



```
Seq. No.
                  296520
                  LIB3116-002-Q1-K1-B1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1944204
BLAST score
                  40
                  3.0e-13
E value
                  56
Match length
                  93
% identity
NCBI Description Oryza sativa mRNA for RicMT, complete cds
                  296521
Seq. No.
                  LIB3116-004-Q1-K1-A10
Seq. ID
Method
                  BLASTN
                  g450504
NCBI GI
BLAST score
                  65
                   4.0e-28
E value
                  97
Match length
                  93
% identity
NCBI Description
                  G.hirsutum rbcS gene for ribulose-1,5-bisphosphate
                  carboxylase, small subunit
                   296522
Seq. No.
Seq. ID
                  LIB3116-004-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g2244919
BLAST score
                  157
E value
                   1.0e-10
Match length
                   62
% identity
                   42
                  (Z97339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  296523
Seq. ID
                  LIB3116-004-Q1-K2-A1
                  BLASTN
Method
                   g3821780
NCBI GI
BLAST score
                   36
                   7.0e-11
E value
Match length
                   48
                   67
% identity
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   296524
                  LIB3116-004-Q1-K2-B2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g22292
BLAST score
                   36
                   4.0e-11
E value
                   48
Match length
% identity
                   94
NCBI Description Z.mays mRNA for glycine-rich protein
```

LIB3116-004-Q1-K2-E3 Seq. ID

Method BLASTX NCBI GI g4098250 BLAST score 270 E value 6.0e-24



Match length 72 % identity 65

NCBI Description (U76611) similar to Solanum tuberosum ci21A gene product encoded by the sequence presented in GenBank Accession

Number U76610 [Solanum tuberosum]

Seq. No. 296526

Seq. ID LIB3116-004-Q1-K2-F7

Method BLASTX
NCBI GI g4218535
BLAST score 352
E value 2.0e-33
Match length 76
% identity 84

NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.

296527

Seq. ID LIB3116-004-Q1-K2-H8

Method BLASTX
NCBI GI g2245028
BLAST score 148
E value 2.0e-09
Match length 97
% identity 34

NCBI Description (Z97341) limonene cyclase [Arabidopsis thaliana]

Seq. No. 296528

Seq. ID LIB3116-005-Q1-K1-C4

Method BLASTN
NCBI GI 9454880
BLAST score 58
E value 8.0e-24
Match length 92
% identity 91

NCBI Description Rice mRNA for WSI724 protein induced by water stress,

complete cds

Seq. No. 296529

Seq. ID LIB3116-005-Q1-K1-F6

Method BLASTX
NCBI GI g2880051
BLAST score 179
E value 3.0e-13
Match length 113
% identity 35

NCBI Description (AC002340) putative protein kinase [Arabidopsis thaliana]

Seq. No. 296530

Seq. ID LIB3116-005-Q1-K1-H6

Method BLASTX
NCBI GI g2058498
BLAST score 199
E value 5.0e-27
Match length 100
% identity 69

NCBI Description (U76029) hemoglobin 1 [Oryza sativa] >gi 2058500 (U76030)

hemoglobin 1 [Oryza sativa]

NCBI GI

BLAST score

g730904

703



```
296531
Seq. No.
                  LIB3116-006-Q1-K1-A1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1495804
BLAST score
                  319
                  1.0e-29
E value
Match length
                  97
% identity
NCBI Description
                 (X96406) 13-lipoxygenase [Solanum tuberosum]
                  296532
Seq. No.
                  LIB3116-006-Q1-K1-A12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4567250
BLAST score
                  212
                  6.0e-17
E value
Match length
                  85
                  49
% identity
NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]
                  296533
Seq. No.
                  LIB3116-006-Q1-K1-B2
Seq. ID
Method
                  BLASTN
                  g2446997
NCBI GI
BLAST score
                  151
E value
                  2.0e-79
Match length
                  284
% identity
                  89
NCBI Description Zea mays FAD7 gene for fatty acid desaturase, complete cds
Seq. No.
                  296534
Seq. ID
                  LIB3116-006-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  g2245012
BLAST score
                  196
                  4.0e-15
E value
Match length
                  50
% identity
NCBI Description (297341) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  296535
                  LIB3116-006-Q1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4056477
BLAST score
                  229
                  6.0e-19
E value
Match length
                  103
% identity
                  48
NCBI Description
                  (AC005896) putative RNA binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  296536
Seq. ID
                  LIB3116-006-Q1-K1-F4
                  BLASTX
Method
```

41541



E value 2.0e-74
Match length 161
% identity 87
NCBI Description 26S PRO

26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING HOMOLOG 5) >gi_626989_pir__S46613 YTA5 protein - yeast (Saccharomyces cerevisiae) >gi_531758_emb_CAA56957_(X81070) probable regulatory subunit of 26S proteasome;

homologue to S4 subunit of human 26S proteasome [Saccharomyces cerevisiae] >gi_683690_emb_CAA88352_(Z48432) homolog to S4 subunit of human 26S proteasome

(X81070) [Saccharomyces cerevisiae]

>gi_1430967_emb_CAA98563_ (Z74055) ORF YDL007w

[Saccharomyces cerevisiae]

Seq. No. 296537

Seq. ID LIB3116-006-Q1-K1-F5

Method BLASTX
NCBI GI g462193
BLAST score 150
E value 9.0e-10
Match length 47
% identity 51

NCBI Description GOLIATH PROTEIN (G1 PROTEIN) >gi 483296 pir JC1495

regulatory protein G1 - fruit fly (Drosophila melanogaster)

>gi 157535 (M97204) goliath protein [Drosophila

melanogaster]

Seq. No. 296538

Seq. ID LIB3116-007-Q1-K1-A7

Method BLASTX
NCBI GI g2293568
BLAST score 250
E value 1.0e-21
Match length 83
% identity 60

NCBI Description (AF012897) HvB12D homolog [Oryza sativa]

Seq. No. 296539

Seq. ID LIB3116-007-Q1-K1-D5

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 9.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 296540

Seq. ID LIB3116-007-Q1-K1-F11

Method BLASTN
NCBI GI g606814
BLAST score 186
E value 1.0e-100
Match length 235
% identity 95

NCBI Description Zea mays Golden Bantam carbonic anhydrase mRNA, complete

cds



```
296541
Seq. No.
                  LIB3116-008-Q1-K1-G10
Seq. ID
Method
                  BLASTX
                  g3913018
NCBI GI
                  372
BLAST score
                  8.0e-36
E value
                  102
Match length
                  73
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
                  aldolase [Oryza sativa]
                  296542
Seq. No.
                  LIB3116-008-Q1-K1-H9
Seq. ID
Method
                  BLASTX
                  g4154352
NCBI GI
                   228
BLAST score
                   6.0e-19
E value
                   93
Match length
% identity
NCBI Description (AF110333) PrMC3 [Pinus radiata]
                   296543
Seq. No.
                   LIB3116-009-Q1-K1-A11
Seq. ID
                   BLASTN
Method
                   g22223
NCBI GI
                   49
BLAST score
                   2.0e-18
E value
Match length
                   165
                   83
% identity
NCBI Description Maize cab-1 gene for chlorophyll a/b-binding protein
                   296544
Seq. No.
                   LIB3116-009-Q1-K1-D2
Seq. ID
                   BLASTX
Method
                   g2501578
NCBI GI
                   363
BLAST score
                   1.0e-34
E value
                   98
Match length
                   74
 % identity
                   ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047
NCBI Description
                   ethylene-responsive protein 1 - Para rubber tree
                   >gi_1209317 (M88254) ethylene-inducible protein [Hevea
                   brasiliensis]
                   296545
 Seq. No.
                   LIB3116-009-Q1-K1-D5
 Seq. ID
                   BLASTX
 Method
                   g128388
 NCBI GI
                   214
 BLAST score
                   3.0e-17
 E value
                   71
 Match length
                   63
 % identity
                   NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
 NCBI Description
```

>gi_82711_pir__A31779 phospholipid transfer protein 9C2

(PHOSPHOLIPID TRANSFER PROTEIN) (PLTP)



precursor - maize >gi_168576 (J04176) phospholipid transfer protein precursor [Zea mays]

 Seq. No.
 296546

 Seq. ID
 LIB3116-009-Q1-K1-H11

 Method
 BLASTX

 NCBI GI
 g115771

 BLAST score
 335

E value 2.0e-31
Match length 100
% identity 69

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll

a/b-binding protein precursor - maize

>gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No. 296547

Seq. ID LIB3116-010-Q1-K1-B10

Method BLASTX
NCBI GI g416731
BLAST score 229
E value 5.0e-19
Match length 66
% identity 68

NCBI Description POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi 82655 pir JQ1107

18.3K protein precursor, pollen - maize

>gi_255569_bbs_113677 (S44171) pollen specific protein [Zea

mays=corn, Peptide, 170 aa] [Zea mays] >gi 1588669 prf 2209273A Zm13 [Zea mays]

Seq. No. 296548

Seq. ID LIB3116-010-Q1-K1-C8

Method BLASTN
NCBI GI g1698669
BLAST score 57
E value 1.0e-23
Match length 77
% identity 94

NCBI Description Zea mays S-like RNase (kin1) mRNA, complete cds

Seq. No. 296549

Seq. ID LIB3116-010-Q1-K1-D5

Method BLASTN
NCBI GI g22528
BLAST score 117
E value 4.0e-59
Match length 245
% identity 89

NCBI Description Zea mays mRNA encoding a zein (clone A20)

Seq. No. 296550

Seq. ID LIB3116-010-Q1-K1-E12

Method BLASTN
NCBI GI g902200
BLAST score 50
E value 2.0e-19



```
Match length
                  87
% identity
                  Z.mays complete chloroplast genome
NCBI Description
Seq. No.
                  296551
Seq. ID
                  LIB3116-010-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  q1171161
BLAST score
                  337
E value
                  9.0e-32
Match length
                  108
% identity
                  55
                  (U41472) pectate lyase homolog [Medicago sativa]
NCBI Description
Seq. No.
                  296552
                  LIB3116-010-Q1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q141602
BLAST score
                  152
                  5.0e-17
E value
Match length
                  99
                  59
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6)
NCBI Description
                  >gi_82658_pir__A22831 19K zein precursor (clone M6) - maize
                  >gi 22538 emb CAA26294 (X02450) zein precursor [Zea mays]
                  296553
Seq. No.
Seq. ID
                  LIB3116-010-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  g141604
BLAST score
                   450
E value
                  7.0e-45
Match length
                  108
                  86
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)
NCBI Description
                  >gi 72310 pir ZIZM91 19K zein precursor (clone cZ19C1) -
                  maize >gi_168678 (M12146) 19 kDa zein protein [Zea mays]
Seq. No.
                  296554
Seq. ID
                  LIB3116-010-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g4539660
BLAST score
                  482
E value
                  9.0e-49
Match length
                  107
                  83
% identity
NCBI Description
                  (AF061282) polyprotein [Sorghum bicolor]
Seq. No.
                  296555
Seq. ID
                  LIB3116-010-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  q3293559
```

Method BLASTX
NCBI GI g3293559
BLAST score 166
E value 1.0e-11
Match length 74
% identity 49

NCBI Description (AF072694) germin-like protein 7 [Oryza sativa]

Seq. ID Method

NCBI GI



```
296556
Seq. No.
Seq. ID
                  LIB3116-011-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  g3451411
BLAST score
                  227
E value
                  5.0e-19
                  79
Match length
% identity
NCBI Description (Z98761) seryl-tRNA synthetase [Helianthus annuus]
                  296557
Seq. No.
                  LIB3116-011-Q1-K1-B7
Seq. ID
                  BLASTN
Method
                  g397395
NCBI GI
BLAST score
                  126
E value
                  1.0e-64
Match length
                  154
                  95
% identity
NCBI Description Z.mays MNB1b mRNA for DNA-binding protein
Seq. No.
                  296558
Seq. ID
                  LIB3116-011-Q1-K1-C5
Method
                  BLASTX
                  g397396
NCBI GI
BLAST score
                  189
E value
                  2.0e-14
Match length
                  66
% identity
                  65
NCBI Description
                  (X66077) DNA-binding protein [Zea mays]
                  296559
Seq. No.
                  LIB3116-011-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q141600
BLAST score
                  283
E value
                  2.0e-25
                  70
Match length
% identity
                  86
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
                  >qi 72315 pir ZIZMB1 19K zein precursor (clone cZ19B1) -
                  maize >gi 168674 (M12143) 19 kDa zein protein [Zea mays]
                  296560
Seq. No.
Seq. ID
                  LIB3116-011-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  q3075395
BLAST score
                  344
                  3.0e - 32
E value
Match length
                  100
% identity
                  (ACOO4484) nodulin-35 homologue [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  296561
```

41546

LIB3116-011-Q1-K1-F10

BLASTX

g4539417

```
BLAST score
E value
                   4.0e-34
Match length
                  119
% identity
                  59
NCBI Description
                  (AL049171) putative protein [Arabidopsis thaliana]
                  296562
Seq. No.
                  LIB3116-011-Q1-K1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3169116
BLAST score
                  200
                  4.0e-16
E value
Match length
                  55
                  71
% identity
                  (AL021366) cICK0721Q.2 (60S Ribosomal Protein L12 LIKE
NCBI Description
                  protein) [Homo sapiens]
                  296563
Seq. No.
Seq. ID
                  LIB3116-011-Q1-K1-G11
Method
                  BLASTX
                  g1706260
NCBI GI
BLAST score
                  151
E value
                  2.0e-10
Match length
                  35
                  80
% identity
NCBI Description
                  cysteine proteinase 1 precursor - maize
                  >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
                  mays]
                  296564
Seq. ID
                  LIB3116-012-Q1-K1-B3
```

CYSTEINE PROTEINASE 1 PRECURSOR >qi 2118131 pir \$59597

Seq. No.

Method BLASTN NCBI GI g3452290 BLAST score 191 E value 1.0e-103 338 Match length % identity 89

NCBI Description Zea mays retrotransposon Huck-1 5' LTR, partial sequence

Seq. No. 296565

Seq. ID LIB3116-012-Q1-K1-B6

Method BLASTX NCBI GI q112994 BLAST score 210 E value 4.0e-19 Match length 67 84 % identity

GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN NCBI Description

>gi_82685_pir__S04536 embryonic abundant protein, glycine-rich - maize >gi 22313 emb CAA31077 (X12564)

ABA-inducible gene protein [Zea mays]

>gi 226091 prf 1410284A abscisic acid inducible gene [Zea

mays]

296566 Seq. No.

LIB3116-012-Q1-K1-C8 Seq. ID



```
Method
                  BLASTN
NCBI GI
                  g167086
BLAST score
                  45
                  3.0e-16
E value
                  153
Match length
                   90
% identity
                  Hordeum vulgare photosystem I protein (PSI-L) mRNA,
NCBI Description
                  complete cds
                  296567
Seq. No.
Seq. ID
                  LIB3116-012-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  g4249416
BLAST score
                  242
E value
                  1.0e-20
Match length
                   66
% identity
                   64
NCBI Description
                   (AC006072) putative exoribonuclease (also contains
                   zinc-finger C2H2-type domain) [Arabidopsis thaliana]
Seq. No.
                   296568
                  LIB3116-013-Q1-K1-A11
Seq. ID
Method
                  BLASTN
NCBI GI
                   g470670
BLAST score
                   60
                   4.0e-25
E value
                  103
Match length
                   89
% identity
                  Zea mays transposable element ILS-1
NCBI Description
Seq. No.
                   296569
                   LIB3116-013-Q1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3877951
BLAST score
                   168
                   5.0e-12
E value
                   58
Match length
                   47
% identity
                   (Z81555) predicted using Genefinder [Caenorhabditis
NCBI Description
                   elegans]
Seq. No.
                   296570
Seq. ID
                   LIB3116-013-Q1-K1-C8
Method
                   BLASTN
NCBI GI
                   g208277
BLAST score
                   34
E value
                   1.0e-09
Match length
                   82
                   85
% identity
NCBI Description
                  rous sarcoma virus gag gene ligated to e.coli lacz gene
                   296571
Seq. No.
                   LIB3116-014-Q1-K1-B2
Seq. ID
```

Method BLASTN NCBI GI q433041 106 BLAST score E value 1.0e-52



```
Match length
                   90
% identity
                  Zea mays W-22 clone PREM-1B retroelement PREM-1, partial
NCBI Description
                   sequence
Seq. No.
                  296572
Seq. ID
                  LIB3116-014-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  q168697
BLAST score
                  262
E value
                  5.0e-23
Match length
                  101
% identity
                   57
```

NCBI Description (M60835) zein [Zea mays]

Seq. No. 296573 LIB3116-014-Q1-K1-H12 Seq. ID Method BLASTX NCBI GI g481190 BLAST score 172 1.0e-12 E value Match length 56 64 % identity

NCBI Description plastocyanin precursor - barley >gi_22705_emb_CAA68696_

(Y00704) plastocyanin precursor [Hordeum vulgare]

>gi_431920_emb_CAA82201_ (Z28347) plastocyanin [Hordeum

vulgare]

Seq. No. 296574

Seq. ID LIB3116-014-Q1-K1-H6

Method BLASTN NCBI GI g3885895 BLAST score 41 E value 4.0e-14 Match length 65 91 % identity

NCBI Description Oryza sativa plastocyanin precursor, mRNA, complete cds

296575 Seq. No.

Seq. ID LIB3116-015-P1-K1-A4

Method BLASTX g4204277 NCBI GI BLAST score 207 2.0e-16 E value Match length 70 57 % identity

(AC004146) Hypothetical protein [Arabidopsis thaliana] NCBI Description

296576 Seq. No.

LIB3116-015-P1-K1-C5 Seq. ID

Method BLASTX NCBI GI g2246625 142 BLAST score E value 8.0e-09 Match length 44 % identity 50

NCBI Description (AF004947) protein kinase [Oryza sativa]



```
296577
Seq. No.
Seq. ID
                  LIB3116-015-P1-K1-E1
                  BLASTN
Method
NCBI GI
                  g2695930
BLAST score
                   45
                   4.0e-16
E value
Match length
                  77
% identity
                  Hordeum vulgare mRNA for hypothetical protein, clone RG49
NCBI Description
Seq. No.
                   296578
                  LIB3116-015-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4455350
BLAST score
                   305
                   2.0e-28
E value
                  70
Match length
                   81
% identity
NCBI Description
                  (AL035524) putative protein [Arabidopsis thaliana]
                   296579
Seq. No.
                  LIB3116-016-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3345477
BLAST score
                  239
                   1.0e-20
E value
Match length
                   56
                   82
% identity
                  (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
                   296580
Seq. No.
Seq. ID
                   LIB3116-016-P1-K1-C10
Method
                   BLASTN
NCBI GI
                   q2065239
BLAST score
                   33
                   3.0e-09
E value
                   37
Match length
                   97
% identity
                  M.musculus mRNA for coxsackie and adenovirus receptor
NCBI Description
                  homologue
                   296581
Seq. No.
Seq. ID
                  LIB3116-016-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   q2982453
BLAST score
                   293
                   2.0e-46
E value
Match length
                   121
                   80
% identity
NCBI Description
                   (AL022223) fructose-bisphosphate aldolase-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   296582
```

Seq. ID LIB3116-016-P1-K1-G4

Method BLASTX NCBI GI g2688822

```
BLAST score 473
E value 9.0e-48
Match length 102
% identity 87
```

NCBI Description (U93272) pyrophosphate-dependent phosphofructo-1-kinase

[Prunus armeniaca]

Seq. No. 296583

Seq. ID LIB3116-017-P1-K1-A5

Method BLASTX
NCBI GI g687677
BLAST score 200
E value 2.0e-15
Match length 71
% identity 54

NCBI Description (U19925) unknown [Arabidopsis thaliana]

Seq. No. 296584

Seq. ID LIB3116-017-P1-K1-C4

Method BLASTN
NCBI GI g3290003
BLAST score 85
E value 4.0e-40
Match length 101
% identity 96

NCBI Description Zea mays pathogenesis related protein-1 (PR-1) mRNA,

complete cds

Seq. No. 296585

Seq. ID LIB3116-017-P1-K1-D2

Method BLASTN
NCBI GI g2065239
BLAST score 36
E value 9.0e-11
Match length 40
% identity 97

NCBI Description M.musculus mRNA for coxsackie and adenovirus receptor

homologue

Seq. No. 296586

Seq. ID LIB3116-017-P1-K1-E9

Method BLASTX
NCBI GI g4510373
BLAST score 157
E value 2.0e-10
Match length 101
% identity 35

NCBI Description (AC007017) putative harpin-induced protein [Arabidopsis

thaliana]

Seq. No. 296587

Seq. ID LIB3116-017-P1-K1-F6

Method BLASTX
NCBI GI g3757521
BLAST score 441
E value 1.0e-43
Match length 134

% identity (AC005167) unknown protein [Arabidopsis thaliana] NCBI Description 296588 Seq. No. Seq. ID LIB3116-017-P1-K1-G11 Method BLASTX NCBI GI q399334 BLAST score 246 E value 2.0e-38 Match length 131 % identity NCBI Description CYSTATIN I PRECURSOR (CORN KERNEL CYSTEINE PROTEINASE INHIBITOR) >gi 322868 pir S27239 cysteine proteinase inhibitor - maize >gi 217962 dbj BAA01472 (D10622) corn cystatin I [Zea mays] Seq. No. 296589 LIB3116-017-P1-K1-H3 Seq. ID Method BLASTX g141598 NCBI GI BLAST score 256 2.0e-22 E value Match length 77 % identity 71 NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE ZG99) >gi_72313_pir__ZIZM99 19K zein precursor (clone ZG99) maize >gi_22519_emb_CAA24717_ (V01470) zein [Zea mays] >gi_22534_emb_CAA24726_ (V01479) zein [Zea mays] Seq. No. 296590 Seq. ID LIB3116-018-P1-K1-B3 Method BLASTN NCBI GI g2062705 BLAST score 38 E value 5.0e-12

42 Match length

98 % identity

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 296591

Seq. ID LIB3116-018-P1-K1-H4

Method BLASTX NCBI GI q3024018 BLAST score 169 E value 2.0e-12 Match length 44 % identity 80

INITIATION FACTOR 5A (EIF-5A) (EIF-4D) NCBI Description

> >gi_1546919_emb_CAA69225 (Y07920) translation initiation factor 5A [Zea mays] >gi 2668738 (AF034943) translation

initiation factor 5A [Zea mays]

296592 Seq. No.

Seq. ID LIB3116-020-P1-K1-A4

Method BLASTX NCBI GI q2245098 BLAST score 319

```
E value 2.0e-29
Match length 96
% identity 61
NCBI Description (297343) ribosomal protein [Arabidopsis thaliana]
```

Seq. ID LIB3116-020-P1-K1-B7

Method BLASTX
NCBI GI g4544445
BLAST score 246
E value 5.0e-21
Match length 105
% identity 50

NCBI Description (AC006592) putative pyrophosphate--fructose 6-phosphate

1-phosphotransferase [Arabidopsis thaliana]

Seq. No. 296594

Seq. ID LIB3116-020-P1-K1-C10

Method BLASTX
NCBI GI 94263509
BLAST score 292
E value 3.0e-26
Match length 126
% identity 51

NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No. 296595

Seq. ID LIB3116-020-P1-K1-C11

Method BLASTX
NCBI GI g4093169
BLAST score 332
E value 6.0e-31
Match length 132
% identity 53

NCBI Description (AF095933) p20-Arc [Dictyostelium discoideum]

Seq. No. 296596

Seq. ID LIB3116-020-P1-K1-D12

Method BLASTX
NCBI GI g1076758
BLAST score 190
E value 2.0e-14
Match length 77
% identity 49

NCBI Description heat-shock protein precursor - rye >gi_2130093_pir__S65776

heat-shock protein, 82K, precursor - rye

>gi 556673 emb CAA82945 (Z30243) heat-shock protein

[Secale cereale]

Seq. No. 296597

Seq. ID LIB3116-020-P1-K1-E3

Method BLASTX
NCBI GI g3096931
BLAST score 140
E value 9.0e-09
Match length 54
% identity 46



(AL023094) putative ribosomal protein S16 [Arabidopsis NCBI Description thaliana] 296598 Seq. No. LIB3116-020-P1-K1-F10 Seq. ID BLASTX Method q3024657 NCBI GI 150 BLAST score 9.0e-21 E value 97

% identity 62 PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) NCBI Description >gi_2668740 (AF034944) translation initiation factor; GOS2 [Zea mays]

Seq. No. 296599

Match length

LIB3116-020-P1-K1-H4 Seq. ID

Method BLASTX q1001355 NCBI GI 172 BLAST score E value 3.0e-12 Match length 119 % identity

NCBI Description (D64006) auxin-induced protein [Synechocystis sp.]

296600 Seq. No.

LIB3116-021-P1-K1-B1 Seq. ID

BLASTX Method g1805254 NCBI GI BLAST score 229 4.0e-26 E value Match length 99 65 % identity

(U62622) monogalactosyldiacylglycerol synthase [Cucumis NCBI Description

sativus]

296601 Seq. No.

LIB3116-021-P1-K1-B7 Seq. ID

BLASTX Method g141600 NCBI GI 277 BLAST score 1.0e-24 E value 109 Match length 60 % identity

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1) NCBI Description

>gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]

296602 Seq. No.

LIB3116-021-P1-K1-C7 Seq. ID

BLASTX Method g1332579 NCBI GI 420 BLAST score 2.0e-41 E value 108 Match length % identity

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. ID Method 296608

BLASTX

LIB3116-021-P1-K1-F11



```
296603
Seq. No.
                  LIB3116-021-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4584852
BLAST score
                  145
                  4.0e-09
E value
                  78
Match length
% identity
                  41
                  (AF014810) proline transporter 3 [Lycopersicon esculentum]
NCBI Description
                  296604
Seq. No.
Seq. ID
                  LIB3116-021-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q3800853
BLAST score
                  352
E value
                  2.0e-33
Match length
                  111
% identity
                  (AF084478) ribulose-1,5-bisphosphate carboxylase/oxygenase
NCBI Description
                  activase precursor [Zea mays]
                  296605
Seq. No.
Seq. ID
                  LIB3116-021-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q168586
BLAST score
                  217
E value
                  6.0e-18
Match length
                  67
% identity
                  67
                  (M58656) pyruvate, orthophosphate dikinase [Zea mays]
NCBI Description
Seq. No.
Seq. ID
                  LIB3116-021-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g4587681
BLAST score
                  225
E value
                  1.0e-18
                  74
Match length
                  53
% identity
                  (AC007197) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  296607
Seq. No.
                  LIB3116-021-P1-K1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q141602
BLAST score
                  273
E value
                  4.0e-24
Match length
                  106
% identity
                  60
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6)
                  >gi 82658 pir A22831 19K zein precursor (clone M6) - maize
                  >gi_22538_emb CAA26294 (X02450) zein precursor [Zea mays]
```

41555

NCBI Description

296613

Seq. No.



```
NCBI GI
                  g99487
BLAST score
                  333
E value
                  3.0e-31
Match length
                  112
% identity
                  59
NCBI Description
                  chlorophyll a/b-binding protein (clone pINEab 43) - Scotch
                  pine >gi 20794 emb CAA41407 (X58517) Type III chlorophyll
                  a /b-binding protein [Pinus sylvestris]
Seq. No.
                  296609
Seq. ID
                  LIB3116-021-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g1619300
BLAST score
                  159
E value
                  9.0e-11
Match length
                  46
% identity
                  65
NCBI Description
                  (X95269) LRR protein [Lycopersicon esculentum]
Seq. No.
                  296610
                  LIB3116-021-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1352200
BLAST score
                  293
E value
                  1.0e-26
Match length
                  78
% identity
                  78
NCBI Description
                  CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)
                  >gi_480909 pir_ S37497 triose
                  phosphate/3-phosphoglycerate/phosphate translocator - maize
                  >gi 405635 emb CAA81349 (Z26595) triose
                  phosphate/phosphate translocator [Zea mays]
Seq. No.
                  296611
Seq. ID
                  LIB3116-022-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g141597
BLAST score
                  188
E value
                  3.0e-14
                  71
Match length
                  58
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
                  >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                  >gi_22545_emb_CAA24728 (V01481) reading frame zein [2]
                  [Zea mays]
Seq. No.
                  296612
Seq. ID
                  LIB3116-022-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g170354
BLAST score
                  452
                  4.0e-45
E value
Match length
                  124
% identity
                  16
```

(M74156) pentameric polyubiquitin [Nicotiana sylvestris]

```
LIB3116-022-P1-K1-A6
Seq. ID
                  BLASTX
Method
                  a4049341
NCBI GI
                  245
BLAST score
                  6.0e-21
E value
                  99
Match length
                  54
% identity
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
                  296614
Seq. No.
                  LIB3116-022-P1-K1-C2
Seq. ID
                  BLASTN
Method
                  q3821780
NCBI GI
                  33
BLAST score
                  5.0e-09
E value
                  37
Match length
                  97
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  296615
Seq. No.
                  LIB3116-022-P1-K1-D3
Seq. ID
                  BLASTX
Method
                  g2760334
NCBI GI
                  169
BLAST score
                  6.0e-12
E value
                  93
Match length
                   41
% identity
NCBI Description (AC002130) F1N21.5 [Arabidopsis thaliana]
                   296616
Seq. No.
                  LIB3116-022-P1-K1-D7
Seq. ID
                   BLASTX
Method
                   g1351014
NCBI GI
                   249
BLAST score
                   2.0e-21
E value
                   101
Match length
% identity
                   40S RIBOSOMAL PROTEIN S8 >gi 968902_dbj_BAA07207 (D38010)
NCBI Description
                   ribosomal protein S8 [Oryza sativa]
                   296617
Seq. No.
                   LIB3116-022-P1-K1-D9
Seq. ID
                   BLASTX
Method
                   g2499488
NCBI GI
BLAST score
                   195
E value
                   5.0e-15
                   74
Match length
                   49
 % identity
                   PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
 NCBI Description
                  .ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                   (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                   (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849)
                   pyrophosphate-dependent phosphofructokinase alpha subunit
```

Seq. No. 296618

Seq. ID LIB3116-022-P1-K1-E3

[Ricinus communis]



Method BLASTX NCBI GI g1871195 BLAST score 163 E value 2.0e-11 91 Match length 37 % identity (U90439) Ca++ dependent protein kinase isolog [Arabidopsis NCBI Description thaliana] >gi 2335093 (AC002339) putative calcium-dependent protein kinase [Arabidopsis thaliana] 296619 Seq. No. LIB3116-022-P1-K1-E6 Seq. ID Method BLASTX g3402684 NCBI GI BLAST score 293 2.0e-26 E value 108 Match length

58 % identity (AC004697) hypothetical protein [Arabidopsis thaliana] NCBI Description

296620 Seq. No. LIB3116-022-P1-K1-E7 Seq. ID Method BLASTN NCBI GI q758354

BLAST score 38 E value 5.0e-12 Match length 190 81 % identity

NCBI Description Z.mays mRNA for plasma membrane H+ ATPase

296621 Seq. No.

Seq. ID LIB3116-022-P1-K1-E9

Method BLASTX NCBI GI g531829 BLAST score 189 1.0e-14 E value Match length 74 % identity 54

(U12390) beta-galactosidase alpha peptide [cloning vector NCBI Description

pSport1]

Seq. No. 296622

Seq. ID LIB3116-022-P1-K1-F12

Method BLASTX NCBI GI g2246378 BLAST score 152 8.0e-10 E value 76 Match length 46 % identity

(Z86094) plastid protein [Arabidopsis thaliana] NCBI Description

296623 Seq. No.

LIB3116-022-P1-K1-F2 Seq. ID

Method BLASTX g70772 NCBI GI BLAST score 265 E value 4.0e-23



Match length 81 % identity 65 NCBI Description histone H4 -

n histone H4 - wheat >gi_70773_pir__HSPM4 histone H4 - garden pea

F

Seq. No. 296624

Seq. ID LIB3116-022-P1-K1-F6

Method BLASTX
NCBI GI g168699
BLAST score 335
E value 3.0e-31
Match length 122
% identity 57

NCBI Description (M60836) zein [Zea mays]

Seq. No. 296625

Seq. ID LIB3116-022-P1-K1-G6

Method BLASTN
NCBI GI g12474
BLAST score 52
E value 3.0e-20
Match length 80
% identity 91

NCBI Description Zea mays chloroplast tV-UAC gene for transfer RNA-Val (UAC)

Seq. No. 296626

Seq. ID LIB3116-025-P1-K1-A11

Method BLASTX
NCBI GI g1352427
BLAST score 306
E value 6.0e-28
Match length 105
% identity 58

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)

(EIF-4C)

Seq. No. 296627

Seq. ID LIB3116-025-P1-K1-B10

Method BLASTX
NCBI GI 94581203
BLAST score 352
E value 3.0e-33
Match length 132
% identity 54

NCBI Description (Y17912) cyclic nucleotide and calmodulin-regulated ion

channel [Arabidopsis thaliana]

Seq. No. 296628

Seq. ID LIB3116-025-P1-K1-B3

Method BLASTX
NCBI GI g825756
BLAST score 170
E value 6.0e-12
Match length 69
% identity 57

NCBI Description (U12391) beta-galactosidase alpha peptide [Cloning vector

pSport2]



```
Seq. No.
                   296629
Seq. ID
                   LIB3116-025-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   q939785
BLAST score
                   363
E value
                   1.0e - 34
Match length
                   120
% identity
                   66
NCBI Description
                   (L46400) MADS box protein [Zea mays]
                   296630
Seq. No.
                   LIB3116-025-P1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2668744
BLAST score
                   325
                   4.0e-30
E value
                   100
Match length
% identity
                   66
                   (AF034946) ubiquitin conjugating enzyme [Zea mays]
NCBI Description
                   296631
Seq. No.
                   LIB3116-025-P1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3024018
                   179
BLAST score
                    3.0e-13
E value
Match length
                    53
% identity
                    70
                   INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
NCBI Description
                   >gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation
                    initiation factor 5A [Zea mays]
                   296632
Seq. No.
Seq. ID
                   LIB3116-025-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g629861
BLAST score
                    215
                    3.0e-17
E value
Match length
                   119
                    48
% identity
NCBI Description
                   zein Zd1, 19K - maize >gi 535020 emb CAA47639 (X67203)
                    zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                    296633
                   LIB3116-025-P1-K1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3913427
BLAST score
                    206
E value
                    3.0e-16
```

Match length 98 50 % identity

NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)

> (SAMDC) >gi_1532073_emb_CAA69075_ (Y07767) S-adenosylmethionine decarboxylase [Zea mays]



```
296634
Seq. No.
                    LIB3116-025-P1-K1-C6
Seq. ID
                    BLASTX
Method
NCBI GI
                    q2224733
BLAST score
                    183
                    1.0e-13
E value
                    125
Match length
                    38
% identity
NCBI Description (AB004933) Aux22e [Vigna radiata]
Seq. No.
                    296635
                    LIB3116-025-P1-K1-C7
Seq. ID
Method
                    BLASTX
                    g548770
NCBI GI
BLAST score
                    346
E value
                    1.0e-32
Match length
                    116
% identity
                    61
                    60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
NCBI Description
                    protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                    ribosomal protein L3 [Oryza sativa]
                    296636
Seq. No.
                    LIB3116-025-P1-K1-C8
Seq. ID
Method
                    BLASTX
NCBI GI
                    g464987
BLAST score
                     274
                     3.0e-24
E value
Match length
                     77
                     68
% identity
                    UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN
NCBI Description
                     LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)
                     >gi_421858_pir__S32672 ubiquitin--protein ligase (EC
6.3.2.19) UBC10 - Arabidopsis thaliana
                     >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating
                     enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin
                     conjugating enzyme [Arabidopsis thaliana]
                     296637
Seq. No.
                     LIB3116-025-P1-K1-D4
 Seq. ID
Method
                     BLASTX
                     g3915131
NCBI GI
                     171
BLAST score
                     2.0e-12
E value
                     89
Match length
                     42
 % identity
                     THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1)
NCBI Description
                     >gi_426442_dbj_BAA04864_ (D21836) thioredoxin h [Oryza
sativa] >gi_454882_dbj_BAA05546_ (D26547) rice thioredoxin
                     h [Oryza sativa] >\overline{gi}_1\overline{9}30072 (U\overline{9}2541) thioredoxin h [Oryza
```

sativa]
Seg. No. 296638

Seq. No. 296638 Seq. ID LIB3116-025-P1-K1-D5

Method BLASTX NCBI GI g168701 BLAST score 233



```
2.0e-19
E value
                  139
Match length
% identity
                  45
                 (M60837) zein [Zea mays]
NCBI Description
                  296639
Seq. No.
                  LIB3116-025-P1-K1-D9
Seq. ID
                  BLASTX
Method
                  g567893
NCBI GI
                  155
BLAST score
                  7.0e-11
E value
                  55
Match length
                  62
% identity
                  (L37382) beta-galactosidase-complementation protein
NCBI Description
                  [Cloning vector]
                  296640
Seq. No.
                  LIB3116-025-P1-K1-E10
Seq. ID
                  BLASTX
Method
                  q3913427
NCBI GI
                   325
BLAST score
                   3.0e-30
E value
                  125
Match length
                   54
% identity
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >gi 1532073_emb_CAA69075_ (Y07767)
                   S-adenosylmethionine decarboxylase [Zea mays]
                   296641
Seq. No.
                   LIB3116-025-P1-K1-F8
Seq. ID
                   BLASTX
Method
                   g1053047
NCBI GI
                   273
BLAST score
                   2.0e-24
E value
                   85
Match length
                   68
% identity
                   (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)
NCBI Description
                   histone H3 [Glycine max] >gi_1053051 (U38427) histone H3
                   [Glycine max]
                   296642
 Seq. No.
                   LIB3116-025-P1-K1-H12
 Seq. ID
                   BLASTX
Method
                   g128388
 NCBI GI
                   317
 BLAST score
                   3.0e-29
 E value
                   107
 Match length
                   64
 % identity
                   NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
 NCBI Description
                   (PHOSPHOLIPID TRANSFER PROTEIN) (PLTP)
                   >gi 82711_pir__A31779 phospholipid transfer protein 9C2
                   precursor - maize >gi_168576 (J04176) phospholipid transfer
```

Seq. No. 296643

Seq. ID LIB3116-025-P1-K2-C6

Method BLASTX

41562

protein precursor [Zea mays]



```
NCBI GI
                  q2224731
BLAST score
                  165
E value
                  6.0e-22
                  108
Match length
                  57
% identity
NCBI Description (AB004932) Aux22d [Vigna radiata]
```

296644 Seq. No. LIB3116-025-P1-K2-F1 Seq. ID Method BLASTX NCBI GI g1216391 BLAST score 174

E value 1.0e-12 Match length 90 % identity

NCBI Description (U39319) myrosinase-associated protein [Brassica napus]

>qi 158901 $\bar{0}$ prf 2209432B myrosinase-associated

protein:ISOTYPE=4 [Brassica napus]

Seq. No. 296645 LIB3116-025-P1-K2-F8 Seq. ID Method BLASTX NCBI GI g417103 BLAST score 219 2.0e-20

E value Match length 69 % identity 84

HISTONE H3.2, MINOR >gi 282871 pir S24346 histone NCBI Description

H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911 emb_CAA56153_(X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_(X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi 2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AFO93633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi 4490755 emb CAB38917.1

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 296646

Seq. ID LIB3116-025-P1-K2-H4

Method BLASTX NCBI GI q130274 BLAST score 182 E value 7.0e-14Match length 57 63 % identity

NCBI Description PLASTOCYANIN >gi 82500 pir S06105 plastocyanin - rice

Seq. ID

Method

BLASTX



```
296647
Seq. No.
                  LIB3116-026-P1-K2-A11
Seq. ID
                  BLASTN
Method
                  q168579
NCBI GI
                  52
BLAST score
                  2.0e-20
E value
                  60
Match length
                  97
% identity
NCBI Description Maize pyruvate, orthophosphate dikinase mRNA, complete cds
                  296648
Seq. No.
                  LIB3116-026-P1-K2-A4
Seq. ID
                  BLASTX
Method
                  g82080
NCBI GI
                   212
BLAST score
                   4.0e-17
E value
                   51
Match length
                   80
% identity
                   chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                   >gi 226872_prf__1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
                   296649
Seq. No.
                   LIB3116-026-P1-K2-B10
Seq. ID
Method
                   BLASTX
                   g4581203
NCBI GI
                   142
BLAST score
                   2.0e-11
E value
                   70
Match length
                   59
% identity
                   (Y17912) cyclic nucleotide and calmodulin-regulated ion
NCBI Description
                   channel [Arabidopsis thaliana]
                                                                       -- ت
                   296650
Seq. No.
                   LIB3116-026-P1-K2-E1
Seq. ID
                   BLASTN
Method
                   g22312
NCBI GI
                   50
BLAST score
                   3.0e-19
E value
                   62
Match length
                   95
% identity
                   Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                   abscisic acid)
                   296651
Seq. No.
                   LIB3116-026-P1-K2-F11
Seq. ID
                   BLASTX
Method
                   q168701
NCBI GI
BLAST score
                   290
                   3.0e-45
E value
Match length
                   132
                    58
 % identity
                   (M60837) zein [Zea mays]
 NCBI Description
 Seq. No.
                    296652
                   LIB3116-026-P1-K2-F6
```



NCBI GI g115786
BLAST score 148
E value 6.0e-10
Match length 53
% identity 64

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB) (LHCP) >gi_82680_pir__A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea

mays]

Seq. No. 296653

Seq. ID LIB3116-026-P1-K2-G6

Method BLASTX
NCBI GI g1173189
BLAST score 170
E value 7.0e-12
Match length 117
% identity 48

NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S12

>gi_2119091_pir__S58629 ribosomal protein S12 - maize
chloroplast >gi_342619 (M17841) ribosomal protein S12 [Zea
mays] >gi_1216141_emb_CAA60309_ (X86563) ribosomal protein

S12 [Zea mays]

Seq. No. 296654

Seq. ID LIB3116-027-P1-K1-B12

Method BLASTX
NCBI GI g3287696
BLAST score 172
E value 2.0e-12
Match length 72
% identity 51

NCBI Description (AC003979) Strong similarity to phosphoribosylanthranilate

transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region.

[Arabidopsis thaliana]

Seq. No. 296655

Seq. ID LIB3116-027-P1-K1-B2

Method BLASTX
NCBI GI g266398
BLAST score 474
E value 1.0e-47
Match length 120
% identity 76

NCBI Description TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR

INHIBITOR) (CHFI) >gi_68849_pir__TIZM1 trypsin/factor XIIa inhibitor precursor - maize >gi_22327_emb_CAA37998_

(X54064) corn Hageman factor inhibitor [Zea mays]

Seq. No. 296656

Seq. ID LIB3116-027-P1-K1-B8

Method BLASTN
NCBI GI g2522426
BLAST score 63
E value 5.0e-27
Match length 195



```
% identity
NCBI Description Cloning vector pWSK29, complete sequence
                  296657
Seq. No.
                  LIB3116-027-P1-K1-C1
Seq. ID
                  BLASTX
Method
                  g485744
NCBI GI
                  250
BLAST score
                  2.0e-21
E value
                  96
Match length
                  55
% identity
NCBI Description (L32792) pyrophosphatase [Beta vulgaris]
                  296658
Seq. No.
                  LIB3116-027-P1-K1-C10
Seq. ID
                  BLASTX
Method
                  q1835731
NCBI GI
                  181
BLAST score
                  3.0e-13
E value
                  83
Match length
% identity
                  46
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                  296659
Seq. No.
                  LIB3116-027-P1-K1-C5
Seq. ID
                  BLASTX
Method
                   g2407279
NCBI GI
BLAST score
                   428
                   3.0e-42
E value
                   129
Match length
                   67
% identity
NCBI Description (AF017362) aldolase [Oryza sativa]
                   296660
Seq. No.
                   LIB3116-027-P1-K1-E7
Seq. ID
                   BLASTX
Method
                   g2493852
NCBI GI
                   189
BLAST score
                   3.0e-14
E value
                   63
Match length
                   56
 % identity
                   CYTOCHROME C OXIDASE POLYPEPTIDE VC
NCBI Description
                   >gi_1070356_emb_CAA92107_ (Z68091) cytochrome c oxidase, Vc
                   subunit [Hordeum vulgare]
                   296661
 Seq. No.
                   LIB3116-027-P1-K1-G11
 Seq. ID
                   BLASTX
 Method
                   q3337356
 NCBI GI
                   230
 BLAST score
 E value
                   4.0e-19
                   115
 Match length
                   48
 % identity
                   (AC004481) putative protein transport protein SEC61 alpha
 NCBI Description
                   subunit [Arabidopsis thaliana]
```

Seq. No. 296662

NCBI GI

```
LIB3116-028-P1-K1-A10
Seq. ID
                  BLASTX
Method
                   g4371282
NCBI GI
                   345
BLAST score
                   2.0e-32
E value
Match length
                  115
% identity
                  (AC006260) putative 60S ribosomal protein L12 [Arabidopsis
NCBI Description
                   thaliana]
                   296663
Seq. No.
                   LIB3116-028-P1-K1-A11
Seq. ID
                   BLASTX
Method
                   q2130024
NCBI GI
                   180
BLAST score
                   3.0e-13
E value
                   64
Match length
                   58
% identity
                   DNA-binding protein ABF2 - wild oat
NCBI Description
                   >gi 1159879_emb_CAA88331_ (Z48431) DNA-binding protein
                   [Avena fatua]
                   296664
Seq. No.
                   LIB3116-028-P1-K1-B1
Seq. ID
                   BLASTX
Method
                   g293093
NCBI GI
                   203
BLAST score
                   5.0e-16
E value
                   79
Match length
                   57
% identity
                   (L01931) ribulose 1,5-bisphosphate carboxylase [Lobelia
NCBI Description
                   296665
Seq. No.
                   LIB3116-028-P1-K1-B4
 Seq. ID
                   BLASTX
Method
NCBI GI
                   g2262100
 BLAST score
                   350
                   3.0e-33
 E value
                   106
Match length
                   61
 % identity
                   (AC002343) unknown protein [Arabidopsis thaliana]
 NCBI Description
                   296666
 Seq. No.
                   LIB3116-028-P1-K1-B5
 Seq. ID
                   BLASTX
 Method
                   g3184282
 NCBI GI
 BLAST score
                   160
                   7.0e-11
 E value
                   116
 Match length
                    38
 % identity
                   (AC004136) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                    296667
 Seq. No.
                    LIB3116-028-P1-K1-B7
 Seq. ID
                    BLASTX
 Method
```

41567

g1673456



```
BLAST score
                  5.0e-27
E value
                  77
Match length
                  80
% identity
NCBI Description (Y09214) rubisco small subunit [Zea mays]
                  296668
Seq. No.
                  LIB3116-028-P1-K1-B9
Seq. ID
                  BLASTX
Method
                  q1711036
NCBI GI
                  177
BLAST score
                  7.0e-13
E value
                  90
Match length
                  44
% identity
                  (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum
NCBI Description
                  sativum]
                  296669
Seq. No.
                  LIB3116-028-P1-K1-C1
Seq. ID
                  BLASTX
Method
                  g99487
NCBI GI
                  275
BLAST score
                  2.0e-24
E value
                  130
Match length
                  46
% identity
                  chlorophyll a/b-binding protein (clone pINEab 43) - Scotch
NCBI Description
                  pine >gi_20794_emb_CAA41407_ (X58517) Type III chlorophyll
                  a /b-binding protein [Pinus sylvestris]
Seq. No.
                  296670
                  LIB3116-028-P1-K1-C8
Seq. ID
Method
                  BLASTX
                   q417103
NCBI GI
                   360
BLAST score
                   2.0e-34
E value
                   96
Match length
% identity
                   HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone
NCBI Description
                   H3.3-like protein - Arabidopsis thaliana
                   >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
                   [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429)
                   histone H3.3 like protein [Arabidopsis thaliana] >gi_488563
                   (U09458) histone H3.2 [Medicago sativa] >gi_488567 (\overline{U}09460)
                   histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone
                   H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2
                   [Medicago sativa] >gi_488577 (U09465) histone H3.2
                   [Medicago sativa] >gi 510911 emb CAA56153 (X79714) histone
                   H3 [Lolium temulentum] >gi 1435157_emb_CAA58445_ (X83422)
                   histone H3 variant H3.3 [Lycopersicon esculentum]
                   >gi 2558944 (AF024716) histone 3 [Gossypium hirsutum]
```

41568

>gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana
tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa]
>gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia
coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone
H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_



```
296671
Seq. No.
                  LIB3116-028-P1-K1-D11
Seq. ID
                  BLASTX
Method
                   g224550
NCBI GI
                   265
BLAST score
                   4.0e-23
E value
                   90
Match length
                   61
% identity
NCBI Description synthase CF0I, ATP [Triticum aestivum]
                   296672
Seq. No.
                   LIB3116-028-P1-K1-D2
Seq. ID
                   BLASTX
Method
                   g121472
NCBI GI
BLAST score
                   218
                   1.0e-17
E value
Match length
                   109
% identity
                   47
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                   >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                   maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
                   [Zea mays] >gi 22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
                   mays] >gi_1684\overline{8}5 (M1\overline{6}066) glutelin-2 [Zea mays]
                   296673
Seq. No.
                   LIB3116-028-P1-K1-D5
Seq. ID
                   BLASTX
Method
                   g112994
NCBI GI
BLAST score
                   252
                   5.0e-22
E value
Match length
                   57
                   84
% identity
                   GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                   >gi_82685_pir__S04536 embryonic abundant protein,
                   glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                   ABA-inducible gene protein [Zea mays]
                   >gi_226091_prf__1410284A abscisic acid inducible gene [Zea
                   mays]
                   296674
Seq. No.
                   LIB3116-028-P1-K1-D7
Seq. ID
                   BLASTX
Method
                   q1710551
NCBI GI
BLAST score
                   194
                   7.0e-15
E value
                   51
Match length
                   75
% identity
                   60S RIBOSOMAL PROTEIN L39 >gi_1177369_emb_CAA64728_
NCBI Description
                    (X95458) ribosomal protein L39 [Zea mays]
Seq. No.
                   296675
                   LIB3116-028-P1-K1-F12
```

Seq. ID

BLASTX Method g2668742 NCBI GI BLAST score 286 E value 1.0e-25



```
Match length
                  67
% identity
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                  296676
Seq. No.
                  LIB3116-028-P1-K1-F2
Seq. ID
                  BLASTX
Method
                  g82040
NCBI GI
                  460
BLAST score
                  4.0e-46
E value
                  119
Match length
                  20
% identity
NCBI Description ubiquitin precursor - flax (fragment) >gi_168304 (M57895)
                  ubiquitin [Linum usitatissimum]
                  296677
Seq. No.
                  LIB3116-028-P1-K1-F4
Seq. ID
                  BLASTX
Method
                  g1835731
NCBI GI
                  209
BLAST score
                   9.0e-17
E value
                   71
Match length
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                   296678
Seq. No.
                  LIB3116-028-P1-K1-F5
Seq. ID
                   BLASTX
Method
                   g1698670
NCBI GI
                   521
BLAST score
                   4.0e-53
E value
                   136
Match length
                   68
% identity
                  (U66241) S-like RNase [Zea mays]
NCBI Description
                   296679
Seq. No.
                   LIB3116-028-P1-K1-F8
Seq. ID
                   BLASTN
Method
                   g559535
NCBI GI
                   68
BLAST score
                   4.0e-30
E value
                   136
Match length
                   88
% identity
NCBI Description Z.mays mRNA for metallothionein
                   296680
Seq. No.
                   LIB3116-028-P1-K1-G3
 Seq. ID
                   BLASTX
Method
                   g3337352
NCBI GI
BLAST score
                   303
 E value
                   1.0e-27
                   122
Match length
 % identity
                   47
```

Seq. No. 296681

NCBI Description

41570

[Arabidopsis thaliana]

(AC004481) putative chromatin structural protein Supt5hp



```
LIB3116-028-P1-K1-G9
Seq. ID
                  BLASTX
Method
                  q4204761
NCBI GI
BLAST score
                  166
                  8.0e-12
E value
                  57
Match length
                  54
% identity
NCBI Description (U51192) peroxidase precursor [Glycine max]
                  296682
Seq. No.
                  LIB3116-028-P1-K1-H2
Seq. ID
                  BLASTX
Method
                  q3096910
NCBI GI
BLAST score
                  168
                  7.0e-12
E value
Match length
                   65
% identity
                  (AJ005813) neoxanthin cleavage enzyme [Arabidopsis
NCBI Description
                   thaliana]
                   296683
Seq. No.
                   LIB3116-028-P1-K1-H9
Seq. ID
                   BLASTX
Method
                   g417544
NCBI GI
BLAST score
                   275
                   3.0e-24
E value
Match length
                   85
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 20 KD PROTEIN) (PSI-D) (PS I SUBUNIT 5)
                   >gi_320209_pir__A60695 photosystem I chain II precursor -
                   cucumber >gi_625966_pir__JQ2132 photosystem I complex 20K
                   protein precursor - cucumber >gi_227772_prf__1710320A
                   photosystem I 20kD protein [Cucumis sativus]
                   296684
Seq. No.
                   LIB3116-030-P1-K1-A10
Seq. ID
                   BLASTX
Method
                   q417154
NCBI GI
                   362
BLAST score
                   1.0e-34
E value
                   110
Match length
                   70
 % identity
                   HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
NCBI Description
                   protein 82 - rice (strain Taichung Native One)
                   >gi 20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                   296685
 Seq. No.
                   LIB3116-030-P1-K1-A6
 Seq. ID
                   BLASTX
 Method
                   g113456
 NCBI GI
                   266
 BLAST score
                   2.0e-23
 E value
                   100
 Match length
                   60
 % identity
```

41571

NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)



```
(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
>gi_22162_emb_CAA40781_ (X57556) adenine nucleotide
translocator [Zea mays]
```

296686 Seq. No. LIB3116-030-P1-K1-B12 Seq. ID BLASTX Method g531829 NCBI GI 175 BLAST score 5.0e-13 E value 77 Match length 53 % identity (U12390) beta-galactosidase alpha peptide [cloning vector NCBI Description pSport1] 296687 Seq. No. LIB3116-030-P1-K1-C5 Seq. ID BLASTX Method q224509 NCBI GI 193 BLAST score 1.0e-14 E value 65

Match length 65 % identity zein E19 [Zea mays] NCBI Description

296688 Seq. No.

LIB3116-030-P1-K1-D3 Seq. ID

BLASTX Method g4039153 NCBI GI 151 BLAST score 8.0e-10 E value Match length 35 71 % identity

(AF104221) low temperature and salt responsive protein NCBI Description LTI6A [Arabidopsis thaliana] >gi_4325217_gb_AAD17302 (AF122005) hydrophobic protein [Arabidopsis thaliana]

296689 Seq. No.

LIB3116-030-P1-K1-E10 Seq. ID

BLASTN Method g2981206 NCBI GI 65 BLAST score 4.0e-28 E value 145 Match length 86 % identity

Zea mays photosystem I complex PsaH subunit precursor NCBI Description

(psaH) mRNA, nuclear gene encoding chloroplast protein,

complete cds

296690 Seq. No.

LIB3116-030-P1-K1-E12 Seq. ID

Method BLASTX q1853970 NCBI GI 143 BLAST score 3.0e-09 E value 66 Match length 45 % identity



NCBI Description

NCBI Description

```
296691
Seq. No.
                  LIB3116-031-P1-K1-C12
Seq. ID
Method
                  BLASTX
                  q115782
NCBI GI
                  214
BLAST score
                  1.0e-17
E value
                   49
Match length
                   82
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB) (LHCP) >gi_72747_pir__CDWT chlorophyll a/b-binding
                   protein precursor - wheat >gi_170674 (M10144) chlorophyll
                   a/b-binding protein precursor [Triticum aestivum]
Seq. No.
                   296692
                   LIB3116-032-P1-K1-E10
Seq. ID
Method
                   BLASTX
                   g82040
NCBI GI
                   354
BLAST score
                   7.0e-34
E value
Match length
                   96
% identity
                   ubiquitin precursor - flax (fragment) >gi_168304 (M57895)
NCBI Description
                   ubiquitin [Linum usitatissimum]
Seq. No.
                   296693
                   LIB3116-032-P1-K1-F4
Seq. ID
                   BLASTX
Method
                   g1931645
NCBI GI
                   185
BLAST score
                   6.0e-14
E value
                   83
Match length
                   49
% identity
                   (U95973) Fe(II) transporter isolog [Arabidopsis thaliana]
NCBI Description
                   296694
Seq. No.
                   LIB3116-033-P1-K1-A12
Seq. ID
                   BLASTN
Method
                   g559535
NCBI GI
                   152
BLAST score
                   3.0e-80
E value
                   192
Match length
                   95
 % identity
 NCBI Description Z.mays mRNA for metallothionein
                   296695
 Seq. No.
                   LIB3116-034-P1-K1-B5
 Seq. ID
                   BLASTX
 Method
                   q123537
 NCBI GI
 BLAST score
                   191
                   2.0e-14
E value
                   93
 Match length
                    45
 % identity
```

(D88122) CPRD46 protein [Vigna unguiculata]

12 KD HEAT SHOCK PROTEIN (GLUCOSE AND LIPID-REGULATED

PROTEIN) >gi_72231_pir__HHBY12 heat shock protein 12 - yeast (Saccharomyces cerevisiae) >gi_3800_emb_CAA39306_



52

mays]

296700

LIB3117-001-Q1-K1-C4

% identity

Seq. No.

Seq. ID

NCBI Description

(X55785) hsp12 [Saccharomyces cerevisiae] >gi_171607 (M60827) 15 kD glucose and lipid regulated protein [Saccharomyces cerevisiae] >gi_559934 emb_CAA86349 (Z46255) hsp12, glp1, len: 109, CAI: 0.65, HS12_YEAST P22943 12 KD HEAT SHOCK PROTEIN [Saccharomyces cerevisiae] >gi_836740 dbj_BAA09224.1 (D50617) 12KD heat shock protein [Saccharomyces cerevisiae] >gi_1100790_dbj_BAA08003_ (D44596) 15kD glucose and lipid regulated protein [Saccharomyces cerevisiae] >gi_1742028_dbj_BAA14033_ (D89864) Sc-Hsp12p [Saccharomyces pastorianus]

```
296696
Seq. No.
                  LIB3117-001-Q1-K1-A6
Seq. ID
                  BLASTN
Method
                  g168681
NCBI GI
                  41
BLAST score
                  8.0e-14
E value
                  137
Match length
                  82
% identity
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
                  >gi 270686_gb_I03333_ Sequence 8 from Patent US
                  296697
Seq. No.
                  LIB3117-001-Q1-K1-B5
Seq. ID
Method
                  BLASTX
                  g3659995
NCBI GI
                  309
BLAST score
                  2.0e-28
E value
                  62
Match length
                  85
% identity
NCBI Description Bifunctional Hageman FactorAMYLASE INHIBITOR FROM MAIZE
                  296698
Seq. No.
                  LIB3117-001-Q1-K1-B9
Seq. ID
Method
                  BLASTX
                  g1655424
NCBI GI
BLAST score
                   147
                   2.0e-09
E value
Match length
                   39
                   77
% identity
                  (D83531) GDP dissociation inhibitor [Arabidopsis thaliana]
NCBI Description
                   >qi 3212878 (AC004005) GDP dissociation inhibitor
                   [Arabidopsis thaliana]
                   296699
Seq. No.
                   LIB3117-001-Q1-K1-C10
Seq. ID
                   BLASTX
Method
                   q419803
NCBI GI
BLAST score
                   280
                   6.0e-25
E value
Match length
                   111
```

41574

zein protein - maize >gi_168705 (M72708) zein protein [Zea

Match length

63

```
Method
                  a3402754
NCBI GI
                  189
BLAST score
                  3.0e-14
E value
                  121
Match length
                  35
% identity
NCBI Description (AL031187) putative protein [Arabidopsis thaliana]
                  296701
Seq. No.
                  LIB3117-001-Q1-K1-C9
Seq. ID
                  BLASTX
Method
                   g419803
NCBI GI
                   353
BLAST score
                   2.0e-33
E value
                   140
Match length
                   54
% identity
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea
                   mays]
                   296702
Seq. No.
                   LIB3117-001-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                   g2832243
NCBI GI
                   167
BLAST score
                   5.0e-12
E value
                   88
Match length
                                                                   ~~<u>~</u>
                   47
% identity
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
                   296703
Seq. No.
                   LIB3117-001-Q1-K1-G3
Seq. ID
                   BLASTN
Method
                   g4140643
NCBI GI
                   68
BLAST score
                   6.0e-30
E value
                   96
Match length
                   93
% identity .
                   Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                   complete sequence
                   296704
Seq. No.
                   LIB3117-001-Q1-K1-H12
Seq. ID
                   BLASTN
Method
                   q312180
NCBI GI
BLAST score
E value
                   6.0e-14
                   105
Match length
 % identity
                   85
NCBI Description Z.mays GapC4 gene
 Seq. No.
                   296705
                   LIB3117-002-Q1-K1-B2
 Seq. ID
 Method
                   BLASTX
                   g3776011
 NCBI GI
 BLAST score
                   141
                    6.0e-09
 E value
```



% identity 51 NCBI Description (AJ010469) RNA helicase [Arabidopsis thaliana]

Seq. No. 296706

Seq. ID LIB3117-002-Q1-K1-C1

Method BLASTN
NCBI GI g2832242
BLAST score 105
E value 4.0e-52
Match length 161
% identity 91

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 296707

Seq. ID LIB3117-002-Q1-K1-C11

Method BLASTX
NCBI GI g1173187
BLAST score 343
E value 1.0e-32
Match length 71
% identity 90

NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673

ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal

protein s12 [Fragaria x ananassa]

Seq. No. 296708

Seq. ID LIB3117-002-Q1-K1-C12

Method BLASTX
NCBI GI g1173187
BLAST score 488
E value 2.0e-49
Match length 104
% identity 88

NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673

ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal

protein s12 [Fragaria x ananassa]

Seq. No. 296709

Seq. ID LIB3117-002-Q1-K1-E7

Method BLASTN
NCBI GI g2832242
BLAST score 36
E value 6.0e-11
Match length 48
% identity 94

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 296710

Seq. ID LIB3117-002-Q1-K1-F12

Method BLASTX
NCBI GI g3914423
BLAST score 208
E value 1.0e-20
Match length 85
% identity 67



```
PROFILIN 4 >gi 2642324 (AF032370) profilin [Zea mays]
NCBI Description
Seq. No.
                  296711
Seq. ID
                  LIB3117-002-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  q141613
BLAST score
                  210
                  7.0e-17
E value
Match length
                  77
% identity
                  55
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
NCBI Description
                  >gi 72305 pir_ZIZM21 22K zein precursor (clone pZ22.1) -
                  maize >gi 22532 emb_CAA24725_ (V01478) zein [Zea mays]
                  296712
Seq. No.
                  LIB3117-002-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4185308
BLAST score
                  162
E value
                  3.0e-11
Match length
                  72
                  49
% identity
NCBI Description
                  (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
                  296713
Seq. No.
Seq. ID
                  LIB3117-002-Q1-K1-F8
Method
                  BLASTN
NCBI GI
                  q4185305
BLAST score
                  88
E value
                  9.0e-42
Match length
                  233
% identity
                  86
NCBI Description
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
                  (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes
Seq. No.
                  296714
                  LIB3117-002-Q1-K1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1848280
BLAST score
                  33
E value
                  4.0e-09
Match length
                  41
                  95
% identity
NCBI Description
                  Sorghum bicolor membrane intrinsic protein (Mipl) mRNA,
                  partial cds
Seq. No.
                  296715
```

Seq. ID LIB3117-002-Q1-K1-G4

Method BLASTN
NCBI GI g168581
BLAST score 111
E value 1.0e-55
Match length 155
% identity 94

NCBI Description Z.mays pyruvate, orthophosphate dikinase (PPDK2) gene, 3'



ena

```
296716
Seq. No.
                  LIB3117-002-Q1-K1-H10
Seq. ID
                  BLASTX
Method
                  g168489
NCBI GI
                  403
BLAST score
                  1.0e-39
E value
                  78
Match length -
                  99
% identity
                  (M16902) glutathione S-transferase I [Zea mays] >gi_168491
NCBI Description
                  (M16901) glutathione S-transferase I [Zea mays]
                  >gi_225458_prf__1303351A transferase,glutathione S [Zea
                  mays]
                  296717
Seq. No.
                  LIB3117-002-Q1-K1-H5
Seq. ID
                  BLASTX
Method
                  g22216
NCBI GI
                  152
BLAST score
                  3.0e-10
E value
                   44
Match length
                   64
% identity
                  (X55722) 22kD zein [Zea mays]
NCBI Description
                   296718
Seq. No.
                  LIB3117-002-Q1-K1-H7
Seq. ID
                   BLASTX
Method
                   g585202
NCBI GI
                   246
BLAST score
                   4.0e-21
E value
                   97
Match length
                   53
% identity
                   GLUTAMINE SYNTHETASE ROOT ISOZYME 2 (GLUTAMATE--AMMONIA
NCBI Description
                   LIGASE) >gi_481807_pir__S39478 glutamate--ammonia ligase
                   (EC 6.3.1.2) 1-2, cytosolic - maize
                   >gi 434326_emb_CAA46720_ (X65927) glutamine synthetase [Zea
                   mays]
                   296719
Seq. No.
                   LIB3117-002-Q1-K1-H8
Seq. ID
                   BLASTX
Method
                   q463152
NCBI GI
                   253
BLAST score
E value
                   2.0e-22
                   66
Match length
                   74
 % identity
                   (L29505) zein [Zea mays] >gi_1094858_prf__2106415A Met-rich
NCBI Description
                   seed storage protein [Zea mays]
 Seq. No.
                   296720
                   LIB3117-003-Q1-K1-A10
 Seq. ID
                   BLASTX
 Method
                   g508545
 NCBI GI
                   144
 BLAST score
```

3.0e-09

41

E value Match length



```
% identity
                 (L34340) zein [Zea mays]
NCBI Description
Seq. No.
                  296721
                  LIB3117-003-Q1-K1-A12
Seq. ID
                  BLASTX
Method
                  g141613
NCBI GI
                  241
BLAST score
                  2.0e-20
E value
Match length
                  111
                   46
% identity
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
NCBI Description
                  >gi_72305_pir__ZIZM21 22K zein precursor (clone pZ22.1) -
                  maize > gi_{225\overline{32}} = mb_{CAA24725} (V01478) zein [Zea mays]
Seq. No.
                   296722
                  LIB3117-003-Q1-K1-B12
Seq. ID
                  BLASTX
Method
                   q224509
NCBI GI
                   222
BLAST score
                   2.0e-20
E value
                   105
Match length
                   57
% identity
NCBI Description zein E19 [Zea mays]
                   296723
Seq. No.
                   LIB3117-003-Q1-K1-B5
Seq. ID
                   BLASTN
Method
                   g168484
NCBI GI
                   84
BLAST score
                   2.0e-39
E value
                   208
Match length
                   85
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                   296724
Seq. No.
                   LIB3117-003-Q1-K1-D11
Seq. ID
                   BLASTX
Method
                   g2828280
NCBI GI
                   348
BLAST score
                   7.0e-33
E value
                   76
Match length
                   83
 % identity
                   (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi_2832633_emb_CAA16762_ (AL021711) putative protein
                   [Arabidopsis thaliana]
                   296725
 Seq. No.
                   LIB3117-003-Q1-K1-D6
 Seq. ID
                   BLASTN
 Method
 NCBI GI
                   q483443
                   40
 BLAST score
                   3.0e-13
 E value
                   48
 Match length
                   96
 % identity
```

NCBI Description Z.mays IBP2 mRNA for initiator-binding protein

```
296726
Seq. No.
                  LIB3117-003-Q1-K1-D8
Seq. ID
                  BLASTN
Method
                  q22292
NCBI GI
                  49
BLAST score
                  8.0e-19
E value
                  101
Match length
% identity
                  87
NCBI Description Z.mays mRNA for glycine-rich protein
                  296727
Seq. No.
                  LIB3117-003-Q1-K1-E8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g82696
                  160
BLAST score
                  4.0e-12
E value
                  73
Match length
                  64
% identity
NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_
                   (X61121) glycine-rich protein [Zea mays]
                  296728
Seq. No.
                  LIB3117-003-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                  g224507
NCBI GI
                   398
BLAST score
                   7.0e-39
E value
                   117
Match length
                   74
% identity
NCBI Description zein A1 [Zea mays]
                   296729
Seq. No.
                   LIB3117-003-Q1-K1-G8
Seq. ID
                   BLASTN
Method
                   g2832242
NCBI GI
                   40
BLAST score
                   4.0e-13
E value
Match length
                   45
                   25
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                   296730
Seq. No.
                   LIB3117-003-Q1-K1-H11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q141597
                   351
BLAST score
E value
                   3.0e-33
                   95
Match length
 % identity
                   83
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
```

>gi 72314 pir ZIZM3 19K zein precursor (clone A30) - maize >gi 22545 emb CAA24728 (V01481) reading frame zein [2]

[Zea mays]

Seq. No. 296731

Seq. ID LIB3117-003-Q1-K1-H6

Method BLASTX

E value

Match length

8.0e-17

71

```
g2832247
NCBI GI
                  230
BLAST score
                  7.0e-23
E value
                  122
Match length
                  57
% identity
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]
                  296732
Seq. No.
                  LIB3117-004-Q1-K1-E10
Seq. ID
                  BLASTX
Method
                  g22220
NCBI GI
                  244
BLAST score
                  1.0e-20
E value
                  114
Match length
% identity
                  53
NCBI Description (X55723) 22 kD zein [Zea mays]
                  296733
Seq. No.
                  LIB3117-004-Q1-K1-G5
Seq. ID
                  BLASTX
Method
                  g2245037
NCBI GI
                  163
BLAST score
                  2.0e-11
E value
                  61
Match length
                  59
% identity
NCBI Description (Z97342) nuclear antigen homolog [Arabidopsis thaliana]
                  296734
Seq. No.
                  LIB3117-005-Q1-K1-A2
Seq. ID
                  BLASTX
Method
                  q1321924
NCBI GI
                   176
BLAST score
                   3.0e-13
E value
                   50
Match length
                   60
% identity
NCBI Description (X92205) NAM [Petunia x hybrida]
                   296735
Seq. No.
                   LIB3117-005-Q1-K1-A8
Seq. ID
                   BLASTX
Method
                   q544421
NCBI GI
                   218
BLAST score
                   6.0e-18
E value
                   52
Match length
                   87
 % identity
                   GLYCINE-RICH RNA-BINDING PROTEIN 1 >gi_485420_pir__S12311
NCBI Description
                   glycine-rich RNA-binding protein (clone S1) - sorghum
                   (fragment) >gi_21623_emb_CAA40863_ (X57663) glycine-rich
                   RNA-binding protein [Sorghum bicolor]
 Seq. No.
                   296736
                   LIB3117-005-Q1-K1-H3
 Seq. ID
                   BLASTX
 Method
                   g224508
 NCBI GI
                   209
 BLAST score
```



```
% identity
NCBI Description zein A20 [Zea mays]
                  296737
Seq. No.
                  LIB3117-006-Q1-K1-B10
Seq. ID
                  BLASTN
Method
                  g535019
NCBI GI
                  36
BLAST score
                  3.0e-11
E value
                  77
Match length
                  87
% identity
NCBI Description Z.mays Zdl tandem genes for zein Zdl (19 kDa Zein)
                  296738
Seq. No.
                  LIB3117-006-Q1-K1-D4
Seq. ID
                  BLASTX
Method
                  q100939
NCBI GI
                  354
BLAST score
                  1.0e-33
E value
                  140
Match length
                   58
% identity
NCBI Description zein precursor - maize
                   296739
Seq. No.
                  LIB3117-006-Q1-K1-D8
Seq. ID
                  BLASTX
Method
                  g1172977
NCBI GI
                   167
BLAST score
                   9.0e-12
E value
Match length
                   84
                   46
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic
                   ribosomal protein L18 [Arabidopsis thaliana]
                   296740
Seq. No.
                   LIB3117-006-Q1-K1-D9
Seq. ID
                   BLASTX
Method
                   q3851333
NCBI GI
BLAST score
                   317
                   1.0e-29
E value
                   79
Match length
                   76
 % identity
                   (Y09302) putative MADS-domain transcription factor [Zea
NCBI Description
                   mays]
                   296741
 Seq. No.
                   LIB3117-006-Q1-K1-E2
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g2832243
                   227
 BLAST score
 E value
                   8.0e-19
                   114
 Match length
 % identity
                   48
                   (AF031569) 22-kDa alpha zein 4 [Zea mays]
 NCBI Description
```

41582

296742

LIB3117-006-Q1-K1-G5

Seq. No.

Seq. ID

Method

NCBI GI

BLAST score



```
BLASTX
Method
                   q3283912
NCBI GI
                   184
BLAST score
                   9.0e-14
E value
                   89
Match length
                   37
% identity
NCBI Description (AF070639) unknown [Homo sapiens]
                   296743
Seq. No.
                   LIB3117-007-Q1-K1-A12
Seq. ID
                   BLASTN
Method
                   g168669
NCBI GI
                   45
BLAST score
                   2.0e-16
E value
                   45
Match length
                   100
% identity
NCBI Description Maize 19 kDa zein mRNA, clone cZ19A2, partial cds
                   296744
Seq. No.
                   LIB3117-007-Q1-K1-D11
Seq. ID
                   BLASTN
Method
                   q2832242
NCBI GI
                   133
BLAST score
                   .8.0e-69
E value
                   188
Match length
                   15
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                   296745
Seq. No.
                   LIB3117-007-Q1-K1-D12
Seq. ID
                   BLASTN
Method
                   g2832242
NCBI GI
                   60
BLAST score
E value
                   3.0e-25
                   208
Match length
                   17
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                    296746
 Seq. No.
                   LIB3117-007-Q1-K1-D8
 Seq. ID
                    BLASTX
Method
                    g141617
 NCBI GI
                    391
 BLAST score
                    6.0e-38
 E value
 Match length
                    111
                    68
 % identity
                    ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
 NCBI Description
                    >gi_100941_pir__S12140 zein Zc1 - maize
                    >gi_100945_pir__B29017 zein 2 - maize
                                            (X53515) zein Zcl [Zea mays]
                    >gi 22515 emb CAA37595
                    >gi_1^-16866\overline{6} (M\overline{1}6460) 16-kDa zein protein [Zea mays]
                    296747
 Seq. No.
                    LIB3117-007-Q1-K1-F2
 Seq. ID
                    BLASTN
```

41583

g2832242

```
E value
                  1.0e-18
Match length
                  262
                  35
% identity
                  Zea mays 22-kDa alpha zein gene cluster, complete sequence
NCBI Description
Seq. No.
                  296748
                  LIB3117-008-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2668742
BLAST score
                  371
E value
                  1.0e-35
                  85
Match length
% identity
NCBI Description
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
Seq. No.
                  296749
Seq. ID
                  LIB3117-008-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g3860273
BLAST score
                  187
E value
                  2.0e-15
Match length
                  74
                  59
% identity
                   (AC005824) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4314398_gb_AAD15608_ (AC006232) hypothetical protein
                   [Arabidopsis thaliana]
                  296750
Seq. No.
                  LIB3117-008-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82654
BLAST score
                  219
E value
                  8.0e-18
Match length
                   41
% identity
                   98
NCBI Description
                  10K zein precursor - maize >gi 22541 emb CAA30409 (X07535)
                  10kDa zein (AA 1 - 150) [Zea mays]
```

Seq. No. 296751 Seq. ID LIB3117-009-Q1-K1-A4

Method BLASTX
NCBI GI g1346109
BLAST score 248
E value 2.0e-21
Match length 73
% identity 64

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (GPB-LR) (RWD) >gi 540535 dbj BAA07404 (D38231)

RWD [Oryza sativa]

Seq. No. 296752

Seq. ID LIB3117-009-Q1-K1-C6

Method BLASTN
NCBI GI g22540
BLAST score 154
E value 3.0e-81
Match length 190



```
% identity
NCBI Description Maize mRNA for 10kDa zein
                  296753
Seq. No.
                  LIB3117-009-Q1-K1-F11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22326
BLAST score
                  96
E value
                  7.0e-47
Match length
                  168
% identity
                  89
NCBI Description Z.mays gene for Hageman factor inhibitor
                  296754
Seq. No.
                  LIB3117-009-Q1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4105697
                  198
BLAST score
E value
                  7.0e-16
Match length
                  64
                  67
% identity
                  (AF049870) thaumatin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  296755
                  LIB3117-009-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3915847
BLAST score
                  282
E value
                  2.0e-25
Match length
                  108
% identity
                  61
                  40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
NCBI Description
                  40S ribosomal protein S2 [Arabidopsis thaliana]
                  296756
Seq. No.
Seq. ID
                  LIB3117-010-Q1-K1-D2
Method
                  BLASTN
NCBI GI
                  g22530
BLAST score
                  68
                  6.0e-30
E value
Match length
                  252
                  81
% identity
NCBI Description Zea mays mRNA fragment encoding a zein (clone B49)
                  296757
Seq. No.
Seq. ID
                  LIB3117-010-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  g467996
BLAST score
                  392
E value
                  4.0e-38
Match length
                  95
% identity
                  84
```

NCBI Description (U04434) flavanone 3-beta-hydroxylase [Zea mays]

Seq. No. 296758

Seq. ID LIB3117-010-Q1-K1-E5

Method BLASTN

```
NCBI GI
                  g22292
BLAST score
                  57
                  2.0e-23
E value
                  117
Match length
% identity
                  88
NCBI Description
                  Z.mays mRNA for glycine-rich protein
                  296759
Seq. No.
Seq. ID
                  LIB3117-010-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g3043428
BLAST score
                  163
E value
                  1.0e-11
Match length
                  40
% identity
                  70
NCBI Description
                  (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
                  296760
Seq. No.
                  LIB3117-011-Q1-K1-B2
Seq. ID
Method
                  BLASTX
                  g112994
NCBI GI
BLAST score
                  352
                  2.0e-33
E value
Match length
                  92
% identity
                  77
NCBI Description
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi 226091 prf 1410284A abscisic acid inducible gene [Zea
                  mays]
Seq. No.
                  296761
Seq. ID
                  LIB3117-011-Q1-K1-D6
Method
                  BLASTN
NCBI GI
                  g2832242
BLAST score
                  425
E value
                  0.0e + 00
                  433
Match length
                  26
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.
                  296762
Seq. ID
                  LIB3117-011-Q1-K1-E11
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  37
E value
                  3.0e-11
                  49
Match length
% identity
                  67
NCBI Description Xenopus laevis cDNA clone 27A6-1
```

296763 Seq. No.

LIB3117-011-Q1-K1-E8 Seq. ID

Method BLASTX NCBI GI g2832638 BLAST score 287



```
7.0e-26
E value
                  73
Match length
                  73
% identity
                  (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
                  296764
Seq. No.
                  LIB3117-011-Q1-K1-F3
Seq. ID
                  BLASTX
Method
                  q1184776
NCBI GI
                  189
BLAST score
                  7.0e-15
E value
                  54
Match length
                  72
% identity
                  (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC4 [Zea mays]
                  296765
Seq. No.
                  LIB3117-011-Q1-K1-F7
Seq. ID
                  BLASTX
Method
                  q468516
NCBI GI
                  189
BLAST score
                  2.0e-14
E value
                  88
Match length
                   48
% identity
NCBI Description (X55724) zein [Zea mays]
                   296766
Seq. No.
                   LIB3117-011-Q1-K1-G6
Seq. ID
                   BLASTX
Method
                   q548770
NCBI GI
                   166
BLAST score
                   1.0e-11
E value
                   32
Match length
                   100
% identity
                   60S RIBOSOMAL PROTEIN L3 >gi 481228 pir S38359 ribosomal
NCBI Description
                   protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                   ribosomal protein L3 [Oryza sativa]
                   296767
 Seq. No.
                   LIB3117-012-Q1-K1-A3
 Seq. ID
                   BLASTN
Method
                   g22524
 NCBI GI
                   63
 BLAST score
 E value
                   5.0e-27
 Match length
                   191
                   83
 % identity
                   Zea mays mRNA encoding a zein (clone ZG31A)
 NCBI Description
                   296768
 Seq. No.
                   LIB3117-012-Q1-K1-F5
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q82660
 BLAST score
                    261
                    7.0e-23
 E value
                   76
 Match length
                   70
 % identity
 NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)
```





```
>gi_809117 emb_CAA24720 (V01473) zein [Zea mays]
                  296769
Seq. No.
                  LIB3117-012-Q1-K1-F6
Seq. ID
                  BLASTN
Method
                  q22524
NCBI GI
                  119
BLAST score
                  2.0e-60
E value
                  211
Match length
                  89
% identity
NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)
                  296770
Seq. No.
                  LIB3117-012-Q1-K1-G6
Seq. ID
Method
                  BLASTX
                  q141605
NCBI GI
                   381
BLAST score
                   6.0e-37
E value
                  89
Match length
                   87
```

% identity NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)

>gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) $maize > gi_1^2 168\overline{68}0$ (M12145) 19 kDa zein protein [Zea mays]

296771 Seq. No. LIB3117-013-Q1-K1-A12 Seq. ID BLASTX Method g1707924 NCBI GI 197 BLAST score 5.0e-15 E value

100 Match length 59 % identity

GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT 1 NCBI Description

PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE

PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE

ADENYL TRANSFERASE) (SHRUNKEN-2) >gi_1947182 (M81603)

shrunken-2 [Zea mays] >gi_444329_prf__1906378A ADP glucose

pyrophosphorylase [Zea mays]

296772 Seq. No.

LIB3117-013-Q1-K1-A6 Seq. ID

BLASTX Method g3980254 NCBI GI 297 BLAST score 5.0e-27 E value 103 Match length % identity

(AJ006053) peroxisomal membrane protein [Arabidopsis NCBI Description

thaliana]

296773 Seq. No.

LIB3117-013-Q1-K1-A7 Seq. ID

BLASTX Method q3980254 NCBI GI 347 BLAST score 9.0e-33 E value 129 Match length



```
% identity
                    (AJ006053) peroxisomal membrane protein [Arabidopsis
NCBI Description
                    thaliana]
                    296774
Seq. No.
                    LIB3117-013-Q1-K1-C11
Seq. ID
                    BLASTN
Method
NCBI GI
                    g22516
                    109
BLAST score
                    2.0e-54
E value
                    265
Match length
                    85
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                    296775
Seq. No.
                    LIB3117-013-Q1-K1-E9
Seq. ID
                    BLASTX
Method
                    q141600
NCBI GI
                    196
BLAST score
                    3.0e-15
E value
                    66
Match length
                    61
% identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
NCBI Description
                    >gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) -
                    \overline{\text{maize}} > \overline{\text{gi}} \cdot 168\overline{674} (M12143) 19 kDa zein protein [Zea mays]
                    296776
Seq. No.
                    LIB3117-013-Q1-K1-G9
Seq. ID
                    BLASTN
Method
                    q22537
NCBI GI
                    122
BLAST score
                     4.0e-62
E value
                     162
Match length
                     66
% identity
NCBI Description Maize mRNA for zein polypeptide (clone M6)
                     296777
Seq. No.
                     LIB3117-013-Q1-K1-H10
 Seq. ID
                     BLASTX
Method
NCBI GI
                     g2245098
                     371
BLAST score
                     1.0e-35
 E value
                     84
Match length
                     77
 % identity
                    (Z97343) ribosomal protein [Arabidopsis thaliana]
 NCBI Description
                     296778
 Seq. No.
                     LIB3117-014-Q1-K1-B10
 Seq. ID
 Method
                     BLASTX
                     g141600
 NCBI GI
 BLAST score
                     176
                     7.0e-13
 E value
                     93
 Match length
 % identity
                     46
                     ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
 NCBI Description
                     >gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) -
                     \overline{\text{maize}} > \overline{\text{gi}} \cdot 168\overline{67}4 \text{ (M12143)} 19 \text{ kDa zein protein [Zea mays]}
```

NCBI GI

BLAST score



```
296779
Seq. No.
                  LIB3117-014-Q1-K1-C1
Seq. ID
                  BLASTX
Method
                  g82696
NCBI GI
                  150
BLAST score
                  9.0e-19
E value
                  56
Match length
                  88
% identity
                  glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
                  296780
Seq. No.
                  LIB3117-014-Q1-K1-H4
Seq. ID
Method
                  BLASTN
                  g22544
NCBI GI
                  236
BLAST score
                   1.0e-130
E value
                  330
Match length
                  83
% identity
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
                   296781
Seq. No.
                   LIB3117-015-Q1-K1-A6
Seq. ID
                   BLASTX
Method
                   g3212852
NCBI GI
                   155
BLAST score
                   3.0e-10
E value
                   109
Match length
                   36
% identity
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                   296782
Seq. No.
                   LIB3117-015-Q1-K1-C7
Seq. ID
                   BLASTX
Method
                   g468516
NCBI GI
                   407
BLAST score
                   8.0e-40
E value
                   106
Match length
                   80
% identity
NCBI Description (X55724) zein [Zea mays]
                   296783
Seq. No.
                   LIB3117-015-Q1-K1-D4
Seq. ID
                   BLASTN
Method
                   g22544
NCBI GI
                   70
BLAST score
                   3.0e-31
E value
                   237
Match length
                   82
 % identity
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
                   296784
 Seq. No.
                   LIB3117-015-Q1-K1-D6
 Seq. ID
                   BLASTX
 Method
```

41590

g2832243

E value 4.0e-12 Match length 39 82

NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 296785

Seq. ID LIB3117-015-Q1-K1-D7

Method BLASTX
NCBI GI 93450889
BLAST score 162
E value 4.0e-11
Match length 63
% identity 57

NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No. 296786

Seq. ID LIB3117-015-Q1-K1-E6

Method BLASTX
NCBI GI g224513
BLAST score 149
E value 7.0e-11
Match length 57
% identity 68

NCBI Description zein M6 [Zea mays]

Seq. No. 296787

Seq. ID LIB3117-015-Q1-K1-E9

Method BLASTX
NCBI GI g2961378
BLAST score 295
E value 1.0e-26
Match length 115
% identity 34

NCBI Description (AL022141) putative protein [Arabidopsis thaliana]

Seq. No. 296788

Seq. ID LIB3117-015-Q1-K1-F4

Method BLASTN
NCBI GI g1060934
BLAST score 102
E value 2.0e-50
Match length 194
% identity 88

NCBI Description Maize mRNA for mLIP15 (DNA-binding factor), complete cds

Seq. No. 296789

Seq. ID LIB3118-001-Q1-K1-D12

Method BLASTX
NCBI GI 94454464
BLAST score 147
E value 5.0e-12
Match length 46
% identity 80

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 296790

Seq. ID LIB3118-001-Q1-K1-E10



Method BLASTX
NCBI GI g2144583
BLAST score 201
E value 5.0e-16
Match length 59
% identity 64

NCBI Description proteinase inhibitor (Bowman-Birk) D-II precursor - soybean >gi_18572_emb_CAA48657_ (X68706) Bowman-Birk proteinase isoinhibitor D-II [Glycine max] >gi_288619_emb_CAA48658_ (X68707) Soybean Bowman-Birk proteinase isoinhibitor D-II [Glycine max] >gi_743636 prf 2013215A Bowman-Birk protease

inhibitor [Glycine max]

Seq. No. 296791

Seq. ID LIB3118-001-Q1-K1-H10

Method BLASTX
NCBI GI g2144584
BLAST score 145
E value 1.0e-09
Match length 72
% identity 50

NCBI Description trypsin inhibitor A (Kunitz) precursor - soybean

>gi 18770_emb CAA45777_ (X64447) trypsin inhibitor subtype

A [Glycine max]

Seq. No. 296792

Seq. ID LIB3118-001-Q1-K1-H12

Method BLASTX
NCBI GI g2144584
BLAST score 153
E value 1.0e-10
Match length 45
% identity 73

NCBI Description trypsin inhibitor A (Kunitz) precursor - soybean

>gi_18770_emb_CAA45777 (X64447) trypsin inhibitor subtype

A [Glycine max]

Seq. No. 296793

Seq. ID LIB3118-002-Q1-K1-B2

Method BLASTN
NCBI GI g662367
BLAST score 76
E value 7.0e-35
Match length 125
% identity 100

NCBI Description Zea mays farnesyl pyrophosphate synthetase (fps) mRNA,

complete cds

Seq. No. 296794

Seq. ID LIB3118-002-Q1-K1-B4

Method BLASTN
NCBI GI g2828011
BLAST score 54
E value 1.0e-21
Match length 194
% identity 84

NCBI Description Zea mays starch synthase I precursor (Ss1) mRNA, nuclear

NCBI Description



gene encoding plastid protein, complete cds

```
Seq. No.
                  296795
Seq. ID
                  LIB3118-002-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  g141605
BLAST score
                  511
                  6.0e-52
E value
Match length
                  129
% identity
                  81
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                  296796
                  LIB3118-002-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82696
BLAST score
                  277
E value
                  8.0e-29
Match length
                  83
% identity
                  86
NCBI Description
                  glycine-rich protein - maize >gi_22293_emb_CAA43431_
                   (X61121) glycine-rich protein [Zea mays]
Seq. No.
                  296797
Seq. ID
                  LIB3118-002-Q1-K1-D5
Method
                  BLASTN
NCBI GI
                  g2832242
BLAST score
                  94
                  1.0e-45
E value
Match length
                  233
% identity
                  11
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.
                  296798
                  LIB3118-002-01-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4206306
BLAST score
                  240
E value
                  3.0e-20
Match length
                  65
% identity
                   68
NCBI Description
                  (AF049110) prpol [Zea mays]
Seq. No.
                  296799
                  LIB3118-002-Q1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g130172
BLAST score
                  145
E value
                  2.0e-09
Match length
                  58
                  50
% identity
```

41593

[Ipomoea batatas]

ALPHA-GLUCAN PHOSPHORYLASE, L ISOZYME PRECURSOR (STARCH PHOSPHORYLASE L) >gi_168276 (M64362) starch phosphorylase



```
Seq. No.
Seq. ID
                   LIB3118-002-Q1-K1-H11
Method
                   BLASTX
NCBI GI
                   q72307
BLAST score
                   379
E value
                   1.0e-36
Match length
                   111
                   75
% identity
NCBI Description
                   22K zein precursor (clone pZ22.3) - maize >qi 168686
                   (J01246) 26.99 kd zein protein [Zea mays]
Seq. No.
                   296801
                   LIB3118-002-Q1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q168586
BLAST score
                   243
                   2.0e-20
E value
Match length
                   69
                   72
% identity
                   (M58656) pyruvate, orthophosphate dikinase [Zea mays]
NCBI Description
                   296802
Seq. No.
                   LIB3118-002-Q1-K1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1710530
                   291
BLAST score
                   3.0e-26
E value
Match length
                   102
% identity
                   54
NCBI Description
                   60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256
                   ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein
                   L27a [Arabidopsis thaliana]
                   296803
Seq. No.
Seq. ID
                   LIB3118-003-Q1-K1-A4
Method
                   BLASTX
NCBI GI
                   g141605
BLAST score
                   152
                   7.0e-10
E value
Match length
                   144
                   33
% identity
NCBI Description
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
                   >qi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) -
                   maize >qi 168680 (M12145) 19 kDa zein protein [Zea mays]
                   296804
Seq. No.
                   LIB3118-003-Q1-K1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g141599
BLAST score
                   218
```

8.0e-18 E value Match length 79 59 % identity

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19A2)

>gi 72316 pir ZIZMA2 19K zein precursor (clone cZ19A2) maize (fragment) >gi 168670 (M12142) 19 kDa zein protein



[Zea mays]

```
Seq. No.
                  296805
Seq. ID
                  LIB3118-003-Q1-K1-B6
Method
                  BLASTX
                  q3492806
NCBI GI
BLAST score
                  246
E value
                  7.0e-21
Match length
                  115
% identity
                  44
                  (AJ225045) adventitious rooting related oxygenase [Malus
NCBI Description
                  domestica]
Seq. No.
                  296806
                  LIB3118-003-Q1-K1-B7
Seq. ID
Method
                  BLASTX
                  g141605
NCBI GI
BLAST score
                  297
E value
                  6.0e-27
Match length
                  109
% identity
                  61
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                  296807
Seq. ID
                  LIB3118-003-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g141598
BLAST score
                  227
                  4.0e-19
E value
Match length
                  84
% identity
                  60
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE ZG99)
NCBI Description
                  >gi 72313 pir ZIZM99 19K zein precursor (clone ZG99) -
                  maize >gi 22519 emb CAA24717 (V01470) zein [Zea mays]
                  >gi 22534 emb CAA24726 (V01479) zein [Zea mays]
                  296808
Seq. No.
Seq. ID
                  LIB3118-003-Q1-K1-D11
Method
                  BLASTN
NCBI GI
                  g602252
BLAST score
                  43
E value
                  4.0e-15
                  71
Match length
% identity
                  90
                  Zea mays enolase (eno2) mRNA, complete cds
NCBI Description
                  296809
Seq. No.
Seq. ID
                  LIB3118-003-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  q82696
BLAST score
                  451
E value
                  5.0e-45
Match length
                  94
% identity
                  93
```

NCBI Description glycine-rich protein - maize >gi 22293 emb CAA43431



% identity

NCBI Description

(X61121) glycine-rich protein [Zea mays]

```
296810
Seq. No.
                  LIB3118-003-Q1-K1-E4
Seq. ID
                  BLASTX
Method
                  g232161
NCBI GI
                  176
BLAST score
                  9.0e-13
E value
                  77
Match length
                  55
% identity
                  19 KD GLOBULIN PRECURSOR (ALPHA-GLOBULIN)
NCBI Description
                  >gi_68857_pir__WMRZ19 19K globulin precursor - rice
                  >gi_20159_emb_CAA45400_ (X63990) 19 kDa globulin precursor
                  [Oryza sativa]
                  296811
Seq. No.
                  LIB3118-003-Q1-K1-E7
Seq. ID
                  BLASTN
Method
                  g21794
NCBI GI
                  50
BLAST score
                  3.0e-19
E value
                  98
Match length
                  88
% identity
NCBI Description Wheat histone H4 gene
                  296812
Seq. No.
                  LIB3118-003-Q1-K1-F11
Seq. ID
                  BLASTN
Method
                   g22292
NCBI GI
                   35
BLAST score
                   2.0e-10
E value
                   59
Match length
                   90
% identity
NCBI Description Z.mays mRNA for glycine-rich protein
                   296813
Seq. No.
                   LIB3118-003-Q1-K1-G3
Seq. ID
                   BLASTX
Method
                   g168697
NCBI GI
                   405
BLAST score
                   2.0e-49
E value
                   132
Match length
                   86
% identity
                  (M60835) zein [Zea mays]
NCBI Description
                   296814
Seq. No.
                   LIB3118-003-Q1-K1-G4
Seq. ID
                   BLASTX
Method
                   g141604
NCBI GI
                   292
BLAST score
E value
                   4.0e-43
                   147
Match length
```

41596

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)

>gi_72310_pir__ZIZM91 19K zein precursor (clone cZ19C1) maize >gi_168678 (M12146) 19 kDa zein protein [Zea mays]



```
296815
Seq. No.
                   LIB3118-005-Q1-K1-A11
Seq. ID
                   BLASTX
Method
                   q2266992
NCBI GI
                   201
BLAST score
                   5.0e-16
E value
                   73
Match length
                   55
% identity
                   (U77412) O-linked GlcNAc transferase [Caenorhabditis
NCBI Description
                   elegans]
                   296816
Seq. No.
                   LIB3118-005-Q1-K1-A5
Seq. ID
                   BLASTX
Method
                   g730461
NCBI GI
                   205
BLAST score
                    4.0e-16
E value
                    56
Match length
                    64
% identity
                    40S RIBOSOMAL PROTEIN YS29A >gi 626904 pir S48503
NCBI Description
                    ribosomal protein S29.e.A, cytosolic - yeast (Saccharomyces cerevisiae) >gi 287628 dbj BAA03507 (D14676) ribosomal
                    protein YS29 [Saccharomyces cerevisiae] >gi_625108 (U19729)
                    Ylr388wp [Saccharomyces cerevisiae]
                    296817
Seq. No.
                    LIB3118-005-Q1-K1-B11
Seq. ID
                    BLASTN
Method
                    g22312
NCBI GI
                    153
BLAST score
                    1.0e-80
E value
                    200
Match length
                    95
% identity
                    Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                    abscisic acid)
                    296818
Seq. No.
                    LIB3118-005-Q1-K1-B3
Seq. ID
                    BLASTX
Method
                    q168699
NCBI GI
                    293
BLAST score
                    2.0e-26
E value
                    79
Match length
                    78
 % identity
 NCBI Description
                    (M60836) zein [Zea mays]
                    296819
 Seq. No.
                    LIB3118-005-Q1-K1-B5
 Seq. ID
 Method
                    BLASTX
                    q168699
 NCBI GI
 BLAST score
                    270
                    6.0e-24
 E value
                    78
 Match length
 % identity
                    73
                    (M60836) zein [Zea mays]
 NCBI Description
```

Seq. No. 296820



```
LIB3118-005-Q1-K1-C3
Seq. ID
                  BLASTN
Method
                  g22544
NCBI GI
                  112
BLAST score
                  2.0e-56
E value
                  167
Match length
                  92
% identity
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)
                  296821
Seq. No.
                  LIB3118-005-Q1-K1-E3
Seq. ID
                  BLASTX
Method
                  g168699
NCBI GI
                  227
BLAST score
                  7.0e-19
E value
                  108
Match length
% identity
                  36
NCBI Description (M60836) zein [Zea mays]
                  296822
Seq. No.
                  LIB3118-005-Q1-K1-F12
Seq. ID
                  BLASTN
Method
                  g535019
NCBI GI
                  66
BLAST score
                  5.0e-29
E value
                  145
Match length
                   44
% identity
NCBI Description Z.mays Zdl tandem genes for zein Zdl (19 kDa Zein)
                   296823
Seq. No.
                  LIB3118-005-Q1-K1-H5
Seq. ID
                   BLASTX
Method
                   g82696
NCBI GI
                   389
BLAST score
                   1.0e-37
E value
                   86
Match length
                   90
% identity
                   glycine-rich protein - maize >gi_22293 emb CAA43431
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
                   296824
 Seq. No.
                   LIB3118-006-Q1-K1-A5
 Seq. ID
                   BLASTX
Method
                   g1705844
NCBI GI
                   263
 BLAST score
                   8.0e-23
 E value
                   85
Match length
                   62
 % identity
                   CHALCONE SYNTHASE RJ5 (NARINGENIN-CHALCONE SYNTHASE)
 NCBI Description
                   >gi 1362040_pir__S56675 naringenin-chalcone synthase
                   homolog RJ5 - garden strawberry (fragment) >gi_643078
                    (U19942) chalcone synthase [Fragaria x ananassa]
                   296825
 Seq. No.
                   LIB3118-006-Q1-K1-A6
 Seq. ID
 Method
                   BLASTX
```

g2911057

NCBI GI



```
BLAST score
                  2.0e-14
E value
                  52
Match length
                  73
% identity
                   (AL021961) caffeoyl-CoA O-methyltransferase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                  296826
Seq. No.
                  LIB3118-006-Q1-K1-A8
Seq. ID
                  BLASTN
Method
                   g5091496
NCBI GI
                   35
BLAST score
                   3.0e-10
E value
                   71
Match length
% identity
                   87
                  Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
NCBI Description
                   complete sequence
                   296827
Seq. No.
                   LIB3118-006-Q1-K1-B10
Seq. ID
                   BLASTX
Method
                   g168586
NCBI GI
                   238
BLAST score
                   3.0e-20
E value
                   72
Match length
% identity
                   68
                   (M58656) pyruvate, orthophosphate dikinase [Zea mays]
NCBI Description
                   296828
Seq. No.
                   LIB3118-006-Q1-K1-B7
Seq. ID
                   BLASTX
Method
                   g2944417
NCBI GI
                   278
BLAST score
                   1.0e-24
E value
                   112
Match length
                   57
% identity
                   (AF049881) peroxidase FLXPER4 [Linum usitatissimum]
NCBI Description
                   296829
Seq. No.
                   LIB3118-006-Q1-K1-E12
Seq. ID
                   BLASTX
Method
                   g2832243
NCBI GI
                   179
BLAST score
                   2.0e-13
E value
                   76
Match length
                   55
 % identity
                   (AF031569) 22-kDa alpha zein 4 [Zea mays]
NCBI Description
                   296830
 Seq. No.
                   LIB3118-006-Q1-K1-H3
 Seq. ID
 Method
                   BLASTX
                   g122106
 NCBI GI
                   227
 BLAST score
                   7.0e-19
 E value
                    53
 Match length
 % identity
                    91
 NCBI Description HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize
```



% identity NCBI Description >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana
>gi_2119028_pir_S60475 histone H4 - garden pea
>gi_21795_emb_CAA24924_(X00043) histone H4 [Triticum
aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis
thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis
thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays]
>gi_168501 (M13370) histone H4 [Zea mays] >gi_168503
(M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone
H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_(Z79638) histone H4 homologue [Sesbania rostrata]
>gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana]
>gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4
[Arabidopsis thaliana] >gi_225838_prf_1314298A histone H4
[Arabidopsis thaliana]

```
Seq. No.
                  296831
                  LIB3118-007-Q1-K1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1184773
BLAST score
                  35
                  2.0e-10
E value
Match length
                  35
                  100
% identity
NCBI Description
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC3
                  (gpc3) mRNA, complete cds
                  296832
Seq. No.
Seq. ID
                  LIB3118-007-Q1-K1-A7
Method
                  BLASTX
                  q168586
NCBI GI
BLAST score
                  235
E value
                   5.0e-20
Match length
                  79
% identity
                  63
NCBI Description (M58656) pyruvate, orthophosphate dikinase [Zea mays]
Seq. No.
                  296833
                  LIB3118-007-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832243
BLAST score
                  165
E value
                  1.0e-11
Match length
                  64
% identity
                  55
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]
Seq. No.
                  296834
Seq. ID
                  LIB3118-007-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g466160
BLAST score
                  336
E value
                  1.0e-31
Match length
                  81
```

HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III >gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis elegans >gi_289769 (L14429) putative [Caenorhabditis



elegans]

```
296835
Seq. No.
                  LIB3118-007-Q1-K1-C6
Seq. ID
                  BLASTX
Method
                  q141613
NCBI GI
BLAST score
                  195
                  3.0e-15
E value
                  90
Match length
                  49
% identity
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
NCBI Description
                  >gi_72305_pir__ZIZM21 22K zein precursor (clone pZ22.1) -
                  maize >gi_22532_emb_CAA24725_ (V01478) zein [Zea mays]
                  296836
Seq. No.
                  LIB3118-007-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                  q82696
NCBI GI
                   259
BLAST score
                   8.0e-23
E value
                   87
Match length
                   62
% identity
                  glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
                   296837
Seq. No.
                   LIB3118-008-Q1-K1-A4
Seq. ID
                   BLASTN
Method
NCBI GI
                   q463151
                   185
BLAST score
                   1.0e-99
E value
                   409
Match length
% identity
NCBI Description Zea mays high sulfur zein gene, complete cds
                   296838
Seq. No.
                   LIB3118-008-Q1-K1-B2
Seq. ID
                   BLASTN
Method
                   g463151
NCBI GI
                   68
BLAST score
                   7.0e-30
E value
                   148
Match length
                   86
 % identity
NCBI Description Zea mays high sulfur zein gene, complete cds
                   296839
 Seq. No.
                   LIB3118-008-Q1-K1-B5
 Seq. ID
 Method
                   BLASTX
                   g550434
 NCBI GI
                   322
 BLAST score
                   8.0e-30
 E value
                   110
 Match length
                   56
 % identity
                   (X81828) cytochrome P450 [Zea mays]
 NCBI Description
```

41601

296840

LIB3118-008-Q1-K1-B7

Seq. No.

Seq. ID



```
Method
                  BLASTX
NCBI GI
                  q266398
                  254
BLAST score
E value
                  4.0e-22
Match length
                  61
% identity
                  79
                  TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR
NCBI Description
                  INHIBITOR) (CHFI) >gi 68849 pir TIZM1 trypsin/factor XIIa
                  inhibitor precursor - maize >qi 22327 emb CAA37998
                  (X54064) corn Hageman factor inhibitor [Zea mays]
Seq. No.
                  296841
                  LIB3118-008-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82696
BLAST score
                  164
                  9.0e-25
E value
Match length
                  86
                  71
% identity
                 glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                  (X61121) glycine-rich protein [Zea mays]
Seq. No.
                  296842
Seq. ID
                  LIB3118-008-Q1-K1-D10
Method
                  BLASTN
NCBI GI
                  q168675
BLAST score
                  52
E value
                  1.0e-20
Match length
                  121
% identity
                  84
NCBI Description Maize mutant zein (zE19) gene, complete cds
Seq. No.
                  296843
Seq. ID
                  LIB3118-008-Q1-K1-D9
                  BLASTN
Method
NCBI GI
                  g168675
BLAST score
                  62
E value
                  2.0e-26
                  150
Match length
                  87
% identity
NCBI Description Maize mutant zein (zE19) gene, complete cds
Seq. No.
                  296844
                  LIB3118-008-Q1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4432814
                  188
BLAST score
E value
                  2.0e-14
Match length
                  93
                  45
% identity
NCBI Description (AC006593) unknown protein [Arabidopsis thaliana]
```

Seq. No. 296845

Seq. ID LIB3118-008-Q1-K1-G6

Method BLASTX NCBI GI g129916 BLAST score 203

E value 1.0e-21 Match length 118 % identity 57

NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY

phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
>gi_21835_emb_CAA33302 (X15232) phosphoglycerate kinase

(AA 1 - 401) [Triticum aestivum]

Seq. No. 296846

Seq. ID LIB3118-008-Q1-K1-G9

Method BLASTN
NCBI GI g22516
BLAST score 141
E value 1.0e-73
Match length 161
% identity 97

NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 296847

Seq. ID LIB3118-009-Q1-K1-A8

Method BLASTX
NCBI GI g100547
BLAST score 156
E value 2.0e-10
Match length 60
% identity 55

NCBI Description globulin precursor - oat

Seq. No. 296848

Seq. ID LIB3118-009-Q1-K1-B3

Method BLASTX
NCBI GI g141600
BLAST score 241
E value 4.0e-29
Match length 104
% identity 69

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)

>gi_72315_pir__ZIZMB1 19K zein precursor (clone cZ19B1) maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]

Seq. No. 296849

Seq. ID LIB3118-009-Q1-K1-B7

Method BLASTN
NCBI GI g22544
BLAST score 70
E value 4.0e-31
Match length 226
% identity 84

NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)

Seq. No. 296850

Seq. ID LIB3118-009-Q1-K1-C6

Method BLASTX
NCBI GI g2982245
BLAST score 162
E value 2.0e-11
Match length 73



% identity NCBI Description (AF051205) hypothetical protein [Picea mariana] 296851 Seq. No. Seq. ID LIB3118-009-Q1-K1-C7 Method BLASTX NCBI GI q3377797 BLAST score 236 E value 7.0e-20 Match length 86 % identity 63 (AF075597) Similar to 60S ribosome protein L19; coded for NCBI Description by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

296852 Seq. No. Seq. ID LIB3118-009-Q1-K1-E3 Method BLASTN g2811133 NCBI GI BLAST score 214 E value 1.0e-117

Match length 277 % identity 95

Zea mays starch synthase isoform zSTSII-1 (zSSIIa) mRNA, NCBI Description

partial cds

Seq. No. 296853

Seq. ID LIB3118-010-Q1-K1-A2

Method BLASTX NCBI GI g141597 BLAST score 166 E value 7.0e-24 109 Match length % identity 66

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)

>gi 72314 pir ZIZM3 19K zein precursor (clone A30) - maize >gi_22545_emb_CAA24728 (V01481) reading frame zein [2]

[Zea mays]

Seq. No. 296854

Seq. ID LIB3118-010-Q1-K1-B7

Method BLASTN NCBI GI g22312 78 BLAST score 6.0e-36 E value Match length 191 % identity 92

NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA =

abscisic acid)

296855 Seq. No.

Seq. ID LIB3118-010-Q1-K1-C8

Method BLASTX NCBI GI g112994 BLAST score 319



```
E value
                  71
Match length
% identity
                  86
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi 226091 prf 1410284A abscisic acid inducible gene [Zea
                  mays]
                   296856
Seq. No.
                  LIB3118-010-Q1-K1-D12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g22216
                   236
BLAST score
                   7.0e-20
E value
                   66
Match length
                   76
% identity
                  (X55722) 22kD zein [Zea mays]
NCBI Description
                   296857
Seq. No.
                   LIB3118-010-Q1-K1-H10
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2062705
BLAST score
                   36
                   5.0e-11
E value
                   36
Match length
                   100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                   296858
Seq. No.
                   LIB3118-011-Q1-K1-A6
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1314428
                   150
 BLAST score
 E value
                   6.0e-79
 Match length
                   150
                   100
 % identity
                   Zea mays ssp. huehuetenangensis Doebley M031 ITS1, 5.8S
 NCBI Description
                   ribosomal RNA, ITS2
                   296859
 Seq. No.
                   LIB3118-011-Q1-K1-B1
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g3264767
                   269
 BLAST score
 E value
                   1.0e-23
                    68
 Match length
 % identity
                    74
                   (AF071893) AP2 domain containing protein [Prunus armeniaca]
 NCBI Description
                    296860
 Seq. No.
```

LIB3118-011-Q1-K1-C10 Seq. ID

BLASTN Method NCBI GI g498774 42 BLAST score 9.0e-15 E value



Match length 70 % identity 90

NCBI Description Z.mays (cv DH5xDH7) hsp70-5 mRNA for heat shock protein

Seq. No.

296861

Seq. ID LIB3118-011-Q1-K1-C4

Method BLASTX
NCBI GI g2119936
BLAST score 171
E value 3.0e-12
Match length 106
% identity 40

NCBI Description translation initiation factor eIF-4A.6 - common tobacco

(fragment)

Seq. No. 296862

Seq. ID LIB3118-011-Q1-K1-C6

Method BLASTX
NCBI GI g224507
BLAST score 522
E value 3.0e-53
Match length 152
% identity 74

NCBI Description zein Al [Zea mays]

Seq. No. 296863

Seq. ID LIB3118-011-Q1-K1-D7

Method BLASTX
NCBI GI g224508
BLAST score 170
E value 3.0e-12
Match length 70
% identity 61

NCBI Description zein A20 [Zea mays]

Seq. No. 296864

Seq. ID LIB3118-011-Q1-K1-E1

Method BLASTN
NCBI GI g168677
BLAST score 55
E value 3.0e-22
Match length 162
% identity 83

NCBI Description Maize 19 kDa zein mRNA, clone cZ19C1, complete cds

Seq. No. 296865

Seq. ID LIB3118-011-Q1-K1-H3

Method BLASTX
NCBI GI g4335745
BLAST score 240
E value 1.0e-20
Match length 99
% identity 43

NCBI Description (AC006284) putative hydrolase (contains an

esterase/lipase/thioesterase active site serine domain

(prosite: PS50187) [Arabidopsis thaliana]

```
296866
Seq. No.
                  LIB3118-012-Q1-K1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22514
                  124
BLAST score
                  2.0e-63
E value
Match length
                  232
% identity
                  88
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                  296867
Seq. No.
                  LIB3118-012-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3080400
                  192
BLAST score
                  8.0e-15
E value
Match length
                  48
                  73
% identity
NCBI Description
                  (AL022603) putative protein [Arabidopsis thaliana]
                  >gi 4455264 emb CAB36800.1 (AL035527) putative protein
                  [Arabidopsis thaliana]
Seq. No.
                  296868
Seq. ID
                  LIB3118-012-Q1-K1-B12
                  BLASTX
Method
NCBI GI
                  q141603
BLAST score
                  154
E value
                  1.0e-22
Match length
                  82
% identity
                  73
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
NCBI Description
                  >gi 72311 pir _ZIZM2 19K zein precursor (clone A20) - maize
                  >gi_22529 emb_CAA24723_ (V01476) zein [Zea mays]
                  296869
Seq. No.
Seq. ID
                  LIB3118-012-Q1-K1-C9
Method
                  BLASTX
                  g2832243
NCBI GI
BLAST score
                  190
E value
                  1.0e-14
Match length
                  81
% identity
                  57
NCBI Description
                  (AF031569) 22-kDa alpha zein 4 [Zea mays]
                  296870
Seq. No.
Seq. ID
                  LIB3118-012-Q1-K1-D6
Method
                  BLASTN
NCBI GI
                  g168702
BLAST score
                  48
                  3.0e-18
E value
Match length
                  116
                  86
% identity
NCBI Description Corn 22 kDa zein protein gene, complete cds
```

296871

BLASTX

LIB3118-012-Q1-K1-E1

Seq. No. Seq. ID

Method



```
q82660
NCBI GI
BLAST score.
                   342
                   3.0e-32
E value
                   100
Match length
% identity
                   70
NCBI Description
                  19K zein precursor (clone ZG31A) - maize (fragment)
                  >gi 809117 emb CAA24720 (V01473) zein [Zea mays]
Seq. No.
                  296872
Seq. ID
                  LIB3118-012-Q1-K1-E5
Method
                  BLASTX
                   q82660
NCBI GI
BLAST score
                   339
                  7.0e-32
E value
Match length
                  104
% identity
                   67
                  19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                   >gi 809117 emb CAA24720 (V01473) zein [Zea mays]
Seq. No.
                   296873
                  LIB3118-012-Q1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g141598
BLAST score
                   313
                   9.0e-29
E value
Match length
                   120
                   58
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE ZG99)
NCBI Description
                   >gi_72313_pir__ZIZM99 19K zein precursor (clone ZG99) -
                  maize >gi_22519_emb_CAA24717_ (V01470) zein [Zea mays]
                   >gi_22534_emb_CAA24726_ (V01479) zein [Zea mays]
Seq. No.
                   296874
Seq. ID
                   LIB3118-012-Q1-K1-F6
                   {\tt BLASTX}
Method
NCBI GI
                   g4559381
BLAST score
                   242
                   1.0e-20
E value
Match length
                   103
                   45
% identity
NCBI Description
                  (AC006526) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   296875
Seq. ID
                   LIB3118-012-Q1-K1-G5
Method
                   BLASTX
NCBI GI
                   q141608
BLAST score
                   325
                   2.0e-30
E value
                   99
Match length
                   72
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943 pir__S15655 -
NCBI Description
                   zein, 19K - maize >gi 22446_emb CAA37651_ (X53582) 19 kDa
                   zein [Zea mays]
```

Seq. No. 296876

Seq. ID LIB3118-012-Q1-K1-G9

Method BLASTN

```
NCBI GI
                   g168681
BLAST score
                   56
E value
                   8.0e-23
Match length
                   144
% identity
                   85
NCBI Description
                   Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
                   >gi 270686 gb I03333 Sequence 8 from Patent US
                   296877
Seq. No.
                   LIB3118-013-Q1-K1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g266398
BLAST score
                   369
E value
                   2.0e-35
Match length
                   86
                   73
% identity
                   TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR
NCBI Description
                   INHIBITOR) (CHFI) >gi_68849_pir__TIZM1 trypsin/factor XIIa
inhibitor precursor - maize >gi_22327_emb_CAA37998_
                   (X54064) corn Hageman factor inhibitor [Zea mays]
Seq. No.
                   296878
Seq. ID
                   LIB3118-013-Q1-K1-A11
Method
                   BLASTX
                   q629861
NCBI GI
                   222
BLAST score
                   2.0e-18
E value
Match length
                   71
% identity
                   63
                   zein Zd1, 19K - maize >gi 535020 emb CAA47639 (X67203)
NCBI Description
                   zein Zdl (19 kDa zein) [Zea mays]
Seq. No.
                   296879
                   LIB3118-013-Q1-K1-A4
Seq. ID
                   BLASTX
Method
                   g2618701
NCBI GI
BLAST score
                   252
E value
                   1.0e-21
                   93
Match length
% identity
                   60
NCBI Description
                   (AC002510) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   296880
Seq. ID
                   LIB3118-013-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   q266398
BLAST score
                   196
                   4.0e-15
E value
                   90
Match length
                   52
% identity
```

TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR NCBI Description

INHIBITOR) (CHFI) >gi_68849_pir__TIZM1 trypsin/factor XIIa inhibitor precursor - maize >gi_22327_emb_CAA37998_

(X54064) corn Hageman factor inhibitor [Zea mays]

Seq. No. 296881

LIB3118-013-Q1-K1-D10 Seq. ID



```
Method
                   BLASTX
NCBI GI
                   q419803
BLAST score
                  267
E value
                  1.0e-23
Match length
                  80
% identity
                   65
                  zein protein - maize > gi 168705 (M72708) zein protein [Zea
NCBI Description
Seq. No.
                  296882
                  LIB3118-013-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g585202
BLAST score
                  214
                  2.0e-17
E value
Match length
                  76
% identity
                   63
NCBI Description
                  GLUTAMINE SYNTHETASE ROOT ISOZYME 2 (GLUTAMATE--AMMONIA
                  LIGASE) >gi 481807 pir S39478 glutamate--ammonia ligase
                   (EC 6.3.1.2) 1-2, cytosolic - maize
                  >gi_434326_emb_CAA46720_ (X65927) glutamine synthetase [Zea
                  mays]
Seq. No.
                   296883
Seq. ID
                  LIB3118-013-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  g129916
BLAST score
                  151
E value
                  4.0e-10
                   90
Match length
% identity
                   41
NCBI Description
                  PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi 66911 pir_TVWTGY
                  phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                   >gi 21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                   (AA 1 - 401) [Triticum aestivum]
Seq. No.
                   296884
Seq. ID
                  LIB3118-013-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  g224507
                  164
BLAST score
E value
                  2.0e-11
                  50
Match length
% identity
                   64
NCBI Description zein Al [Zea mays]
                   296885
Seq. No.
Seq. ID
                  LIB3118-014-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                   q4158230
BLAST score
                   290
E value
                   2.0e-26
```

Seq. No. 296886

85

71

NCBI Description (Y18625) amylogenin [Triticum aestivum]

Match length

% identity

Seq. No.

Seq. ID

296891

LIB3118-014-Q1-K1-E10



```
Seq. ID
                  LIB3118-014-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  g129081
BLAST score
                  224
E value
                  2.0e-18
Match length
                  75
% identity
                  63
NCBI Description
                  OLEOSIN ZM-II (OLEOSIN 18 KD) (LIPID BODY-ASSOCIATED
                  PROTEIN L2) >gi 100904 pir A35040 oleosin 18 - maize
                  >gi_168509 (J05212) oleosin KD18 (L2) [Zea mays]
                  296887
Seq. No.
Seq. ID
                  LIB3118-014-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  g3328122
BLAST score
                  167
                  4.0e-12
E value
Match length
                  53
% identity
                  66
                  (AF073473) phosphoglycerate kinase precursor [Solanum
NCBI Description
                  tuberosum]
Seq. No.
                  296888
Seq. ID
                  LIB3118-014-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  q2829924
BLAST score
                  143
E value
                  6.0e-09
                  58
Match length
                  48
% identity
NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  296889
Seq. ID
                  LIB3118-014-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  g629862
BLAST score
                  469
E value
                  4.0e-47
Match length
                  108
% identity
                  86
NCBI Description zein Zd1, 19K - maize >gi 535021 emb CAA47640 (X67203)
                  zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                  296890
Seq. ID
                  LIB3118-014-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  g282881
BLAST score
                  218
E value
                  1.0e-17
                  109
Match length
% identity
                  43
                 receptor-like protein kinase precursor - Arabidopsis
NCBI Description
                  thaliana >gi 166846 (M84658) receptor-like protein kinase
                  [Arabidopsis thaliana]
```

41611

å,



```
Method
                  BLASTX
NCBI GI
                  g944842
BLAST score
                  140
E value
                  4.0e-09
Match length
                  65
% identity
                  54
                  (X80023) ATP/ADP carrier protein [Triticum turgidum]
NCBI Description
                  296892
Seq. No.
                  LIB3118-014-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141614
BLAST score
                  325
E value
                  3.0e-30
Match length
                  123
% identity
                  60
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)
NCBI Description
                  >gi_82662_pir_B22831 22K zein precursor (clone M1) - maize
                  >gi_22527_emb_CAA24722_ (V01475) reading frame zein [Zea
                  mays] >gi 224510 prf 1107201D zein M1 [Zea mays]
Seq. No.
                  296893
Seq. ID
                  LIB3118-014-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  g629861
BLAST score
                  331
E value
                   6.0e-31
Match length
                   98
% identity
                  70
                  zein Zd1, 19K - maize >gi 535020_emb CAA47639_ (X67203)
NCBI Description
                  zein Zd1 (19 kDa zein) [Zea mays]
                  296894
Seq. No.
Seq. ID
                  LIB3136-001-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g4337179
BLAST score
                  152
                   4.0e-10
E value
                   63
Match length
                   49
% identity
NCBI Description
                  (AC006416) This gene is continued on the 5' end of BAC
                  T12M14. [Arabidopsis thaliana]
                  296895
Seq. No.
                  LIB3136-001-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2511531
BLAST score
                  220
                   6.0e-18
E value
Match length
                  95
                   58
% identity
NCBI Description
                  (AF008120) alpha tubulin 1 [Eleusine indica]
                  >gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1
```

[Eleusine indica]

Seq. No. 296896

Seq. ID LIB3136-002-P1-K1-B11



Method BLASTX NCBI GI q4056469 BLAST score 192 2.0e-24 E value Match length 84 74 % identity NCBI Description

(AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967,

gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and

gb_Z25043 come from t

Seq. No. 296897

Seq. ID LIB3136-002-P1-K1-C1

Method BLASTX NCBI GI q2827143 BLAST score 175 E value 9.0e-13 Match length 107 % identity 40

(AF027174) cellulose synthase catalytic subunit NCBI Description

[Arabidopsis thaliana]

Seq. No. 296898

LIB3136-002-P1-K1-D2 Seq. ID

BLASTX Method NCBI GI g136745 BLAST score 712 2.0e-75 E value Match length 151 % identity

FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVONOID NCBI Description

3-O-GLUCOSYLTRANSFERASE) (BRONZE-1) (BZ-W22 ALLELE)

>qi 82690 pir S01037 flavonol 3-0-qlucosyltransferase (EC 2.4.1.91) (allele Bz-W22) - maize >gi 22210 emb CAA30760 (X07937) UDPglucose flavonoid glycosyl transferase [Zea mays] >gi_22506_emb_CAA31857_ (X13502) UFGT (AA 1 - 471)

[Zea mays]

Seq. No. 296899

LIB3136-002-P1-K1-E8 Seq. ID

Method BLASTX NCBI GI g1350969 BLAST score 207 E value 1.0e-16 Match length 62 66 % identity

NCBI Description 40S RIBOSOMAL PROTEIN S26 (S31) >gi_971284_dbj_BAAO7208_

(D38011) ribosomal protein S31 [Oryza sativa]

Seq. No. 296900

LIB3136-002-P1-K1-G9 Seq. ID

Method BLASTX NCBI GI q4582787 BLAST score 221 1.0e-18 E value Match length 54

E value

Match length

% identity

9.0e-46 95



```
% identity
NCBI Description (AJ012281) adenosine kinase [Zea mays]
                  296901
Seq. No.
Seq. ID
                  LIB3136-002-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g3334115
BLAST score
                  213
                  3.0e-17
E value
Match length
                  74
% identity
                  64
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                  (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 2463664
                   (AF006489) adenine nucleotide translocator 1 [Gossypium
                  hirsutum]
                  296902
Seq. No.
Seq. ID
                  LIB3136-003-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  g3935148
BLAST score
                  172
E value
                  4.0e-23
Match length
                  110
% identity
                  55
NCBI Description (AC005106) T25N20.12 [Arabidopsis thaliana]
Seq. No.
                  296903
Seq. ID
                  LIB3136-003-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  q584893
BLAST score
                  164
E value
                  1.0e-11
Match length
                  80
% identity
                  47
NCBI Description SERINE CARBOXYPEPTIDASE III PRECURSOR
                  >gi 283002 pir S22530 carboxypeptidase III (EC 3.4.16.-) -
                  rice >gi_218153_dbj_BAA01757_ (D10985) serine
                  carboxypeptidase III [Oryza sativa]
Seq. No.
                  296904
                  LIB3136-003-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827534
BLAST score
                  264
E value
                  3.0e-23
                  92
Match length
% identity
                  63
NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]
Seq. No.
                  296905
Seq. ID
                  LIB3136-003-Q1-K1-C1
                  BLASTX
Method
NCBI GI
                  q2492636
BLAST score
                  457
```



NCBI Description ACONITASE (ACONITATE HYDRATASE) (CITRATE HYDRO-LYASE) >gi 1084317 pir S49849 aconitate hydratase (EC 4.2.1.3) muskmelon (fragment) >gi_599723 emb_CAA58047_ (X82840) aconitase [Cucumis melo] Seq. No. 296906 LIB3136-003-Q1-K1-E11 Seq. ID Method BLASTX NCBI GI q3236259 BLAST score 245 E value 7.0e-21 Match length 102 % identity (AC004684) putative alcohol dehydrogenase [Arabidopsis NCBI Description thaliana] 296907 Seq. No. LIB3136-004-Q1-K1-C4 Seq. ID Method BLASTN NCBI GI g2431768 BLAST score 104 E value 1.0e-51 180 Match length % identity 89 NCBI Description Zea mays acidic ribosomal protein Pla (rppla) mRNA, complete cds 296908 Seq. No. Seq. ID LIB3136-004-01-K1-D1 Method BLASTX NCBI GI g1931647 BLAST score 325 E value 3.0e-30 Match length 77 % identity 81 (U95973) endomembrane protein EMP70 precusor isolog NCBI Description [Arabidopsis thaliana] 296909 Seq. No. Seq. ID LIB3136-004-Q1-K1-F2 Method BLASTX NCBI GI g2062167 BLAST score 391 6.0e-38 E value Match length 123 % identity 58 (AC001645) Proline-rich protein APG isolog [Arabidopsis NCBI Description thaliana]

Seq. No. 296910

Seq. ID LIB3136-004-Q1-K1-F9

Method BLASTN
NCBI GI g551482
BLAST score 40
E value 4.0e-13
Match length 126
% identity 83



NCBI Description Zea mays ABA- and ripening-inducible-like protein mRNA, complete cds

Seq. No. 296911

Seq. ID LIB3136-004-Q1-K1-G1

Method BLASTX
NCBI GI g2262099
BLAST score 177
E value 4.0e-13
Match length 74
% identity 46

NCBI Description (AC002343) thaumatin isolog [Arabidopsis thaliana]

Seq. No. 296912

Seq. ID LIB3136-004-Q1-K1-G9

Method BLASTX
NCBI GI g2108252
BLAST score 271
E value 5.0e-24
Match length 112
% identity 56

NCBI Description (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]

>gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2
[Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_

(AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]

Seq. No. 296913

Seq. ID LIB3136-004-Q1-K1-H1

Method BLASTX
NCBI GI g1839188
BLAST score 150
E value 1.0e-09
Match length 56
% identity 55

NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No. 296914

Seq. ID LIB3136-005-Q1-K1-A11

Method BLASTX
NCBI GI g2244888
BLAST score 144
E value 3.0e-09
Match length 46
% identity 48

NCBI Description (Z97338) similarity to cytochrome P450 [Arabidopsis

thaliana]

Seq. No. 296915

Seq. ID LIB3136-005-Q1-K1-B4

Method BLASTN
NCBI GI g1845194
BLAST score 184
E value 4.0e-99
Match length 271
% identity 93

NCBI Description Z.mays mRNA for HMGcl protein

```
296916
Seq. No.
                  LIB3136-005-Q1-K1-C11
Seq. ID
                  BLASTX
Method
                  g2495171
NCBI GI
BLAST score
                   468
                  4.0e-47
E value
                  96
Match length
                   93
% identity
                  DELTĄ-AMINOLEVULINIC ĄCID DEHYDRATASE PRECURSOR
NCBI Description
                   (PORPHOBILINOGEN SYNTHASE) (ALADH)
                  >gi_1041423_emb_CAA63139_ (X92402) aminolevulinate
                  dehydratase [Hordeum vulgare]
                   296917
Seq. No.
                  LIB3136-005-Q1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3451067
                   154
BLAST score
                   1.0e-10
E value
Match length
                   64
% identity
                  (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
                   296918
Seq. No.
                   LIB3136-005-Q1-K1-E2
Seq. ID
Method
                   BLASTX
                   g2326947
NCBI GI
BLAST score
                   288
                   4.0e-26
E value
                   91
Match length
% identity
                   (Z50801) Chlorophyll a/b-binding protein CP29 precursor
NCBI Description
                   [Zea mays]
                   296919
Seq. No.
                   LIB3136-005-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   g893294
NCBI GI
                   183
BLAST score
                   7.0e-14
E value
                   86
```

Match length 50 % identity

(L43362) 4-coumarate:CoA ligase isoform 2 [Oryza sativa] NCBI Description

Seq. No. 296920

Seq. ID LIB3136-005-Q1-K1-F11

BLASTX Method NCBI GI q2511531 BLAST score 258 6.0e-29 E value 86 Match length 76 % identity

(AF008120) alpha tubulin 1 [Eleusine indica] NCBI Description

>gi 3163944 emb CAA06618 (AJ005598) alpha-tubulin 1

[Eleusine indica]

296921 Seq. No.

NCBI GI

E value

BLAST score

g642134

2.0e-15

157



```
LIB3136-005-Q1-K1-H1
Seq. ID
                  BLASTX
Method
                  g1076421
NCBI GI
BLAST score
                   185
                   8.0e-14
E value
Match length
                   46
                   80
% identity
                   transcription factor TGA3 - Arabidopsis thaliana >gi_304113
NCBI Description
                   (L10209) transcription factor [Arabidopsis thaliana]
                   296922
Seq. No.
Seq. ID
                   LIB3136-006-Q1-K1-A10
Method
                   BLASTX
NCBI GI
                   q2911059
BLAST score
                   459
                   5.0e-46
E value
Match length
                   99
% identity
                   84
                  (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
                   296923
Seq. No.
Seq. ID
                   LIB3136-006-Q1-K1-B10
Method
                   BLASTX
                   g2980806
NCBI GI
                   207
BLAST score
                   2.0e-16
E value
Match length
                   60
% identity
                   58
                  (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
                   296924
Seq. No.
Seq. ID
                   LIB3136-006-Q1-K1-B3
Method
                   BLASTX
                   g2109457
NCBI GI
BLAST score
                   244
E value
                   6.0e-21
                   84
Match length
% identity
                   61
NCBI Description (AF001501) chitinase [Oryza sativa]
                   296925
Seq. No.
Seq. ID
                   LIB3136-006-Q1-K1-B7
Method
                   BLASTX
                   g2702280
NCBI GI
BLAST score
                   668
                   2.0e-70
E value
                   140
Match length
                   89
% identity
                   (AC003033) photomorphogenesis repressor COP1 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   296926
                   LIB3136-006-Q1-K1-D7
Seq. ID
                   BLASTX
Method
```

41,618



```
Match length
% identity
                   68
                   (D45355) protein kinase [Arabidopsis thaliana]
NCBI Description
                  >gi 3063704_emb_CAA18595.1_ (AL022537) protein kinase AME3
                   [Arabidopsis thaliana]
Seq. No.
                   296927
                  LIB3136-007-Q1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3043428
BLAST score
                   355
E value
                   9.0e-34
                   89
Match length
                   75
% identity
                  (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
NCBI Description
                   296928
Seq. No.
                   LIB3136-007-Q1-K1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2921304
BLAST score
                   309
E value
                   9.0e-55
Match length
                   129
% identity
                   86
                  (AF033496) herbicide safener binding protein [Zea mays]
NCBI Description
Seq. No.
                   296929
Seq. ID
                   LIB3136-008-Q1-K1-A12
Method
                   BLASTX
                   g2829910
NCBI GI
BLAST score
                   581
                   3.0e-60
E value
Match length
                   136
                   28
% identity
                   (AC002291) Unknown protein, contains regulator of
NCBI Description
                   chromosome condensation motifs [Arabidopsis thaliana]
                   296930
Seq. No.
Seq. ID
                   LIB3136-008-Q1-K1-B8
                   BLASTX
Method
                   g3928543
NCBI GI
                   146
BLAST score
E value
                   1.0e-09
                   42
Match length
% identity
                   (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   296931
Seq. No.
```

Seq. ID LIB3136-008-Q1-K1-C7

BLASTX Method NCBI GI g3548802 BLAST score 337 E value 1.0e-31 Match length 132 % identity 52

NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana]

Seq. No.

296937



>gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein
[Nicotiana tabacum] [Arabidopsis thaliana]

```
Seq. No.
                  296932
Seq. ID
                  LIB3136-008-Q1-K1-F12
                  BLASTX
Method
NCBI GI
                  g1076781
                  300
BLAST score
                  3.0e-27
E value
                  66
Match length
                  92
% identity
                  transcription factor HBP-la(c14) - wheat
NCBI Description
                  >gi_497895_dbj_BAA02304_ (D12920) transcription factor
                  HBP-la(c14) [Triticum aestivum]
Seq. No.
                  296933
                  LIB3136-008-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4566505
                  152
BLAST score
E value
                  5.0e-10
Match length
                  45
% identity
                  67
                   (AF102868) beta-D-glucan exohydrolase isoenzyme ExoI
NCBI Description
                   [Hordeum vulgare]
                  296934
Seq. No.
Seq. ID
                  LIB3136-008-Q1-K1-H1
                  BLASTN
Method
NCBI GI
                  g22484
BLAST score
                  54
E value
                  7.0e-22
Match length
                  86
                  93
% identity
NCBI Description Z.mays RNA for superoxide dismutase Sod4A
                  296935
Seq. No.
Seq. ID
                  LIB3136-008-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  g3163946
BLAST score
                  162
                  1.0e-11
E value
                   65
Match length
% identity
                  58
NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]
                  296936
Seq. No.
Seq. ID
                  LIB3136-009-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g2984709
BLAST score
                  286
E value
                  7.0e-32
                  121
Match length
% identity
                   66
NCBI Description
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
```



```
LIB3136-010-Q1-K1-A11
Seq. ID .
Method
                  BLASTN
                  q2773153
NCBI ·GI
                  122
BLAST score
                  4.0e-62
E value
Match length
                  158
% identity
                  Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                   (Asr1) mRNA, complete cds
                  296938
Seq. No.
                  LIB3136-010-Q1-K1-A7
Seq. ID
Method
                  BLASTX
                   g2425066
NCBI GI
BLAST score
                   226
                   2.0e-18
E value
                   50
Match length
                   94
% identity
                  (AF019147) cysteine proteinase Mir3 [Zea mays]
NCBI Description
                   296939
Seq. No.
                  LIB3136-010-Q1-K1-C5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2773153
BLAST score
                   67
E value
                   3.0e-29
Match length
                   158
                   87
% identity
                  Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                   (Asr1) mRNA, complete cds
                   296940
Seq. No.
                   LIB3136-010-Q1-K1-C6
Seq. ID
Method
                   BLASTX
                   q1699023
NCBI GI
BLAST score
                   346
E value
                   1.0e-32
                   99
Match length
                   70
% identity
                   (U78866) putative arginine-aspartate-rich RNA binding
NCBI Description
                   protein [Arabidopsis thaliana] >gi 1699051 (U78867)
                   putative aspartate-arginine-rich mRNA binding protein
                   [Arabidopsis thaliana]
Seq. No.
                   296941
Seq. ID
                   LIB3136-010-Q1-K1-E5
Method
                   BLASTX
NCBI GI
                   q3757521
BLAST score
                   245
E value
                   7.0e-21
Match length
                   120
```

% identity 45

(AC005167) unknown protein [Arabidopsis thaliana] NCBI Description

296942 Seq. No.

Seq. ID LIB3136-010-Q1-K1-F3

Method BLASTN



```
g3885883
NCBI GI
                  43
BLAST score
                  3.0e-15
E value
                  83
Match length
                  90
% identity
                  Oryza sativa 60S ribosomal protein L21 (RPL21) mRNA,
NCBI Description
                  complete cds
                  296943
Seq. No.
                  LIB3136-011-Q1-K1-A5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1171429
                   217
BLAST score
                   9.0e-18
E value
                   95
Match length
                   48
% identity
                  (U44028) CKC [Arabidopsis thaliana]
NCBI Description
                   296944
Seq. No.
                  LIB3136-011-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3831455
BLAST score
                   209
                   1.0e-16
E value
Match length
                   64
% identity
                   64
                   (AC005700) putative ubiquitin activating enzyme
NCBI Description
                   [Arabidopsis thaliana]
                   296945
Seq. No.
                   LIB3136-011-Q1-K1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2984709
                   402
BLAST score
                   2.0e-39
E value
                   105
Match length
                   76
% identity
                   (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
NCBI Description
                   296946
Seq. No.
                   LIB3136-011-Q1-K1-D6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3212869
                   416
BLAST score
E value
                   5.0e-41
                   113
Match length
% identity
                   (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                   296947
Seq. No.
Seq. ID
                   LIB3136-011-Q1-K1-E3
Method
                   BLASTX
                   g4454010
NCBI GI
BLAST score
                   310
E value
                   1.0e-28
Match length
                   97
                   64
% identity
```

Seq. No.

Seq. ID

296953

LIB3136-012-Q1-K1-B1



```
(AL035396) putative protein [Arabidopsis thaliana]
NCBI Description
                  296948
Seq. No.
Seq. ID
                  LIB3136-011-Q1-K1-E7
                  BLASTX
Method
NCBI GI
                  g82696
BLAST score
                  376
                  3.0e-36
E value
                  79
Match length
% identity
                  92
                  glycine-rich protein - maize >gi 22293 emb CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
                   296949
Seq. No.
                  LIB3136-011-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4646221
BLAST score
                   192
                  9.0e-15
E value
Match length
                   45
% identity
                   80
                   (AC007290) putative membrane-associated protein, 3' partial
NCBI Description
                   [Arabidopsis thaliana]
                   296950
Seq. No.
                   LIB3136-011-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1497987
BLAST score
                   296
                   5.0e-27
E value
                   90
Match length
% identity
                   63
                  (U62798) SCARECROW [Arabidopsis thaliana]
NCBI Description
                   296951
Seq. No.
                  LIB3136-011-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                   g2393724
NCBI GI
BLAST score
                   154
E value
                   3.0e-10
                   77
Match length
                   36
% identity
                  (U80819) glutathione-S-transferase homolog [Mus musculus]
NCBI Description
Seq. No.
                   296952
Seq. ID
                  LIB3136-012-Q1-K1-A5
                   BLASTX
Method
                   g3746431
NCBI GI
BLAST score
                   251
                   2.0e-24
E value
Match length
                   86
                   70
% identity
                   (AF038585) pyruvate dehydrogenase kinase isoform 1; PDK1
NCBI Description
                   [Zea mays]
```

```
Method BLASTX
NCBI GI g3822403
BLAST score 185
E value 7.0e-14
Match length 51
% identity 63
```

NCBI Description (AF087932) hydroperoxide lyase [Arabidopsis thaliana]

 Seq. No.
 296954

 Seq. ID
 LIB3136-012-Q1-K1-C11

 Method
 BLASTX

 NCBI GI
 g119350

 BLAST score
 137

 E value
 1.0e-08

 Match length
 30

Match length 30 % identity 90

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi 16271 emb CAA41114 (X58107) enolase

[Arabidopsis thaliana]

>gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696

[Arabidopsis thaliana]

Seq. No. 296955

Seq. ID LIB3136-012-Q1-K1-E5

Method BLASTX
NCBI GI g3415134
BLAST score 343
E value 2.0e-32
Match length 122
% identity 59

NCBI Description (AF082024) Phyb1 [Pimpinella brachycarpa]

Seq. No. 296956

Seq. ID LIB3136-012-Q1-K1-G12

Method BLASTX
NCBI GI g3043415
BLAST score 327
E value 9.0e-31
Match length 72
% identity 89

NCBI Description (Y17053) At-hsc70-3 [Arabidopsis thaliana]

Seq. No. 296957

Seq. ID LIB3136-012-Q1-K1-H9

Method BLASTX
NCBI GI g4490316
BLAST score 146
E value 3.0e-09
Match length 54
% identity 46

NCBI Description (AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No. 296958

Seq. ID LIB3136-013-Q1-K1-C10

Method

NCBI GI



```
BLASTN
Method
NCBI GI
                  g2431766
BLAST score
                  151
                  9.0e-80
E value
Match length
                  171
                  98
% identity
NCBI Description
                  Zea mays acidic ribosomal protein P3a (rpp3a) mRNA,
                  complete cds
Seq. No.
                  296959
Seq. ID
                  LIB3136-013-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g1778093
BLAST score
                  344
E value
                  5.0e-33
Match length
                  122
% identity
                  63
NCBI Description
                  (U64902) putative sugar transporter; member of major
                  facilitative superfamily; integral membrane protein [Beta
                  vulgaris]
                  296960
Seq. No.
Seq. ID
                  LIB3136-013-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  g4646217
BLAST score
                  305
E value
                  5.0e-28
Match length
                  103
% identity
                  56
NCBI Description
                  (AC007290) putative phosphoprotein phosphatase [Arabidopsis
                  thaliana]
                  296961
Seq. No.
Seq. ID
                  LIB3136-013-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  q3249105
BLAST score
                  146
E value
                  8.0e-10
Match length
                  60
% identity
                  50
NCBI Description
                  (AC003114) Contains similarity to protein phosphatase 2C
                  (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                  296962
                  LIB3136-013-Q1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2894534
BLAST score
                  403
E value
                  2.0e-39
                  91
Match length
% identity
                  86
NCBI Description
                  (AJ224327) aquaporin [Oryza sativa]
Seq. No.
                  296963
Seq. ID
                  LIB3136-013-Q1-K1-F3
```

41625

BLASTX

q3355468



```
BLAST score
E value
                  6.0e-18 -
                  72
Match length
                  68
% identity
                   (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                  thaliana]
                  296964
Seq. No.
Seq. ID
                  LIB3136-013-Q1-K1-F9
                  BLASTN
Method
NCBI GI
                  g3821780
                  36
BLAST score
                  8.0e-11
E value,
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  296965
Seq. No.
Seq. ID
                  LIB3136-013-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  q542157
BLAST score
                  219
                  3.0e-18
E value
Match length
                  61
                  70
% identity
NCBI Description ribosomal 5S RNA-binding protein - Rice
                  296966
Seq. No.
                  LIB3136-013-Q1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4107009
BLAST score
                  340
                   6.0e-32
E value
                  70
Match length
                   94
% identity
NCBI Description (D82039) OSK1 [Oryza sativa]
                   296967
Seq. No.
Seq. ID
                  LIB3136-013-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                   g3107931
BLAST score
                  158
                   4.0e-11
E value
Match length
                   79
                   47
% identity
                  (AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]
NCBI Description
Seq. No.
                   296968
                  LIB3136-013-Q1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2781433
```

Method BLASTX
NCBI GI g2781433
BLAST score 286
E value 1.0e-25
Match length 94
% identity 56

NCBI Description (AF030052) RSW1-like cellulose synthase catalytic subunit

[Oryza sativa subsp. japonica]

Seq. ID



```
Seq. No.
                    296969
                    LIB3136-014-Q1-K1-A8
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g3122013
  BLAST score
                    185
                     9.0e-14
  E value
                    80
  Match length
                     47
  % identity
                    DNAJ PROTEIN >gi 1750265 (U72720) DnaJ [Streptococcus
  NCBI Description
                    pneumoniae]
  Seq. No.
                     296970
  Seq. ID
                    LIB3136-014-Q1-K1-C7
  Method
                    BLASTX
  NCBI GI
                     q4432983
  BLAST score
                     233
                     1.0e-19
  E value
  Match length
                     53
                     83
  % identity
  NCBI Description (D87044) protein kinase catalytic domain (fragment) [Zea
                    mays]
  Seq. No.
                     296971
  Seq. ID
                     LIB3136-014-Q1-K2-C11
  Method
                     BLASTX
  NCBI GI
                     q3163946
  BLAST score
                     273
                     5.0e-32
  E value
  Match length
                     96
                     75
  % identity
  NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]
                     296972
  Seq. No.
                     LIB3136-014-Q1-K2-D1
  Seq. ID
                     BLASTX
  Method
                     q3913239
  NCBI GI
  BLAST score
                     448
                     1.0e-44
  E value
                     93
  Match length
                     92
   % identity
  NCBI Description
                     PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP
                     SYNTHASE) >gi 2612941 (AF024512) CLA1 transketolase-like
                     protein [Oryza sativa]
                     296973
  Seq. No.
                     LIB3136-015-Q1-K1-A2
  Seq. ID
                     BLASTX
  Method
                     g3236249
  NCBI GI
  BLAST score
                     445
                     3.0e-44
  E value
                     138
  Match length
                     59
   % identity
  NCBI Description (AC004684) hypothetical protein [Arabidopsis thaliana]
   Seq. No.
                     296974
```

41627

LIB3136-015-Q1-K1-A6

NCBI GI

BLAST score



```
BLASTX
Method
NCBI GI
                  g4165550
BLAST score
                  217
                  1.0e-17
E value
                   49
Match length
                   86
% identity
                  (AJ004915) apgm [Malus domestica]
NCBI Description
                  296975
Seq. No.
Seq. ID
                  LIB3136-015-Q1-K1-B2
Method
                  BLASTX
                  g3928084
NCBI GI
                   184
BLAST score
                   7.0e-14
E value
Match length
                   101
                   43
% identity
                   (AC005770) retrotransposon-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   296976
Seq. No.
Seq. ID
                   LIB3136-015-Q1-K1-C10
Method
                   BLASTX
NCBI GI
                   g1418331
                   218
BLAST score
                   1.0e-17
E value
                   98
Match length
                   51
% identity
                   (X95909) receptor like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   296977
Seq. No.
Seq. ID
                   LIB3136-015-Q1-K1-C4
Method
                   BLASTX
NCBI GI
                   g4512674
BLAST score
                   160
                   7.0e-11
E value
Match length
                   111
                   37
% identity
NCBI Description (AC006931) hypothetical protein [Arabidopsis thaliana]
                   296978
Seq. No.
                   LIB3136-015-Q1-K1-D10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3913427
                   287
BLAST score
                   6.0e-26
E value
Match length
                   88
                   67
% identity
                   S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >qi 1532073 emb CAA69075 (Y07767)
                   S-adenosylmethionine decarboxylase [Zea mays]
                   296979
Seq. No.
Seq. ID
                   LIB3136-015-Q1-K1-D6
Method
                   BLASTX
```

g3913464

E value 5.0e-25
Match length 101
% identity 55

NCBI Description BETAINE-ALDEHYDE DEHYDROGENASE (BADH)

>gi_2244604_dbj_BAA21098_ (AB001348) betaine aldehyde

dehydrogenase [Oryza satīva]

Seq. No. 296980

Seq. ID LIB3136-015-Q1-K1-G1

Method BLASTX
NCBI GI g3309086
BLAST score 228
E value 7.0e-19
Match length 56
% identity 79

NCBI Description (AF076253) calcineurin B-like protein 3 [Arabidopsis

thaliana]

Seq. No. 296981

Seq. ID LIB3136-015-Q1-K1-H7

Method BLASTX
NCBI GI g1550738
BLAST score 141
E value 9.0e-09
Match length 68
% identity 46

NCBI Description (Y08061) endomembrane-associated protein [Arabidopsis

thaliana] >gi 2982443 emb CAA18251 (AL022224)

endomembrane-associated protein [Arabidopsis thaliana]

Seq. No. 296982

Seq. ID LIB3136-016-Q1-K1-C3

Method BLASTX
NCBI GI g4587512
BLAST score 360
E value 2.0e-34
Match length 132
% identity 54

NCBI Description (AC007060) Strong similarity to gi_2245113

glycerol-3-phosphate permease homolog from Arabidopsis thaliana BAC gb_Z97343 and a member of the PF_00083 Sugar

transporter family

Seq. No. 296983

Seq. ID LIB3136-016-Q1-K1-D1

Method BLASTX
NCBI GI g3075394
BLAST score 173
E value 5.0e-13
Match length 71
% identity 52

NCBI Description (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana] >gi 3559809 emb CAA09311 (AJ010713) fiddlehead

protein [Arabidopsis Thaliana]

Seq. No. 296984

Seq. ID LIB3136-016-Q1-K1-D5

BLAST score

E value

150

1.0e-09



```
BLASTX
Method
                   g3337350
NCBI GI
BLAST score
                   370
E value
                   2.0e-43
                   127
Match length
                   72
% identity
NCBI Description
                   (AC004481) putative permease [Arabidopsis thaliana]
                   296985
Seq. No.
                   LIB3136-016-Q1-K1-E1
Seq. ID
                   BLASTX
Method
                   g4314378
NCBI GI
BLAST score
                   148
                   8.0e-10
E value
Match length
                   89
                   40
% identity
                  (AC006232) putative lipase [Arabidopsis thaliana]
NCBI Description
                   296986
Seq. No.
Seq. ID
                   LIB3136-016-Q1-K1-E8
Method
                   BLASTX
NCBI GI
                   g82696
                   208
BLAST score
                   9.0e-17
E value
                   69
Match length
                   59
% identity
                   glycine-rich protein - maize >gi 22293 emb CAA43431
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
                   296987
Seq. No.
Seq. ID
                   LIB3136-016-Q1-K1-F10
Method
                   BLASTX
NCBI GI
                   g3152608
BLAST score
                   517
                   1.0e-52
E value
Match length
                   126
% identity
                   (AC004482) putative BEL1-like homeotic protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   296988
                   LIB3136-016-Q1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2384758
BLAST score
                   204
E value
                   4.0e-16
Match length
                   67
                   60
% identity
                   (AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza
NCBI Description
                   sativa]
Seq. No.
                   296989
Seq. ID
                   LIB3136-016-Q1-K1-G2
Method
                   BLASTX
NCBI GI
                   g1899175
```

E value

Match length

NCBI Description

% identity



```
Match length
                  45
% identity
                  (U90262) calcium-dependent calmodulin-independent protein
NCBI Description
                  kinase CDPK [Cucurbita pepo]
                  296990
Seq. No.
                  LIB3136-016-Q1-K1-H7
Seq. ID
                  BLASTX
Method
                  g2894592
NCBI GI
                  153
BLAST score
                  1.0e-10
E value
                   64
Match length
% identity
NCBI Description (AL021889) predicted protein [Arabidopsis thaliana]
                   296991
Seq. No.
                   LIB3136-017-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                   g3135543
NCBI GI
                   326
BLAST score
                   2.0e-30
E value
Match length
                   104
% identity
                   64
NCBI Description (AF062393) aquaporin [Oryza sativa]
                   296992
Seq. No.
                   LIB3136-017-Q1-K1-E8
Seq. ID
Method
                   BLASTX
                   g3075397
NCBI GI
                   242
BLAST score
                   2.0e-20
E value
                   63
Match length
 % identity
                   67
NCBI Description (AC004484) hypothetical protein [Arabidopsis thaliana]
                   296993
Seq. No.
                   LIB3136-017-Q1-K1-F11
 Seq. ID
                   BLASTN
 Method
                   g296593
 NCBI GI
                   60
 BLAST score
                   5.0e-25
 E value
                   76
 Match length
                   95
 % identity
 NCBI Description H. vulgare pZE40 gene
                   296994
 Seq. No.
                   LIB3136-017-Q1-K1-H7
 Seq. ID
                   BLASTX
 Method
                   q1705651
 NCBI GI
                   341
 BLAST score
```

41631

20 KD NUCLEAR CAP BINDING PROTEIN (NCBP 20 KD SUBUNIT)

>gi_1582342_prf__2118330A cap-binding protein [Homo

(CBP20) >gi_984139_emb_CAA58962_ (X84157) subunit of the dimeric cap binding complex CBC [Homo sapiens]

4.0e-32

92

Method

BLASTX



sapiens]

```
Seq. No.
                  296995 -
                  LIB3136-018-Q1-K1-C11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2463510
BLAST score
                  87
                  2.0e-41
E value
Match length
                  101
% identity
                  25
NCBI Description
                  Z.mays small nuclear RNA genes snoR1.1, snoR2.2, snoR3.2,
                  U14.1a, U14.1b, U14.1c and U14.1d
Seq. No.
                  296996
Seq. ID
                  LIB3136-018-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  g2351374
BLAST score
                  147
                  3.0e-09
E value
                  29
Match length
                  100
% identity
NCBI Description
                  (U54560) putative 26S proteasome subunit athMOV34
                   [Arabidopsis thaliana]
                  296997
Seq. No.
Seq. ID
                  LIB3136-018-Q1-K1-F8
Method
                  BLASTX
                  g349379
NCBI GI
BLAST score
                  271
E value
                  8.0e-24
Match length
                  115
% identity
                  56
                  (L22847) HAHB-1 [Helianthus annuus]
NCBI Description
                  296998
Seq. No.
                  LIB3136-018-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2213594
BLAST score
                  445
E value
                  3.0e-44
Match length
                  133
                  59
% identity
NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]
                  296999
Seq. No.
Seq. ID
                  LIB3136-019-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g4388534
BLAST score
                  165
E value
                  5.0e-12
Match length
                  33
                  100
% identity
NCBI Description (Y15179) F1-ATP synthase, beta subunit [Sorghum bicolor]
Seq. No.
                  297000
Seq. ID
                  LIB3136-019-Q1-K1-C9
```

```
q2961375
NCBI GI
BLAST score
                   242
E value
                   4.0e-21
Match length
                   68
% identity
                   72
                   (AL022141) NAM like protein [Arabidopsis thaliana]
NCBI Description
                   297001
Seq. No.
                   LIB3136-019-Q1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1346396
BLAST score
                   154
E value
                   1.0e-10
Match length
                   33
                   73
% identity
                   PUTATIVE RECEPTOR PROTEIN KINASE ZMPK1 PRECURSOR
NCBI Description
                   >gi 100913 pir S10930 probable receptor protein kinase (EC
                   2.7.1.-) precursor - maize >gi 22432 emb CAA36611 (X52384)
                   precursor protein (AA -26 to 791) [Zea mays]
                   >gi_22436_emb_CAA47962_ (X67733) receptor-like protein kinase [Zea mays] >gi_226927_prf__1611404A receptor protein
                   kinase [Zea mays]
Seq. No.
                   297002
Seq. ID
                   LIB3136-019-Q1-K1-G9
Method
                   BLASTX
NCBI GI
                   q3478637
BLAST score
                   349
                   4.0e-33
E value
Match length
                   117
                   55
% identity
NCBI Description (AC005546) R29425_1 [Homo sapiens]
                   297003
Seq. No.
Seq. ID
                   LIB3136-019-Q1-K1-H1
Method
                   BLASTX
NCBI GI
                   g2497824
                   203
BLAST score
                   5.0e-16
E value
Match length
                   110
% identity
NCBI Description
                   DNA REPLICATION LICENSING FACTOR MCM6 (P105MCM)
                   >gi 1688042 dbj BAA12699 (D84557) HsMcm6 [Homo sapiens]
                   297004
Seq. No.
Seq. ID
                   LIB3136-020-Q1-K1-A10
Method
                   BLASTX
NCBI GI
                   g445613
BLAST score
                   319
E value
                   1.0e-29
Match length
                   87
```

% identity 69

NCBI Description ribosomal protein L7 [Solanum tuberosum]

297005 Seq. No.

Seq. ID LIB3136-020-Q1-K1-B5

Method BLASTX



```
NCBI GI
                  g1352679
BLAST score
                  216
E value
                  1.0e-17
Match length
                  119
% identity
                  42
                  PROTEIN PHOSPHATASE 2C ABI1 (PP2C) >gi 2129699 pir A54588
NCBI Description
                  protein phosphatase ABII - Arabidopsis thaliana
                  >gi 509419 emb CAA55484 (X78886) ABI1 [Arabidopsis
                  thaliana]
                  297006
Seq. No.
                  LIB3136-020-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832677
BLAST score
                  233
                  2.0e-19
E value
Match length
                  62
% identity
                  69
                  (AL021712) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Seq. ID
                  LIB3136-020-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  q445612
BLAST score
                  242
                  2.0e-20
E value
                  62
Match length
                  73
% identity
NCBI Description ribosomal protein S19 [Solanum tuberosum]
Seq. No.
                  297008
Seq. ID
                  LIB3136-020-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  q3618320
BLAST score
                  466
E value
                  1.0e-46
Match length
                  135
% identity
                  67
                  (AB001888) zinc finger protein [Oryza sativa]
NCBI Description
                  297009
Seq. No.
                  LIB3136-020-Q1-K1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1245938
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
```

% identity 100

NCBI Description rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,

heart atrium, mRNA, 2998 nt]

Seq. No. 297010

Seq. ID LIB3136-021-Q1-K1-E11

Method BLASTX NCBI GI g4417276 BLAST score 174 2.0e-12 E value

```
Match length
                   50
                 . 68
% identity
NCBI Description (AC007019) unknown protein [Arabidopsis thaliana]
                  297011
Seq. No.
                  LIB3136-021-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462748
BLAST score .
                  465
                  1.0e-46
E value
Match length
                  97
% identity
                  94
NCBI Description
                   (AC002292) putative Clathrin Coat Assembly protein
                   [Arabidopsis thaliana]
                   297012
Seq. No.
                  LIB3136-021-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2625154
BLAST score
                   162
E value
                   3.0e-13
Match length
                   77
% identity
                  (AF032877) alpha-tubulin [Chloromonas sp. ANT3]
NCBI Description
                   297013
Seq. No.
Seq. ID
                  LIB3136-021-Q1-K1-F6
Method
                  BLASTX
                  g1170937
NCBI GI
                   440
BLAST score
                   1.0e-43
E value
Match length
                   88
                   97
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >qi 450549 emb CAA81481 (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
                   297014
Seq. No.
Seq. ID
                   LIB3136-022-Q1-K1-A10
Method
                   BLASTX
NCBI GI
                   g2498778
BLAST score
                   333
                   4.0e-31
E value
Match length
                   136
                   52
% identity
                  PIR7A PROTEIN >gi 629799 pir S47086 pir7a protein - rice
NCBI Description
                   >gi_498744_emb_CAA84025_ (Z34271) Pir7a [Oryza sativa]
```

Seq. No. 297015

Seq. ID LIB3136-022-Q1-K1-C8

Method BLASTX
NCBI GI g135398
BLAST score 497
E value 2.0e-50
Match length 91
% identity 100



NCBI Description TUBULIN ALPHA-1 CHAIN >gi_82731_pir__S15773 tubulin alpha-1 chain - maize >gi_22147_emb_CAA33734_ (X15704)

alphal-tubulin [Zea mays]

Seq. No. 297016

Seq. ID LIB3136-022-Q1-K1-D6

Method BLASTX
NCBI GI g4191810
BLAST score 248
E value 3.0e-21
Match length 124
% identity 41

NCBI Description (AB006532) DNA helicase [Homo sapiens]

Seq. No. 297017

Seq. ID LIB3136-022-Q1-K1-G8

Method BLASTX
NCBI GI g82696
BLAST score 308
E value 2.0e-28
Match length 82
% identity 76

NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_

(X61121) glycine-rich protein [Zea mays]

Seq. No. 297018

Seq. ID LIB3136-023-Q1-K1-A2

Method BLASTX
NCBI GI g3341509
BLAST score 164
E value 2.0e-11
Match length 74
% identity 45

NCBI Description (AJ231133) caffeic acid 3-0-Methyltransferase [Saccharum

officinarum]

Seq. No. 297019

Seq. ID LIB3136-023-Q1-K1-C10

Method BLASTX
NCBI GI g4530585
BLAST score 175
E value 1.0e-12
Match length 50
% identity 64

NCBI Description (AF130978) B12D protein [Ipomoea batatas]

Seq. No. 297020

Seq. ID LIB3136-023-Q1-K1-D3

Method BLASTN
NCBI GI 9440170
BLAST score 63
E value 6.0e-27
Match length 107
% identity 96

NCBI Description Z.mays (C6000237) trpA gene

Seq. No. 297021

```
LIB3136-023-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4056421
BLAST score
                  256
E value
                  5.0e-22
Match length
                  77
% identity
                  61
                   (AC005322) Similar to gb Z30094 basic transcripion factor
NCBI Description
                  2, 44 kD subunit from Homo sapiens. EST gb W43325 comes
                  from this gene. [Arabidopsis thaliana]
                  297022
Seq. No.
                  LIB3136-024-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2496731
BLAST score
                  295
E value
                  1.0e-26
Match length
                  91
% identity
                  66
                  HYPOTHETICAL 30.2 KD PROTEIN Y40V >gi 2182566 (AE000089)
NCBI Description
                  Y4oV [Rhizobium sp. NGR234]
Seq. No.
                  297023
Seq. ID
                  LIB3136-024-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g2191175
BLAST score
                  158
                  1.0e-10
E value
Match length
                  117
                  32
% identity
NCBI Description
                  (AF007270) A IG002P16.24 gene product [Arabidopsis
                  thaliana]
Seq. No.
                  297024
Seq. ID
                  LIB3136-025-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  g3850569
BLAST score
                  254
E value
                  5.0e-22
                  97
Match length
% identity
                  49
                  (AC005278) ESTs gb T21276, gb T45403, and gb AA586113 come
NCBI Description
                  from this gene. [Arabidopsis thaliana]
                  297025
Seq. No.
Seq. ID
                  LIB3136-025-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  q2668742
BLAST score
                  364
E value
                  8.0e-35
Match length
                  84
% identity
                  83
```

297026 Seq. No.

Seq. ID LIB3136-025-Q1-K1-G3

Method BLASTX

41637

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

```
NCBI GI
                   g498643
BLAST score
                   350
E value
                   3.0e-34
Match length
                   92
                   93
% identity
                  (U10270) G-box binding factor 1 [Zea mays]
NCBI Description
                   297027
Seq. No.
Seq. ID
                   LIB3136-026-Q1-K1-A11
Method
                   BLASTX
NCBI GI
                   g2909846
BLAST score
                   321
                   7.0e-30
E value
Match length
                   75
% identity
                   81
                   (AF045570) (S)-adenosyl-L-methionine:delta 24-sterol
NCBI Description
                   methyltransferase [Zea mays]
Seq. No.
                   297028
                   LIB3136-026-Q1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g544250
BLAST score
                   243
E value
                   1.0e-20
Match length
                   81
                   64
% identity
                   ER LUMEN PROTEIN RETAINING RECEPTOR (HDEL RECEPTOR)
NCBI Description
                   >gi_541860_pir__A49677 endoplasmic reticulum retention
receptor Erd2 - Arabidopsis thaliana
                   297029
Seq. No.
Seq. ID
                   LIB3136-027-P1-K1-A10
                   BLASTX
Method
NCBI GI
                   q2497538
BLAST score
                   260
E value
                   4.0e-23
Match length
                   70
                   77
% identity
                  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 466350 (L08632)
NCBI Description
                   pyruvate kinase [Glycine max]
                   297030
Seq. No.
                   LIB3136-027-P1-K1-D1
Seq. ID
Method
                   BLASTX
                   g4249390
NCBI GI
BLAST score
                   152
                   3.0e-10
E value
```

Standard Comments

Match length 67 % identity

NCBI Description (AC005966) Similar to gb AF039182 probable aldo-keto

reductase from Fragaria \bar{x} ananassa. This gene may be cut off. EST gb U74151 comes from this gene. [Arabidopsis

thaliana]

297031 Seq. No.

Seq. ID LIB3136-027-P1-K1-D11

Method BLASTX

BLAST score

E value

216

1.0e-17

```
q1008904
NCBI GI
BLAST score
                    197
E value
                    2.0e-15
Match length
                    71
% identity
                   (L43094) xyloglucan endotransglycosylase [Tropaeolum majus]
NCBI Description
                    297032
Seq. No.
                    LIB3136-027-P1-K1-F10
Seq. ID
                    BLASTN
Method
NCBI GI
                    g559535
BLAST score
                    222
                    1.0e-122
E value
Match length
                    314
                    93
% identity
NCBI Description Z.mays mRNA for metallothionein
                    297033
Seq. No.
                    LIB3136-027-P1-K1-G12
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2952328
BLAST score
                    246
E value
                    3.0e-21
Match length
                    69
% identity
                    65
                    (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza
NCBI Description
                    sativa]
                    297034
Seq. No.
Seq. ID
                    LIB3136-028-Q1-K1-A11
Method
                    BLASTN
                    g602605
NCBI GI
                    67
BLAST score
                    2.0e-29
E value
Match length
                    95
% identity
                    48
NCBI Description Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin
                    297035
Seq. No.
Seq. ID
                    LIB3136-028-Q1-K1-B8
Method
                    BLASTX
NCBI GI
                    g119958
BLAST score
                    212
E value
                    3.0e-17
Match length
                    39
                    97
% identity
                    FERREDOXIN III PRECURSOR (FD III) >gi_168473 (M73831) ferredoxin [Zea mays] >gi_1864001_dbj_BAA19251_ (AB001387) Fd III [Zea mays] >gi_444686_prf__1907324C
NCBI Description
                    ferredoxin: ISOTYPE=III [Zea mays]
                    297036
Seq. No.
Seq. ID
                    LIB3136-028-Q1-K1-D7
Method
                    BLASTX
NCBI GI
                    g2252634
```

BLAST score

Match length

% identity

E value

235

112

62

8.0e-29



```
Match length
% identity
                   51
                   (U95973) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   297037
Seq. No.
                  LIB3136-028-Q1-K1-E10
Seq. ID
                  BLASTX
Method
                  g1172818
NCBI GI
BLAST score
                   315
                   3.0e-29
E value
                   83
Match length
                   77
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal
                   protein S16 [Oryza sativa] >gi_1096552_prf__2111468A
                   ribosomal protein S16 [Oryza sativa]
                   297038
Seq. No.
Seq. ID
                   LIB3136-028-Q1-K1-H10
Method
                   BLASTX
NCBI GI
                   g2267595
BLAST score
                   173
E value
                   1.0e-12
Match length
                   69
% identity
                   52
NCBI Description · (AF009412) plastocyanin precursor [Oryza sativa]
                   297039
Seq. No.
Seq. ID
                  LIB3136-029-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                   g1350720
BLAST score
                   162
E value
                   2.0e-11
Match length
                   62
                   56
% identity
                  60S RIBOSOMAL PROTEIN L32
NCBI Description
Seq. No.
                   297040
Seq. ID
                   LIB3136-029-Q1-K1-G6
Method
                   BLASTX
NCBI GI
                   g168489
BLAST score
                   276
                   1.0e-24
E value
Match length
                   81
                   68
% identity
NCBI Description
                   (M16902) glutathione S-transferase I [Zea mays] >gi 168491
                   (M16901) glutathione S-transferase I [Zea mays]
                   >gi_225458_prf__1303351A transferase,glutathione S [Zea
                   mays]
Seq. No.
                   297041
Seq. ID
                   LIB3136-029-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                   q3786009
```



NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 297042 LIB3136-030-Q1-K1-D8 Seq. ID Method BLASTX NCBI GI g2668742

BLAST score 277 5.0e-25 E value Match length 63 87 % identity

(AF034945) glycine-rich RNA binding protein [Zea mays] NCBI Description

Seq. No. 297043

LIB3136-030-Q1-K1-G2 Seq. ID Method

BLASTX q70642 NCBI GI BLAST score 510 E value 4.0e-52 Match length 105 19 % identity

NCBI Description ubiquitin precursor - Arabidopsis thaliana

>gi_17678_emb_CAA31331_ (X12853) polyubiquitin (AA 1 - 382) [Arabidopsis thaliana] >gi_987519 (U33014) polyubiquitin [Arabidopsis thaliana] >gi_226499_prf__1515347A

poly-ubiquitin [Arabidopsis thaliana]

Seq. No. 297044

Seq. ID LIB3136-030-Q1-K1-G7

Method BLASTX NCBI GI g2589164 BLAST score 256 2.0e-22 E value Match length 79 66 % identity

NCBI Description (D88452) aldehyde oxidase-2 [Zea mays]

297045 Seq. No.

LIB3136-030-Q1-K1-G8 Seq. ID

Method BLASTX NCBI GI g1350969 BLAST score 146 E value 8.0e-10 Match length 61 % identity 51

40S RIBOSOMAL PROTEIN S26 (S31) >gi_971284_dbj_BAA07208_ NCBI Description

(D38011) ribosomal protein S31 [Oryza sativa]

Seq. No. 297046

Seq. ID LIB3136-030-Q1-K1-H8

Method BLASTX NCBI GI g1877393 BLAST score 258 E value 2.0e-22 Match length 103 % identity 57

NCBI Description (Y11527) serine/threonine protein kinase [Oryza sativa]



```
297047
Seq. No.
                  LIB3136-032-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2384760
BLAST score
                  265
                  2.0e-31
E value
Match length
                  99
                  72
% identity
                  (AF016897) GDP dissociation inhibitor protein OsGDI2 [Oryza
NCBI Description
                  sativa]
                  297048
Seq. No.
Seq. ID
                  LIB3136-032-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  g3033400
BLAST score
                  153
                  4.0e-10
E value
Match length
                  76
% identity
                  42
NCBI Description
                  (AC004238) putative Ser/Thr protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  297049
Seq. ID
                  LIB3136-032-Q1-K1-B9
                  BLASTX
Method
NCBI GI
                  q3183405
BLAST score
                  175
                  1.0e-12
E value
                  84
Match length
% identity
                  43
NCBI Description
                  HYPOTHETICAL 11.3 KD PROTEIN C2C6.07 IN CHROMOSOME I
                  >gi 3451305 emb CAA20442 (AL031324) very hypothetical
                  protein [Schizosaccharomyces pombe]
Seq. No.
                  297050
                  LIB3136-032-Q1-K1-D8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1778148
BLAST score
                  59
E value
                  1.0e-24
Match length
                  207
                  83
% identity
NCBI Description
                  Zea mays plastid phosphate/phosphoenolpyruvate translocator
                  precursor (MZPPT4) mRNA, complete cds
Seq. No.
                  297051
Seq. ID
                  LIB3136-032-Q1-K1-D9
Method
                  BLASTN
NCBI GI
                  g2341060
BLAST score
                  53
E value
                  5.0e-21
Match length
                  210
                  87
% identity
```

Seq. No. 297052

NCBI Description

mRNA, complete cds

Zea mays translational initiation factor eIF-4A (tif-4A3)

```
LIB3136-032-Q1-K1-E6
Seq. ID
                  BLASTN
Method
                   q435312
NCBI GI
BLAST score
                   45
                   4.0e-16
E value
                  192
Match length
% identity
                  86
                  Z.mays mRNA for beta-D-glucosidase
NCBI Description
                  297053
Seq. No.
                  LIB3136-032-Q1-K1-H8
Seq. ID
Method
                  BLASTX
                  g1001263
NCBI GI
BLAST score
                   167
E value
                   7.0e-12
Match length
                   86
% identity
                   41
NCBI Description
                  (D64003) hypothetical protein [Synechocystis sp.]
Seq. No.
                   297054
                   LIB3136-033-Q1-K1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4432844
BLAST score
                   139
                   1.0e-08
E value
Match length
                   53
                   47
% identity
                  (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                   297055
Seq. No.
Seq. ID
                  LIB3136-033-Q1-K1-A8
Method
                   BLASTX
NCBI GI
                   g1552860
BLAST score
                   146
E value
                   3.0e-09
Match length
                   85
% identity
                   38
                   (Z80343) hypothetical protein Rv3777 [Mycobacterium
NCBI Description
                   tuberculosis]
                   297056
Seq. No.
                  LIB3136-033-Q1-K1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g606811
BLAST score
                   173
                   6.0e-13
E value
Match length
                   60
% identity
                   33
NCBI Description
                  (U08401) carbonic anhydrase [Zea mays]
Seq. No.
                   297057
                   LIB3136-033-Q1-K1-G7
Seq. ID
Method
                   BLASTN
                   g2921303
NCBI GI
BLAST score
                   85
```

5.0e-40

317

E value Match length



Seq. No. 297058

Seq. ID LIB3136-034-Q1-K1-A8

Method BLASTN
NCBI GI g170784
BLAST score 37
E value 2.0e-11
Match length 93
% identity 85

NCBI Description Wheat ubiquitin carrier protein (UBC1) mRNA, complete cds

Seq. No. 297059

Seq. ID LIB3136-034-Q1-K1-B6

Method BLASTX
NCBI GI g4027891
BLAST score 312
E value 5.0e-29
Match length 77
% identity 66

NCBI Description (AF049350) alpha-expansin precursor [Nicotiana tabacum]

Seq. No. 297060

Seq. ID LIB3136-034-Q1-K1-D2

Method BLASTX
NCBI GI g2668742
BLAST score 186
E value 2.0e-14
Match length 63
% identity 63

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 297061

Seq. ID LIB3136-034-Q1-K1-E10

Method BLASTX
NCBI GI g1084479
BLAST score 148
E value 2.0e-09
Match length 30
% identity 97

NCBI Description H+-transporting ATP synthase (EC 3.6.1.34) delta chain -

maize (fragment) >gi 311237 emb CAA46804 (X66005)

H(+)-transporting ATP synthase [Zea mays]

Seq. No. 297062

Seq. ID LIB3136-035-Q1-K1-A11

Method BLASTX
NCBI GI g2281086
BLAST score 353
E value 2.0e-33
Match length 127
% identity 51

NCBI Description (AC002333) indole-3-acetate beta-glucosyltransferase isolog

[Arabidopsis thaliana]

% identity

NCBI Description



```
297063
Seq. No.
                  LIB3136-036-Q1-K1-A4
Seq. ID
                  BLASTX
Method
                  g312179
NCBI GI
                  477
BLAST score
                  2.0e-48
E value
Match length
                  92
                  99
% identity
                  (X73151) glyceraldehyde 3-phosphate dehydrogenase
NCBI Description
                  (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic
                  glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]
                  >gi_1185554 (U45858) glyceraldehyde-3-phosphate
                   dehydrogenase [Zea mays]
                   297064
Seq. No.
                   LIB3136-036-Q1-K1-B12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1431629
                   292
BLAST score
                   2.0e-26
E value
                   138
Match length
                   46
% identity
NCBI Description (X99348) pectinacetylesterase precursor [Vigna radiata]
                   297065
Seq. No.
                   LIB3136-036-Q1-K1-C7
Seq. ID
                   BLASTX
Method
                   q3080420
NCBI GI
BLAST score
                   158
                   1.0e-10
E value
                   62
Match length
% identity
                   50
                   (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                   thaliana]
                   297066
Seq. No.
                   LIB3136-036-Q1-K1-G1
Seq. ID
                   BLASTX
Method
                   q4056425
NCBI GI
                   239
BLAST score
                   9.0e-21
E value
                   73
Match length
 % identity
                   (AC005322) ESTs gb_H36249, gb_AA59732 and gb_AA651219 come
NCBI Description
                   from this gene. [Arabidopsis thaliana]
                   297067
 Seq. No.
                   LIB3136-036-Q1-K1-H10
 Seq. ID
                   BLASTN
 Method
                   g258165
 NCBI GI
                    41
 BLAST score
                   7.0e-14
 E value
                    49
 Match length
                    96
```

Mutant, 299 nt]

Wx (wx-B5)=waxy gene {long terminal repeat} [maize, Genomic



```
297068
Seq. No.
                  LIB3136-037-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q12426
BLAST score
                  245
                  6.0e-21
E value
Match length
                  62
                  81
% identity
NCBI Description
                  (X17438) NDH-C protein (AA 1 - 120) [Zea mays]
                  297069
Seq. No.
                  LIB3136-038-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3892709
BLAST score
                  426
                  3.0e-42
E value
Match length
                  93
% identity
                  78
NCBI Description
                  (AL033545) putative protein [Arabidopsis thaliana]
Seq. No.
                  297070
Seq. ID
                  LIB3136-038-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g2191187
BLAST score
                  273
                  4.0e-24
E value
Match length
                  89
% identity
                  61
                   (AF007271) contains similarity to a DNAJ-like domain
NCBI Description
                   [Arabidopsis thaliana]
                  297071
Seq. No.
Seq. ID
                  LIB3136-039-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  q2130051
BLAST score
                  262
                  1.0e-25
E value
Match length
                  79
                  76
% identity
NCBI Description
                  xylose isomerase (EC 5.3.1.5) - barley
                  >gi 1296807 emb CAA64544 (X95256) xylose isomerase
                   [Hordeum vulgare] >gi 1588664 prf 2209268A xylose
                  isomerase [Hordeum vulgare]
Seq. No.
                  297072
Seq. ID
                  LIB3136-039-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g2827143
BLAST score
                  417
E value
                  4.0e-41
Match length
                  105
% identity
                  78
NCBI Description
                   (AF027174) cellulose synthase catalytic subunit
                   [Arabidopsis thaliana]
```

Seq. No. 297073

Seq. ID LIB3136-040-P1-K1-A10

Match length

```
Method
NCBI GI
                   g3643608
BLAST score
                   206
E value
                   3.0e-16
Match length
                   104
% identity
                   45
                  (AC005395) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   297074
Seq. No.
                  LIB3136-040-P1-K1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                   g22163
BLAST score
                   100
                   4.0e-49
E value
Match length
                   212
                   87
% identity
                  Z.mays MANT2 mRNA for adenine nucleotide translocator
NCBI Description
                   (ADP/ATP translocase)
Seq. No.
                   297075
Seq. ID
                   LIB3136-040-P1-K1-B8
Method
                   BLASTX
NCBI GI
                   g606815
BLAST score
                   351
E value
                   3.0e - 33
Match length
                   93
                   28
% identity
                  (U08403) carbonic anhydrase [Zea mays]
NCBI Description
                   297076
Seq. No.
Seq. ID
                   LIB3136-040-P1-K1-C2
Method
                   BLASTN
NCBI GI
                   g413915
BLAST score
                   54
E value
                   2.0e-21
Match length
                   90
% identity
                   92
                  Rice mRNA for isocitrate dehydrogenase, partial cds
NCBI Description
                   >gi_3106666_dbj_D42386_D42386 Rice callus cDNA, AK088
                   297077
Seq. No.
                   LIB3136-040-P1-K1-D12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3264597
BLAST score
                   98
E value
                   7.0e-48
Match length
                   255
% identity
                   84
NCBI Description
                  Zea mays trypsin inhibitor mRNA, complete cds
                   297078
Seq. No.
                   LIB3136-040-P1-K1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g541112
BLAST score
                   186
E value
                   7.0e-14
```

```
% identity
NCBI Description
                  hypothetical protein f678 - Escherichia coli >gi_304982
                  (L19201) ORF f678 [Escherichia coli]
                  297079
Seq. No.
                  LIB3136-042-P1-K1-E9
Seq. ID
Method
                  BLASTX
                  g1296955
NCBI GI
BLAST score
                  284
E value
                  1.0e-25
Match length
                  62
                  45
% identity
NCBI Description
                  (X95402) duplicated domain structure protein [Oryza sativa]
                  297080
Seq. No.
Seq. ID
                  LIB3136-043-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g2191140
BLAST score
                  147
E value
                  2.0e-09
Match length
                  91
% identity
                  47
NCBI Description
                  (AF007269) contains weak similarity to MYB-related proteins
```

[Arabidopsis thaliana]

Seq. No. 297081 Seq. ID LIB3136-044-P1-K1-E3

BLASTN Method NCBI GI g248336 BLAST score 69 E value 2.0e-30 137 Match length % identity

NCBI Description polyubiquitin [maize, Genomic, 3841 nt]

297082 Seq. No.

LIB3136-044-P1-K1-H10 Seq. ID

Method BLASTX NCBI GI g2191172 BLAST score 175 4.0e-13 E value Match length 44 73 % identity

(AF007270) contains similarity to GATA-type zinc fingers NCBI Description

(PS:PS00344) [Arabidopsis thaliana]

Seq. No. 297083

Seq. ID LIB3136-045-Q1-K1-A2

Method BLASTX NCBI GI q4490317 BLAST score 157 E value 2.0e-10 Match length 89 % identity

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

297084 Seq. No.

```
LIB3136-045-Q1-K1-B6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4263722
                  509
BLAST score
                  8.0e-52
E value
Match length
                  126
                  79
% identity
                  (AC006223) putative glucan synthase [Arabidopsis thaliana]
NCBI Description
                  297085
Seq. No.
Seq. ID
                  LIB3136-045-Q1-K1-C1
Method
                  BLASTN
NCBI GI
                  g1546918
BLAST score
                  33
E value
                  4.0e-09
Match length
                  49
% identity
                  92
NCBI Description Z.mays mRNA for translation initiation factor 5A
                  297086
Seq. No.
Seq. ID
                  LIB3136-045-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g4336205
                  259
BLAST score
                  7.0e-23
E value
                  81
Match length
% identity
                  68
                  (AF077372) cytochrome b5 reductase [Zea mays]
NCBI Description
Seq. No.
                  297087
Seq. ID
                  LIB3136-045-Q1-K1-C8
Method
                  BLASTX
                  g4218120
NCBI GI
BLAST score
                  172
E value
                  3.0e-20
Match length
                  99
                  58
% identity
                  (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  297088
Seq. No.
                  LIB3136-045-Q1-K1-E4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1172809
BLAST score
                  370
E value
                  2.0e-35
Match length
                  113
% identity
                  70
                  60S RIBOSOMAL PROTEIN L10 (QM PROTEIN HOMOLOG) >gi 468056
NCBI Description
                   (U06108) QM protein [Zea mays]
```

Seq. No. 297089

Seq. ID LIB3136-045-Q1-K1-F2

Method BLASTX NCBI GI g1321661 BLAST score 164 E value 1.0e-11

Match length % identity

NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

Seq. No.

297090

Seq. ID

LIB3136-045-Q1-K1-F7

BLASTX Method q1532135 NCBI GI BLAST score 207 2.0e-16 E value 47 Match length 85 % identity

(U49442) chloroplast mRNA-binding protein CSP41 precursor NCBI Description

[Spinacia oleracea]

297091 Seq. No.

LIB3136-045-Q1-K1-G11 Seq. ID

Method BLASTX NCBI GI q2826882 BLAST score 175 3.0e-13 E value Match length 62 % identity 56

NCBI Description (AJ223634) transcription factor IIA small subunit

[Arabidopsis thaliana]

Seq. No. Seq. ID 297092

LIB3136-045-Q1-K1-H10

BLASTX Method NCBI GI g3513727 BLAST score 209 E value 1.0e-16 Match length 110 37 % identity

(AF080118) contains similarity to TPR domains (Pfam: NCBI Description

TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi 4539358 emb CAB40052.1 (AL049525) putative

protein [Arabidopsis thaliana]

Seq. No. 297093

Seq. ID LIB3136-045-Q1-K1-H7

Method BLASTX g2497539 NCBI GI BLAST score 194 E value 6.0e-27 104 Match length 65 % identity

NCBI Description PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi 169703

(M64736) ATP:pyruvate phosphotransferase [Ricinus communis]

Seq. No. 297094

Seq. ID LIB3136-045-Q1-K1-H9

Method BLASTX NCBI GI g3513727 BLAST score 235 E value 1.0e-19

```
Match length 10 % identity 50
```

NCBI Description (AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative

protein [Arabidopsis thaliana]

 Seq. No.
 297095

 Seq. ID
 LIB3136-047-Q1-K1-B3

 Method
 BLASTX

NCBI GI g4567249
BLAST score 261
E value 3.0e-23
Match length 61
% identity 75

NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No. 297096

Seq. ID LIB3136-047-Q1-K1-E11

Method BLASTX
NCBI GI g2668742
BLAST score 201
E value 3.0e-16
Match length 45
% identity 87

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 297097

Seq. ID LIB3136-047-Q1-K1-E12

Method BLASTX
NCBI GI g421787
BLAST score 207
E value 2.0e-16
Match length 109
% identity 45

NCBI Description jacalin prepropeptide - jackfruit >gi 289162 (L03796)

jacalin [Artocarpus integrifolia]

Seq. No. 297098

Seq. ID LIB3136-047-Q1-K1-F5

Method BLASTX
NCBI GI g576192
BLAST score 357
E value 1.0e-34
Match length 82
% identity 91

NCBI Description Dioscoreophyllum cumminsii >gi_576193_pdb_1MOL_B

Dioscoreophyllum cumminsii

Seq. No. 297099

Seq. ID LIB3136-048-Q1-K1-A5

Method BLASTN
NCBI GI g550541
BLAST score 121
E value 2.0e-61
Match length 350

NCBI Description

297105

Seq. No.



% identity Z.mays CYP71C4 mRNA for cytochrome P-450 NCBI Description 297100 Seq. No. Seq. ID LIB3136-048-Q1-K1-C8 Method BLASTN NCBI GI g236729 BLAST score 53 4.0e-21 E value Match length 117 % identity 86 metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt] NCBI Description 297101 Seq. No. LIB3136-048-Q1-K1-D1 Seq. ID Method BLASTX g3759184 NCBI GI BLAST score 169 4.0e-12 E value Match length 54 % identity 61 NCBI Description (AB018441) phi-1 [Nicotiana tabacum] Seq. No. 297102 Seq. ID LIB3136-048-Q1-K1-F4 Method BLASTX NCBI GI g729103 BLAST score 184 E value 4.0e-14 50 Match length 72 % identity NCBI Description CHALCONE--FLAVONONE ISOMERASE >gi 542181 pir S41570 chalcone isomerase (EC 5.5.1.6) - maize >gi 396149_emb_CAA80441_ (Z22760) chalcone flavonone isomerase [Zea mays] Seq. No. 297103 Seq. ID LIB3136-048-Q1-K1-G2 Method BLASTX NCBI GI g4204372 BLAST score 299 E value 3.0e-27 79 Match length 77 % identity (U62748) acidic ribosomal protein P2a-2 [Zea mays] NCBI Description 297104 Seq. No. Seq. ID LIB3136-049-Q1-K1-A12 Method BLASTX NCBI GI g3982632 BLAST score 513 E value 3.0e-52 Match length 104 % identity 93 (AF056160) disease resistance gene analog PIC20 [Zea mays]

NCBI GI

BLAST score

q550437

146



```
LIB3136-049-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g347855
BLAST score
                  288
E value
                  8.0e-26
Match length
                  138
% identity
                  43
                  (L21753) glucose transporter [Saccharum hybrid cultivar
NCBI Description
                  H65-7052]
                  297106
Seq. No.
                  LIB3136-049-Q1-K1-B5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
                  6.0e-11
E value
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  297107
Seq. No.
Seq. ID
                  LIB3136-049-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  g1711036
                  178
BLAST score
                  2.0e-13
E value
Match length
                   44
                  77
% identity
                  (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum
NCBI Description
                  sativum]
Seq. No.
                  297108
                  LIB3136-049-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4586039
BLAST score
                  363
                  1.0e-34
E value
                  108
Match length
% identity
                   66
                  (AC007109) unknown protein [Arabidopsis thaliana]
NCBI Description
                  297109
Seq. No.
Seq. ID
                  LIB3136-049-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                   g4586027
BLAST score
                   159
E value
                   3.0e-11
Match length
                   46
                   67
% identity
                  (AC007109) putative ribosomal protein L14 [Arabidopsis
NCBI Description
                   thaliana]
                   297110
Seq. No.
Seq. ID
                  LIB3136-049-Q1-K1-F9
Method
                  BLASTN
```

Seq. No.

```
E value
Match length
                  274
                  89
% identity
                  Z.mays CYP71C2 mRNA for cytochrome P-450
NCBI Description
Seq. No.
                  297111
Seq. ID
                  LIB3136-050-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g4572673
BLAST score
                  209
                  6.0e-17
E value
Match length
                  89
% identity
                  54
NCBI Description
                  (AC006954) putative sarcosine oxidase [Arabidopsis
                  thaliana]
                  297112
Seq. No.
                  LIB3136-050-Q1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455338
BLAST score
                  265
                  4.0e-23
E value
Match length
                  91
% identity
                  55
NCBI Description
                  (AL035525) putative protein [Arabidopsis thaliana]
Seq. No.
                  297113
Seq. ID
                  LIB3136-051-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  g1619300
BLAST score
                  166
E value
                  7.0e-12
                  71
Match length
                  51
% identity
                  (X95269) LRR protein [Lycopersicon esculentum]
NCBI Description
                  297114
Seq. No.
Seq. ID
                  LIB3136-051-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  g2668744
BLAST score
                   340
                   4.0e-32
E value
                  70
Match length
% identity
                   90
                  (AF034946) ubiquitin conjugating enzyme [Zea mays]
NCBI Description
                  297115
Seq. No.
                  LIB3136-051-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2668742
BLAST score
                   382
E value
                   4.0e-37
Match length
                  80
% identity
                   94
NCBI Description
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
```



```
Seq. ID
                  LIB3136-051-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g2244965
BLAST score
                  144
                  6.0e-09
E value
Match length
                  74
% identity
                  39
                  (Z97340) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                  297117
Seq. No.
Seq. ID
                  LIB3136-051-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g2288969
BLAST score
                  227
                  5.0e-19
E value
Match length
                  61
% identity
                  77
                  (Y12862) glutathione transferase [Zea mays]
NCBI Description
                  297118
Seq. No.
Seq. ID
                  LIB3136-051-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  q2119187
BLAST score
                  237
                  8.0e-20
E value
Match length
                  47
                  96
% identity
                  transmembrane protein, glucose starvation-induced - maize
NCBI Description
                  >gi_575731_emb CAA57955 (X82633) transmembrane protein
                  [Zea mays]
Seq. No.
                  297119
Seq. ID
                  LIB3136-051-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  g1272505
BLAST score
                  140
E value
                  1.0e-08
Match length
                  45
% identity
                  73
NCBI Description
                  (D49551) peroxidase [Oryza sativa]
Seq. No.
                  297120
Seq. ID
                  LIB3136-052-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g1173055
BLAST score
                  244
E value
                  3.0e-34
                  82
Match length
                  94
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir__S42497
                  ribosomal protein L11.e - alfalfa >gi 1076504 pir S51819
                  RL5 ribosomal protein - alfalfa >gi_463252_emb_CAA55090_
                  (X78284) RL5 ribosomal protein [Medicago sativa]
```

Seq. No. 297121

Seq. ID LIB3136-052-Q1-K1-C9

Method BLASTX

Method

NCBI GI

BLASTX

g1362103

```
NCBI GI
                  g1711240
                  145
BLAST score
E value
                  3.0e-09
                  48
Match length
                  52
% identity
NCBI Description
                  (D86728) TIS [Mus musculus]
Seq. No.
                  297122
                  LIB3136-052-Q1-K1-D6
Seq. ID
Method
                  BLASTX
                  g120670
NCBI GI
BLAST score
                  346
E value
                  1.0e-32
                  67
Match length
                  99
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 100879 pir S06879 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) C - maize
                  >gi 295853 emb CAA33620 (X15596) GAPDH [Zea mays]
Seq. No.
                  297123
Seq. ID
                  LIB3136-052-Q1-K1-D9
Method
                  BLASTN
NCBI GI
                  g1532072
BLAST score
                  56
                  9.0e-23
E value
Match length
                  104
% identity
                  88
                  Z.mays mRNA for S-adenosylmethionine decarboxylase
NCBI Description
Seq. No.
                  297124
Seq. ID
                  LIB3136-052-Q1-K1-F3
Method
                  BLASTN
                  a644492
NCBI GI
BLAST score
                  43
E value
                  5.0e-15
Match length
                  156
                  89
% identity
NCBI Description Corn elongation factor lalpha gene, complete cds
Seq. No.
                  297125
                  LIB3136-054-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1168536
BLAST score
                  183
                  4.0e-14
E value
Match length
                  66
                  58
% identity
                  PHYTEPSIN PRECURSOR (ASPARTIC PROTEINASE)
NCBI Description
                  >gi_100567_pir__S19697 aspartic proteinase (EC 3.4.23.-)
                  precursor - barley >gi_18904_emb_CAA39602_ (X56136)
                  aspartic proteinase [Hordeum vulgare]
                  297126
Seq. No.
Seq. ID
                  LIB3136-054-Q1-K1-A5
```



```
BLAST score
                  3.0e-16
E value
Match length
                  89
                  51
% identity
                  ubiquitin conjugating enzyme - tomato
NCBI Description
                  >gi 886679 emb CAA58111 (X82938) ubiquitin conjugating
                  enzyme [Lycopersicon esculentum]
                  297127
Seq. No.
                  LIB3136-054-Q1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4586255
BLAST score
                  181
E value
                  4.0e-25
Match length
                  79
                  73
% identity
NCBI Description
                  (AL049640) putative protein [Arabidopsis thaliana]
Seq. No.
                  LIB3136-054-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3421413
BLAST score
                  171
                  4.0e-12
E value
Match length
                  63
                  60
% identity
                  (AF081922) protein phosphatase 2A 55 kDa B regulatory
NCBI Description
                  subunit [Oryza sativa] >gi 3421415 (AF081923) protein
                  phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]
Seq. No.
                  297129
                  LIB3136-054-Q1-K1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1854377
BLAST score
                  59
                  1.0e-24
E value
Match length
                  271
                  81
% identity
NCBI Description
                  Saccharum officinarum RNA for Sucrose-Phosphate Synthase,
                  complete cds
                  297130
Seq. No.
Seq. ID
                  LIB3136-054-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g4106389
BLAST score
                  182
                  2.0e-13
E value
Match length
                  79
% identity
                  54
NCBI Description
```

(AF074849) MEI1 [Arabidopsis thaliana]

Seq. No. 297131

Seq. ID LIB3136-055-Q1-K1-B12

Method BLASTN NCBI GI g2894376 BLAST score 39 E value 2.0e-12



Match length 90 % identity

NCBI Description Hordeum vulgare DNA for chromosome 4H

Seq. No.

297132

Seq. ID Method

LIB3136-055-Q1-K1-H10 BLASTX

NCBI GI g2791896 BLAST score 147 E value 1.0e-09 Match length 92 37 % identity

(Y08997) 146kDa nuclear protein [Xenopus laevis] NCBI Description

Seq. No.

297133

LIB3136-056-Q1-K1-B12 Seq. ID

Method BLASTX NCBI GI g2506277 BLAST score 154 1.0e-10 E value Match length 56 52 % identity

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60

KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >qi 806808

(U21139) chaperonin precursor [Pisum sativum]

Seq. No.

297134 Seq. ID LIB3136-056-Q1-K1-B2

Method BLASTX g115786 NCBI GI BLAST score 301 E value 1.0e-27 77 Match length 79 % identity

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB) (LHCP) >gi 82680 pir A29119 chlorophyll a/b-binding protein - maize >gi 22357 emb CAA68451 (Y00379) LHCP [Zea

mays]

297135 Seq. No.

LIB3136-056-Q1-K1-B3 Seq. ID

Method BLASTX NCBI GI g4586112 BLAST score 194 E value 8.0e-15 Match length 84 % identity 45

NCBI Description (ALO49638) putative protein [Arabidopsis thaliana]

Seq. No. 297136

Seq. ID LIB3136-056-Q1-K1-B4

Method BLASTX NCBI GI g3789952 BLAST score 166 E value 1.0e-11 Match length 52 % identity 62

. -



(AF094775) chlorophyll a/b-binding protein presursor [Oryza NCBI Description sativa] 297137 Seq. No. LIB3136-056-Q1-K1-C11 Seq. ID Method BLASTX NCBI GI g3668091 BLAST score 368 3.0e-35 E value Match length 103 % identity 61 NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana] 297138 Seq. No. LIB3136-056-01-K1-D12 Seq. ID Method BLASTX NCBI GI g4538903 BLAST score 214 E value 3.0e-17 Match length 134 % identity 40 NCBI Description (AL049482) putative protein [Arabidopsis thaliana] 297139 Seq. No. LIB3136-056-Q1-K1-E1 Seq. ID Method BLASTX NCBI GI g4589962 BLAST score 163 1.0e-11 E value Match length 77 % identity 47 NCBI Description (AC007169) putative fructokinase [Arabidopsis thaliana] 297140 Seq. No. LIB3136-056-Q1-K1-G5 Seq. ID Method BLASTX NCBI GI g1514643 BLAST score 158 E value 1.0e-10 56 Match length 55 % identity NCBI Description (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza] 297141 Seq. No. Seq. ID LIB3136-056-Q1-K1-G8 Method BLASTX NCBI GI g1709970

BLAST score 428 E value 3.0e-42 Match length 125 % identity 66

NCBI Description 60S RIBOSOMAL PROTEIN L10A

Seq. No. 297142

Seq. ID LIB3136-057-Q1-K1-C2

Method BLASTX g1272685 NCBI GI

```
BLAST score
                  1.0e-57
E value .
                  116
Match length
                  89
% identity
                  (Z24449) acetyl CoA carboxylase [Zea mays]
NCBI Description
                  297143
Seq. No.
                  LIB3136-057-Q1-K1-D10
Seq. ID
                  BLASTX
Method
                  q1769901
NCBI GI
                  161
BLAST score
                  1.0e-11
E value
                   54
Match length
% identity
                   57
                  (X95737) proline transporter 1 [Arabidopsis thaliana]
NCBI Description
                   >gi_2088642 (AF002109) proline transporter 1 [Arabidopsis
                   thaliana]
                   297144
Seq. No.
                   LIB3136-057-Q1-K1-E10
Seq. ID
                   BLASTN
Method
                   g22646
NCBI GI
                   54
BLAST score
                   2.0e-21
E value
Match length
                   131
% identity
NCBI Description Z.mays MFS18 mRNA
                   297145
Seq. No.
                   LIB3136-057-Q1-K1-F7
Seq. ID
                   BLASTX
Method
                   g3292827
NCBI GI
                   328
BLAST score
                   6.0e-31
E value
                   78
Match length
% identity
                   (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
                   297146
Seq. No.
                   LIB3136-058-Q1-K1-B5
Seq. ID
                   BLASTX
Method
                   q2765837
NCBI GI
                   157
BLAST score
E value
                   2.0e-10
Match length
                   76
                   47
 % identity
                   (Z96936) NAP16kDa protein [Arabidopsis thaliana]
 NCBI Description
                   297147
 Seq. No.
                   LIB3136-058-Q1-K1-B6
 Seq. ID
 Method
                   BLASTX
                    g4539009
 NCBI GI
                    267
 BLAST score
                    1.0e-23
 E value
                    99
 Match length
                    51
 % identity
 NCBI Description (AL049481) putative protein [Arabidopsis thaliana]
```

NCBI GI

```
2
```

```
297148
Seq. No.
                  LIB3136-058-Q1-K1-C5
Seq. ID
Method
                  BLASTX
                  g746540
NCBI GI
BLAST score
                  210
                  1.0e-16
E value
                  97
Match length
                  44
% identity
NCBI Description (U23521) No definition line found [Caenorhabditis elegans]
Seq. No.
                  297149
Seq. ID
                  LIB3136-058-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  g520544
BLAST score
                  217
E value
                  1.0e-17
                  107
Match length
% identity
                  53
NCBI Description (U12195) betaine aldehyde dehydrogenase [Sorghum bicolor]
Seq. No.
                  297150
Seq. ID
                  LIB3136-058-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  g2674203
BLAST score
                  345
E value
                  1.0e-32
Match length
                  124
                  58
% identity
NCBI Description
                  (AF036328) CLP protease regulatory subunit CLPX
                   [Arabidopsis thaliana]
Seq. No.
                  297151
Seq. ID
                  LIB3136-058-Q1-K1-D6
Method
                  BLASTX
                  g4038471
NCBI GI
BLAST score
                  196
                  2.0e-15
E value
Match length
                  62
% identity
                   66
NCBI Description (AF111029) 40S ribosomal protein S27 homolog [Zea mays]
                  297152
Seq. No.
Seq. ID
                  LIB3136-058-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g4262236
BLAST score
                  245
E value
                   7.0e-21
Match length
                  74
% identity
                   65
NCBI Description
                  (AC006200) putative ribose 5-phosphate isomerase
                   [Arabidopsis thaliana]
Seq. No.
                   297153
Seq. ID
                  LIB3136-058-Q1-K1-F7
Method
                  BLASTX
```

41661

g2832625



```
BLAST score
                   4.0e-10
E value
Match length
                   60
% identity
                   53
NCBI Description
                   (AL021711) putative protein [Arabidopsis thaliana]
                   297154
Seq. No.
                   LIB3136-058-Q1-K1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3618312
BLAST score
                   258
                   2.0e-22
E value
Match length
                   80
% identity
                   65
                  (AB001884) zinc finger protein [Oryza sativa]
NCBI Description
                   297155
Seq. No.
Seq. ID
                   LIB3136-059-Q1-K1-C11
Method
                   BLASTX
NCBI GI
                   g464705
BLAST score
                   154
                   2.0e-10
E value
Match length
                   66
% identity
                   58
                   40S RIBOSOMAL PROTEIN S13 >gi_419802_pir__S30146 ribosomal
NCBI Description
                   protein S13.e - maize >gi 288059 emb CAA44311 (X62455) cytoplasmatic ribosomal protein S13 [Zea mays]
                   297156
Seq. No.
Seq. ID
                   LIB3136-059-Q1-K1-D9
Method
                   BLASTX
NCBI GI
                   g3047117
BLAST score
                   342
E value
                   1.0e-32
Match length
                   84
                   80
% identity
                   (AF058919) similar to ATP-dependent RNA helicases
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   297157
Seq. ID
                   LIB3136-059-Q1-K1-E7
Method
                   BLASTX
NCBI GI
                   q1076719
BLAST score
                   154
E value
                   4.0e-10
                   39
Match length
                   67
% identity
                   glycine rich protein - barley (fragment)
NCBI Description
                   >gi_728596_emb_CAA88559_ (Z48625) glycine rich protein
                   [Hordeum vulgare]
Seq. No.
                   297158
```

Seq. ID LIB3136-059-Q1-K1-F10

Method BLASTX
NCBI GI g2132925
BLAST score 160
E value 8.0e-11



Match length 122 % identity 33

NCBI Description probable membrane protein YOR245c - yeast (Saccharomyces

cerevisiae) >gi_1420558_emb_CAA99466_ (Z75153) ORF YOR245c

[Saccharomyces cerevisiae]

Seq. No. 297159

Seq. ID LIB3136-059-Q1-K1-F12

Method BLASTX
NCBI GI g4512653
BLAST score 410
E value 3.0e-45
Match length 150
% identity 61

NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]

Seq. No. 297160

Seq. ID LIB3136-059-Q1-K1-G12

Method BLASTX
NCBI GI g3687249
BLAST score 201
E value 8.0e-16
Match length 54
% identity 74

NCBI Description (AC005169) putative copia-like transposable element

[Arabidopsis thaliana]

Seq. No. 297161

Seq. ID LIB3136-060-Q1-K1-A4

Method BLASTX
NCBI GI g1871180
BLAST score 196
E value 3.0e-15
Match length 48
% identity 73

NCBI Description (U90439) unknown protein [Arabidopsis thaliana]

Seq. No. 297162

Seq. ID LIB3136-060-Q1-K1-B8

Method BLASTN
NCBI GI g2062705
BLAST score 34
E value 9.0e-10
Match length 34
% identity 100

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 297163

Seq. ID LIB3136-060-Q1-K1-C11

Method BLASTX
NCBI GI g2388580
BLAST score 253
E value 1.0e-21
Match length 86
% identity 50

NCBI Description (AC000098) Similar to Sequence 10 from patent 5477002

(gb_1253956). [Arabidopsis thaliana]

```
297164
Seq. No.
                  LIB3136-060-Q1-K1-D1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g167082
BLAST score
                  35
E value
                  3.0e-10
Match length
                  35
% identity
                  100
NCBI Description
                  H.vulgare peroxidase BP 2A (Prx6) gene, complete cds
                  297165
Seq. No.
                  LIB3136-060-Q1-K1-D11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2293566
BLAST score
                  211
                  6.0e-27
E value
Match length
                  128
% identity
                  57
                  (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
NCBI Description
                  297166
Seq. No.
Seq. ID
                  LIB3136-060-Q1-K1-F8
Method
                  BLASTN
NCBI GI
                  q3057119
BLAST score
                  34
                  7.0e-10
E value
Match length
                  66
% identity
                  88
NCBI Description Zea mays starch synthase DULL1 (dull1) mRNA, complete cds
Seq. No.
                  297167
                  LIB3136-060-Q1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q266578
BLAST score
                  259
                  2.0e-22
E value
Match length
                  56
                  82
% identity
NCBI Description
                  METALLOTHIONEIN-LIKE PROTEIN 1 >gi 100898 pir S17560
                  metallothionein-like protein - maize >gi 236730 bbs 57629
                  (S57628) metallothionein homologue [Zea mays, Peptide, 76
                  aa] [Zea mays] >gi 559536 emb CAA57676 (X82186)
                  metallothionein- like protein [Zea mays]
                  >gi_228095_prf__1717215A metallothionein-like protein [Zea
                  mays]
Seq. No.
                  297168
Seq. ID
                  LIB3137-001-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g2642648
BLAST score
                  314
                  5.0e-29
E value
Match length
                  87
% identity
NCBI Description
                  (AF033852) cytosolic heat shock 70 protein; HSC70-3
```

[Spinacia oleracea] >gi 2660768 (AF034616) cytosolic heat

% identity



shock 70 protein [Spinacia oleracea] >gi_2660770 (AF034617)
cytosolic heat shock 70 protein [Spinacia oleracea]

297169 Seq. No. Seq. ID LIB3137-001-Q1-K1-F4 Method BLASTX NCBI GI q417745 BLAST score 240 E value 2.0e-20 Match length 91 % identity 58 ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE NCBI Description HYDROLASE) (ADOHCYASE) >gi 170773 (L11872) S-adenosyl-L-homocysteine hydrolase [Triticum aestivum] 297170 Seq. No. LIB3137-001-Q1-K1-F5 Seq. ID Method BLASTX NCBI GI q3242075 BLAST score 146 1.0e-09 E value Match length 49 % identity 59 NCBI Description (Z97059) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana] Seq. No. 297171 Seq. ID LIB3137-001-Q1-K1-G12 BLASTN Method g22229 NCBI GI BLAST score 132 E value 2.0e-68 203 Match length 91 % identity NCBI Description Z.mays cab-m7 gene for light harvesting chlorophyll a/b binding protein 297172 Seq. No. LIB3137-001-Q1-K1-H4 Seq. ID Method BLASTX g1430887 NCBI GI BLAST score 185 E value 7.0e-14 Match length 36 100 % identity NCBI Description (X99197) 70 kD heatshockprotein [Medicago sativa] Seq. No. 297173 Seq. ID LIB3137-002-Q1-K1-A2 Method BLASTX NCBI GI g2668742 BLAST score 344 E value 2.0e-32 79 Match length

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

```
Seq. No.
                  LIB3137-002-Q1-K1-E8
Seq. ID
                  BLASTX
Method
                  g2995953
NCBI GI
                  145
BLAST score
                  5.0e-09
E value
                  63
Match length
                  49
% identity
NCBI Description (AF053565) glutaredoxin I [Mesembryanthemum crystallinum]
                   297175
Seq. No.
                  LIB3137-002-Q1-K1-E9
Seq. ID
                   BLASTX
Method
                   a3024657
NCBI GI
                   378
BLAST score
                   1.0e-36
E value
                   103
Match length
                   72
% identity
NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
                   >gi_2668740 (AF034944) translation initiation factor; GOS2
                   [Zea mays]
                   297176
Seq. No.
                   LIB3137-002-Q1-K1-F3
Seq. ID
Method
                   BLASTX
                   q2984709
                                                        - 57
NCBI GI
                   336
BLAST score
                   1.0e-31
E value
                   72
Match length
% identity
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                   297177
Seq. No.
                   LIB3137-002-Q1-K1-F8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q578549
BLAST score
                   152
                   3.0e-10
 E value
                   43
Match length
 % identity
                   72
 NCBI Description (Z22614) ubiquitin [Tetrahymena pyriformis]
                   297178
 Seq. No.
                   LIB3137-002-Q1-K1-G2
 Seq. ID
 Method
                   BLASTN
                   g551482
 NCBI GI
                   106
 BLAST score
                   1.0e-52
 E value
                   231
 Match length
                   95
 % identity
                   Zea mays ABA- and ripening-inducible-like protein mRNA,
 NCBI Description
                   complete cds
                    297179
 Seq. No.
                   LIB3137-002-Q1-K1-G6
 Seq. ID
```

41666

BLASTX

g1703374

Method

NCBI GI



BLAST score 7.0e-17 E value 92 Match length 53 % identity NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 2129457 pir S66337 ADP-ribosylation factor 1 - Chlamydomonas reinhardtii >qi 861205 (U27120) ADP-ribosylation factor [Chlamydomonas reinhardtii] 297180 Seq. No. LIB3137-002-Q1-K1-G8 Seq. ID Method BLASTX NCBI GI q1362010 202 BLAST score 4.0e-16 E value Match length 55 20 % identity NCBI Description ubiquitin-like protein 9 - Arabidopsis thaliana Seq. No. 297181 Seq. ID LIB3137-002-Q1-K1-H4 Method BLASTX NCBI GI · g4588012 BLAST score 180 3.0e-18 E value Match length 104 49 % identity (AF085717) putative callose synthase catalytic subunit NCBI Description [Gossypium hirsutum] Seq. No. 297182 Seq. ID LIB3137-003-Q1-K1-B10 Method BLASTX q1769887 NCBI GI BLAST score 171 E value 3.0e-12 Match length 42 81 % identity NCBI Description (X95736) amino acid permease 6 [Arabidopsis thaliana] Seq. No. 297183 Seq. ID LIB3137-003-Q1-K1-B3 Method BLASTX NCBI GI q1321661 BLAST score 293 E value 1.0e-26 Match length 65 % identity 86 NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

Seq. No. 297184

Seq. ID LIB3137-003-Q1-K1-C10

Method BLASTX
NCBI GI g3293031
BLAST score 288
E value 6.0e-26
Match length 109

% identity (AJ007574) amino acid carrier [Ricinus communis] NCBI Description 297185 Seq. No. LIB3137-003-Q1-K1-D3 Seq. ID Method BLASTX NCBI GI q3776578 BLAST score 195 E value 6.0e-15 Match length 112 % identity 36 NCBI Description (AC005388) ESTs gb F13915 and gb F13916 come from this gene. [Arabidopsis thaliana] Seq. No. 297186

Seq. ID LIB3137-003-Q1-K1-D8 Method BLASTX NCBI GI g115815 BLAST score 246 5.0e-21 E value

94 Match length % identity 55

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-M9) (LHCP) >gi_100866_pir__S13098 chlorophyll a/b-binding protein precursor - maize

>gi 22355_emb_CAA39376_ (X55892) light-harvesting chlorophyll a/b binding protein [Zea mays]

297187 Seq. No.

Seq. ID LIB3137-003-Q1-K1-G12

Method BLASTX NCBI GI q1174592 BLAST score 280 5.0e-36 E value Match length 106 % identity 73

NCBI Description TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin

- garden pea >gi 525332 (U12589) alpha-tubulin [Pisum

sativum]

Seq. No. 297188

Seq. ID LIB3137-003-Q1-K1-G6

Method BLASTX g2499611 NCBI GI BLAST score 281 E value 5.0e-25 Match length 63 % identity 81

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7)

(ATMPK7) >gi_629548_pir__S40473 mitogen-activated protein kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana

>gi_457406_dbj_BAA04870_ (D21843) MAP kinase [Arabidopsis

thaliana]

Seq. No. 297189

Seq. ID LIB3137-004-Q1-K1-D1

Method BLASTX 188



268

NCBI GI BLAST score g113595

```
1.0e-30
E value
Match length
                  81
                  85
% identity
                  ALDOSE REDUCTASE (AR) (ALDEHYDE REDUCTASE)
NCBI Description
                  >qi 100562 pir S15024 aldose reductase-related protein -
                  barley >gi 18891 emb CAA40747 (X57526) aldose
                  reductase-related protein [Hordeum vulgare]
Seq. No.
                  297190
Seq. ID
                  LIB3137-004-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  q4038037
BLAST score
                  192
E value
                  1.0e-14
Match length
                  134
% identity
                  15
NCBI Description
                  (AC005936) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  297191
Seq. ID
                  LIB3137-004-Q1-K1-E5
Method
                  BLASTX
                  g2505870
NCBI GI
BLAST score
                  142
                  5.0e-09
E value
Match length
                  88
% identity
                  42
                  (Y12227) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  297192
                  LIB3137-004-Q1-K1-F8
Seq. ID
Method
                  BLASTX
                  q1171579
NCBI GI
BLAST score
                  241
E value
                  2.0e-20
Match length
                   61
                  72
% identity
                  (X95342) cytochrome P450 [Nicotiana tabacum]
NCBI Description
Seq. No.
                  297193
                  LIB3137-004-Q1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913793
BLAST score
                  290
E value
                  5.0e-26
Match length
                  82
% identity
                   68
NCBI Description
                  GLUTATHIONE PEROXIDASE 2 >gi_2569989_emb_CAA75009_ (Y14707)
                  glutathione peroxidase [Helianthus annuus]
Seq. No.
                  297194
Seq. ID
                  LIB3137-005-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  g488573
BLAST score
                  427
E value
                  4.0e-42
```

```
Match length
% identity
                  99
                                                               **...
                  (U09463) histone H3.2 [Medicago sativa]
NCBI Description
                  297195
Seq. No.
                  LIB3137-005-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4325344
BLAST score
                  240
E value
                  4.0e-20
Match length
                  61
% identity
                  70
NCBI Description
                  (AF128393) similar to beta-transducins (Pfam: PF00400,
                  Score=71.7, E=1.5e-17, N=6) [Arabidopsis thaliana]
Seq. No.
                  297196
Seq. ID
                  LIB3137-005-Q1-K1-B5
Method
                  BLASTN
NCBI GI
                  g902200
BLAST score
                  90
E value
                  6.0e-43
Match length
                  207
% identity
                  43
                  Z.mays complete chloroplast genome
NCBI Description
Seq. No.
                  297197
Seq. ID
                  LIB3137-005-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g2340108
BLAST score
                  321
E value
                  6.0e-30
Match length
                  57
% identity
                  100
                  (U65948) starch branching enzyme IIa [Zea mays]
NCBI Description
                  297198
Seq. No.
                  LIB3137-005-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g122084
BLAST score
                  363
                  1.0e-34
E value
Match length
                  80
                  93
% identity
                  HISTONE H3 >gi_70754_pir__HSBH3 histone H3 - barley
NCBI Description
                  (fragment) >gi_167061 (M34928) histone H3 protein [Hordeum
                  vulgare] >gi_225348_prf__1301219A histone H3 [Hordeum
                  vulgare var. distichum]
                  297199
Seq. No.
Seq. ID
                  LIB3137-005-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  q2760606
BLAST score
                  654
E value
                  1.0e-68
Match length
                  143
% identity
                  86
```

NCBI Description (AB001568) phospholipid hydroperoxide glutathione



peroxidase-like protein [Arabidopsis thaliana] >gi_3004869 (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis thaliana] >gi_4539451_emb_CAB39931.1_ (AL049500) phospholipid hydroperoxide glutathione peroxidase [Arabidopsis thaliana]

 Seq. No.
 297200

 Seq. ID
 LIB3137-005-Q1-K1-C11

 Method
 BLASTX

 NCBI GI
 g136640

 BLAST score
 611

 100-63

BLAST score 611 E value 1.0e-63 Match length 115 % identity 98

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 170785 (M62720)

ubiquitin carrier protein [Triticum aestivum]

Seq. No. 297201

Seq. ID LIB3137-005-Q1-K1-C12

Method BLASTX
NCBI GI g136640
BLAST score 173
E value 2.0e-12
Match length 100
% identity 45

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 170785 (M62720)

ubiquitin carrier protein [Triticum aestivum]

Seq. No. 297202

Seq. ID LIB3137-005-Q1-K1-C8

Method BLASTX
NCBI GI g168523
BLAST score 518
E value 8.0e-53
Match length 101
% identity 99

NCBI Description (M31483) glyceraldehyde-3-phosphate dehydrogenase precursor

[Zea mays]

Seq. No. 297203

Seq. ID LIB3137-005-Q1-K1-D10

Method BLASTX
NCBI GI g3372230
BLAST score 487
E value 4.0e-49
Match length 133
% identity 68

NCBI Description (AF017074) RNA polymerase I, II and III 16.5 kDa subunit

[Arabidopsis thaliana] >gi_4585968_gb_AAD25604.1_AC005287_6 (AC005287) RNA polymerase I, II and III 16.5 kDa subunit

[Arabidopsis thaliana]

Seq. No. 297204

Seq. ID LIB3137-005-Q1-K1-D5

Method BLASTX

```
NCBI GI
                  q3915826
BLAST score
                  387
                  1.0e-37
E value
Match length
                  101
                  74
% identity
                  60S RIBOSOMAL PROTEIN L5
NCBI Description
Seq. No.
                  297205
                  LIB3137-005-Q1-K1-D9
Seq. ID
Method
                  BLASTX
                  g2213583
NCBI GI
BLAST score
                  377
E value
                  3.0e-36
Match length
                  141
% identity
                  55
NCBI Description (AC000348) T7N9.3 [Arabidopsis thaliana]
Seq. No.
                  297206
Seq. ID
                  LIB3137-005-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  g1370174
BLAST score
                  559
E value
                  2.0e-57
Match length
                  122
% identity
                  86
NCBI Description (Z73936) RAB1Y [Lotus japonicus]
                  297207
Seq. No.
Seq. ID
                  LIB3137-005-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g2921304
                  558
BLAST score
                  1.0e-57
E value
Match length
                  121
                  93
% identity
NCBI Description (AF033496) herbicide safener binding protein [Zea mays]
                  297208
Seq. No.
                  LIB3137-005-Q1-K1-F11
Seq. ID
Method
                  BLASTX
                  g2253219
NCBI GI
BLAST score
                  540
                  2.0e-55
E value
Match length
                  128
% identity
                  83
NCBI Description (AF002689) actin 2 [Podocarpus macrophyllus]
Seq. No.
                  297209
Seq. ID
                  LIB3137-005-Q1-K1-G10
Method
                  BLASTX
```

Method BLASTX
NCBI GI g122085
BLAST score 439
E value 2.0e-43
Match length 133
% identity 73

NCBI Description HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482 pir S04099 histone H3 (variant H3R-21)

Seq. No.



297210

- rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi 168506 $(M3\overline{5}388)$ histone H3 [Zea mays] >gi_169655 (M7 $\overline{7}493$) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi 169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone $\overline{3}$ [Zea mays] >gi $\overline{1040764}$ (M35 $\overline{3}87$) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ Histone H3 [Asparagus officinalis] $\overline{gi_1667592}$ (U $\overline{77296}$) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb M17131 and gb M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb T42306 come from this gene. [Arabidopsis thaliana] >gi 225459 prf 1303352A histone H3 [Helicoverpa zea]
>gi 225839 prf 1314298B histone H3 [Arabidopsis thaliana]

```
LIB3137-005-Q1-K1-G11
Seq. ID
Method
                  BLASTX
                  g4490293
NCBI GI
BLAST score
                  607
                   4.0e-63
E value
Match length
                  153
% identity
                   (AL035678) WD-repeat protein-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   297211
Seq. No.
                   LIB3137-005-Q1-K1-G9
Seq. ID
Method
                   BLASTX
                   q70774
NCBI GI
                   409
BLAST score
E value
                   6.0e-40
                   82
Match length
                   99
% identity
                  histone H4 (TH091) - wheat >gi 170747 (M12277) histone H4
NCBI Description
                   [Triticum aestivum]
                   297212
Seq. No.
                   LIB3137-005-Q1-K1-H11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4193388
```

Seq. No. 297213

508 1.0e-51

130 77

brasiliensis]

BLAST score

% identity

NCBI Description

E value Match length

(AF091455) translationally controlled tumor protein [Hevea



```
LIB3137-005-Q1-K1-H9
Seq. ID
                  BLASTX
Method
                  a2245069
NCBI GI
                  364
BLAST score
                  6.0e-35
E value
                  98
Match length
% identity
                 (Z97342) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  297214
Seq. No.
                  LIB3137-006-Q1-K1-D9
Seq. ID
                  BLASTX
Method
                  q4507793
NCBI GI
                  167
BLAST score
                  1.0e-11
E value
                  42
Match length
% identity
                  ubiquitin-conjugating enzyme E2N (homologous to yeast
NCBI Description
                  UBC13) >gi_2501432 sp_Q16781 UBCC HUMAN
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_2146981_pir__JC4894
                  ubiquitin-conjugating enzyme (EC 6.3.2.-) E2 - human
                  >gi 1181558 dbj_BAA11675_ (D83004) ubiquitin-conjugating
                  enzyme E2 UbcH-ben [Homo sapiens]
                  297215
Seq. No.
                  LIB3137-007-Q1-K1-B3
Seq. ID
                  BLASTX
Method
                  g4091008
NCBI GI
                  200
BLAST score
                  7.0e-16
E value
Match length
% identity
                  (AF040700) methionyl-tRNA synthetase [Oryza sativa]
NCBI Description
                   297216
Seq. No.
                   LIB3137-007-Q1-K1-E12
Seq. ID
                  BLASTX
Method
                   q2335101
NCBI GI
BLAST score
                   271
                   7.0e-24
E value
                   87
Match length
% identity
                  (AC002339) unknown protein [Arabidopsis thaliana]
NCBI Description
                   297217
Seq. No.
                   LIB3137-007-Q1-K1-E8
Seq. ID
Method
                   BLASTX
                   q1076800
NCBI GI
BLAST score
                   362
                   2.0e-34
E value
                   74
Match length
                   92
 % identity
                   L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
 NCBI Description
                   maize >gi_600116_emb CAA84406_ (Z34934) cytosolic ascorbate
                   peroxidase [Zea mays] >gi_1096503_prf__2111423A ascorbate
```

peroxidase [Zea mays]



```
297218
Seq. No.
                  LIB3137-007-Q1-K1-G8
Seq. ID
Method
                  BLASTX
                  g112994
NCBI GI
                  346
BLAST score
                  7.0e-33
E value
                  78
Match length
                  88
% identity
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >qi 226091 prf 1410284A abscisic acid inducible gene [Zea
                  mays]
                  297219
Seq. No.
                  LIB3137-007-Q1-K1-H1
Seq. ID
                  BLASTX
Method
                   q4586117
NCBI GI
                   399
BLAST score
                   4.0e-39
E value
                   100
Match length
                   73
% identity
                  (AL049638) putative protein [Arabidopsis thaliana]
NCBI Description
                   297220
Seq. No.
                   LIB3137-008-Q1-K1-B3
Seq. ID
                   BLASTX
Method
                   g1129145
NCBI GI
                   188
BLAST score
                   2.0e-14
E value
                   88
Match length
                   45
% identity
NCBI Description (X75329) acetyl-CoA C-acyltransferase [Mangifera indica]
                   297221
Seq. No.
                   LIB3137-008-Q1-K1-C6
Seq. ID
                   BLASTX
Method
                   q4335756
NCBI GI
BLAST score
                   185
                   7.0e-14
E value
                   80
Match length
                   50
% identity
NCBI Description (AC006284) putative ankyrin [Arabidopsis thaliana]
                   297222
Seq. No.
                   LIB3137-008-Q1-K1-E6
Seq. ID
Method
                   BLASTX
                   q4455129
NCBI GI
BLAST score
                   191
E value
                   2.0e-14
                   116
Match length
                   37
 % identity
                   (AF127761) ribonucleoprotein ZRNP1 [Homo sapiens]
NCBI Description
```

41675

297223

Seq. No.

Seq. No.

297228



```
LIB3137-008-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g120670
                  341
BLAST score
                  2.0e-32
E value
Match length
                  78
                  85
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 100879 pir_ S06879 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) C - maize
                  >gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]
Seq. No.
                  297224
Seq. ID
                  LIB3137-008-Q1-K1-F6
Method
                  BLASTN
NCBI GI
                  q168490
BLAST score
                  44
                  8.0e-16
E value
                  92
Match length
                  87
% identity
                  Maize glutathione S-transferase (GST-I) mRNA, complete cds
NCBI Description
Seq. No.
                  297225
Seq. ID
                  LIB3137-009-Q1-K1-D12
                  BLASTX
Method
NCBI GI
                  g2119187
BLAST score
                  157
                  9.0e-11
E value
                  31
Match length
                  94
% identity
                  transmembrane protein, glucose starvation-induced - maize
NCBI Description
                  >gi 575731 emb CAA57955 (X82633) transmembrane protein
                  [Zea mays]
Seq. No.
                  297226
Seq. ID
                  LIB3137-009-Q1-K1-D3
Method
                  BLASTX
                  g3256035
NCBI GI
BLAST score
                  365
E value
                  8.0e-35
Match length
                  140
                  51
% identity
                  (Y14274) putative serine/threonine protein kinase [Sorghum
NCBI Description
                  bicolor]
Seq. No.
                  297227
Seq. ID
                  LIB3137-009-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  q2384673
BLAST score
                  164
E value
                  2.0e-11
Match length
                  67
% identity
                  49
                  (AF012658) putative potassium transporter AtKT3p
NCBI Description
                  [Arabidopsis thaliana]
```



```
LIB3137-009-Q1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2623298
BLAST score
                  261
E value
                  7.0e-23 ·--
Match length
                  108
% identity
                   (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis
NCBI Description
                  thaliana]
                  297229
Seq. No.
                  LIB3137-009-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4510339
BLAST score
                  144
                  2.0e-09
E value
Match length
                  36
                  81
% identity
                   (AC006921) putative ABC transporter protein [Arabidopsis
NCBI Description
                  thaliana]
                  297230
Seq. No.
                  LIB3137-009-Q1-K1-G4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3414828
BLAST score
                  113
                   6.0e-57
E value
Match length
                  121
% identity
                   98
NCBI Description
                  Zea mays subsp. mays race Tuxpeno globulin-1 gene, partial
                  cds
Seq. No.
                  297231
Seq. ID
                  LIB3137-009-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  g4567273
BLAST score
                  305
E value
                  8.0e-28
Match length
                  102
% identity
                  58
NCBI Description
                  (AC006841) putative vacuolar proton ATPase subunit
                   [Arabidopsis thaliana]
Seq. No.
                  297232
Seq. ID
                  LIB3137-009-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  q1170937
BLAST score
                  159
                  2.0e-11
E value
```

Match length 35 % identity 86

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_450549 emb CAA81481 (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 297233

```
LIB3137-010-Q1-K1-A12
Seq. ID
                  BLASTX
Method
                  g1495251
NCBI GI
                  259
BLAST score
                  2.0e-22
E value
Match length
                  126
% identity
NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana]
                  297234
Seq. No.
                  LIB3137-010-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4512667
                  312
BLAST score
                  8.0e-29
E value
                  112
Match length
                  56
% identity
NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]
                  297235
Seq. No.
                  LIB3137-010-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1911166
BLAST score
                  163
                  5.0e-23
E value
                  107
Match length
% identity
NCBI Description (X94400) soluble-starch-synthase [Solanum tuberosum]
                   297236
Seq. No.
                  LIB3137-010-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3785977
                   252
BLAST score
E value
                   9.0e-22
                   111
Match length
% identity
                   (AC005560) putative growth regulator protein [Arabidopsis
NCBI Description
                   thaliana]
                   297237
Seq. No.
                   LIB3137-010-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                   g115786
NCBI GI
                   279
BLAST score
                   5.0e-25
E value
                   80
Match length
                   68
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
```

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TIPE I PRECURSOR (CAB) (LHCP) >gi_82680_pir_A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea

mays]

Seq. No. 297238

Seq. ID LIB3137-010-Q1-K1-G2

Method BLASTX NCBI GI g4455225



```
BLAST score
E value
                  6.0e-12
Match length
                  57
                  56
% identity
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
                  297239
Seq. No.
                  LIB3137-010-Q1-K1-G6
Seq. ID
                  BLASTX
Method
                  g3511285
NCBI GI
                  315
BLAST score
                  3.0e-29
E value
                  99
Match length
% identity
                  61
NCBI Description (AF081534) cellulose synthase [Populus alba x Populus
                  tremula]
                  297240
Seq. No.
                  LIB3137-010-Q1-K1-G8
Seq. ID
                  BLASTX
Method
                  g548605
NCBI GI
                  200
BLAST score
                  1.0e-15
E value
                   83
Match length
                   63
% identity
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                   >gi_539055_pir__A48527 photosystem I protein psaK precursor
                   - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
                   297241
Seq. No.
                   LIB3137-010-Q1-K1-H6
Seq. ID
Method
                   BLASTX
                   g129232
NCBI GI
BLAST score
                   157
E value
                   6.0e-14
                   90
Match length
                   58
% identity
                   ORYZAIN BETA CHAIN PRECURSOR >gi_67645_pir__KHRZOB oryzain
NCBI Description
                   (EC 3.4.22.-) beta precursor - rice
                   >gi 218183 dbj BAA14403 (D90407) oryzain beta precursor
                   [Oryza sativa]
                   297242
Seq. No.
                   LIB3137-011-Q1-K1-C12
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1213278
BLAST score
                   54
E value
                   2.0e-21
Match length
                   54
                   100
 % identity
```

NCBI Description Z.mays ZEMb gene

297243 Seq. No.

LIB3137-011-Q1-K1-C4 Seq. ID

BLASTN Method

E value

2.0e-10



```
NCBI GI
BLAST score
                   42
                   1.0e-14
 E value
                   90
Match length
                   87
 % identity
NCBI Description Z.mays mRNA for dehydrin (dhn3)
                   297244
 Seq. No.
                   LIB3137-011-Q1-K1-C7
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q82684
 BLAST score
                   164
 E value
                   1.0e-11
                   64
 Match length
 % identity
                   dehydrin 3 - maize >gi 18964 emb CAA33364_ (X15290)
 NCBI Description
                   dehydrin (AA 1-167) [Zea mays]
                   297245
 Seq. No.
                   LIB3137-012-Q1-K1-A8
 Seq. ID
                   BLASTX
 Method
                   q425194
 NCBI GI
 BLAST score
                   291
 E value
                   7.0e-28
                    99
 Match length
                   70
 % identity
                    (L26243) heat shock protein [Spinacia oleracea] >gi_2660772
 NCBI Description
                    (AF034618) cytosolic heat shock 70 protein [Spinacia
                    oleracea]
                    297246
 Seq. No.
                    LIB3137-012-Q1-K1-B12
 Seq. ID
 Method
                    BLASTN
                    g1698669
 NCBI GI
 BLAST score
                    40
                    2.0e-13
 E value
                    129
 Match length
                    84
 % identity
 NCBI Description Zea mays S-like RNase (kin1) mRNA, complete cds
                    297247
 Seq. No.
                    LIB3137-012-Q1-K1-B3
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g2832616
                    221
 BLAST score
                    6.0e-18
 E value
 Match length
                    131
 % identity
                    41
                    (AL021711) heat shock transcription factor - like protein
 NCBI Description
                    [Arabidopsis thaliana]
                    297248
 Seq. No.
 Seq. ID
                    LIB3137-012-Q1-K1-C12
                    BLASTX
 Method
                    g2098575
 NCBI GI
                    156
 BLAST score
```

```
86
```

```
Match length 86 % identity 42
```

NCBI Description (AC002115) F25451_2 [Homo sapiens]

Seq. No. 297249

Seq. ID LIB3137-012-Q1-K1-D4

Method BLASTX
NCBI GI g2098575
BLAST score 300
E value 2.0e-27
Match length 74
% identity 73

NCBI Description (AC002115) F25451_2 [Homo sapiens]

Seq. No. 297250

Seq. ID LIB3137-012-Q1-K1-D6

Method BLASTN
NCBI GI g3821780
BLAST score 37
E value 2.0e-11
Match length 37
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 297251

Seq. ID LIB3137-012-Q1-K1-E9

Method BLASTX
NCBI GI g129591
BLAST score 333
E value 4.0e-31
Match length 96
% identity 71

NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_ (X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 297252

Seq. ID LIB3137-012-Q1-K1-F12

Method BLASTX
NCBI GI g2708806
BLAST score 206
E value 2.0e-16
Match length 71
% identity 61

NCBI Description (AF037359) superoxide dismutase [Paulownia kawakamii]

Seq. No. 297253

Seq. ID LIB3137-012-Q1-K1-G5

Method BLASTX
NCBI GI g3335378
BLAST score 267
E value 2.0e-23
Match length 78
% identity 72

NCBI Description (AC003028) Myb-related transcription activator [Arabidopsis

thaliana]

Seq. No. 297254

```
LIB3137-012-Q1-K1-H5
Seq. ID
                  BLASTN
Method
                  g2687357
NCBI GI
                  66
BLAST score
                  6.0e-29
E value
Match length
                  122
                  89
% identity
                  Zea mays nonphototropic hypocotyl 1 (nph1) mRNA, complete
NCBI Description
                  cds
                  297255
Seq. No.
                  LIB3137-013-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                  q2580440
NCBI GI
                  245
BLAST score
                  6.0e-21
E value
                  61
Match length
% identity
                  72
NCBI Description (D87261) PCF2 [Oryza sativa]
                   297256
Seq. No.
                  LIB3137-013-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q730919
                   195
BLAST score
                   4.0e-15
E value
                   75
Match length
                   55
% identity
                   T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON)
NCBI Description
                   (CCT-EPSILON) (TCP-K19) >gi_542112_pir__S40461 t-complex
                   polypeptide 1 - oat >gi_435173_emb_CAA53396_ (X75777) T
                   complex polypeptide 1 [Avena sativa]
                   297257
Seq. No.
                   LIB3137-013-Q1-K1-B7
Seq. ID
                   BLASTX
Method
                   g295355
NCBI GI
                   300
BLAST score
                   5.0e-30
E value
                   118
Match length
                   56
 % identity
                  (L13653) peroxidase [Lycopersicon esculentum]
NCBI Description
                   297258
 Seq. No.
                   LIB3137-013-Q1-K1-D2
 Seq. ID
                   BLASTX
Method
                   q4469023
NCBI GI
                   223
BLAST score
                   2.0e-36
 E value
                   93
 Match length
                   87
 % identity
                   (AL035602) putative protein [Arabidopsis thaliana]
 NCBI Description
                   297259
 Seq. No.
                   LIB3137-013-Q1-K1-D8
 Seq. ID
```

41682

BLASTX

q3004950

Method

NCBI GI



```
BLAST score
                  1.0e-32
E value
                  86
Match length
                  79
% identity
NCBI Description (AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays]
Seq. No.
                  297260
                  LIB3137-013-Q1-K1-E7
Seq. ID
                  BLASTX
Method
                  g1170242
NCBI GI
BLAST score
                  200
E value
                  4.0e-16
Match length
                  55
                  76
% identity
                  FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME
NCBI Description
                  SYNTHETASE) >gi_474966_dbj_BAA05101_ (D26105)
                  ferrochelatase [Hordeum vulgare]
Seq. No.
                  297261
                  LIB3137-013-Q1-K1-G3
Seq. ID
                  BLASTN
Method
                   q313759
NCBI GI
BLAST score
                   48
                   5.0e-18
E value
                   60
Match length
                   95
% identity
NCBI Description Z.mays hsp 70-1 gene for heat shock protein
                   297262
Seq. No.
                   LIB3137-013-Q1-K1-G7
Seq. ID
                   BLASTX
Method
                   g3915029
NCBI GI
                   202
BLAST score
E value
                   7.0e-16
                   70
Match length
% identity
                   57
                   ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
NCBI Description
                   (STEAROYL-ACP DESATURASE) >gi_976257_dbj_BAA07631_ (D38753)
                   stearyl-ACP desaturase [Oryza sativa]
                   297263
Seq. No.
                   LIB3137-013-Q1-K1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q465835
                   155
BLAST score
                   1.0e-10
E value
Match length
                   85
                   44
 % identity
                   HYPOTHETICAL 272.0 KD PROTEIN C50C3.6 IN CHROMOSOME III
NCBI Description
                   >gi 630577 pir__S44625 C50C3.6 protein - Caenorhabditis
                   elegans >gi_289658 (L14433) putative [Caenorhabditis
                   elegans]
```

Seq. No. 297264

Seq. ID LIB3137-014-Q1-K1-A10

Method BLASTX NCBI GI g1345683

Match length

122



```
BLAST score
                    2.0e-19
  E value
Match length
                    48
  % identity
                    94
                    CATALASE ISOZYME 3 >qi 487045 pir S37379 catalase (EC
  NCBI Description
                    1.11.1.6) 3 - maize >gi 168437 (L05934) catalase [Zea mays]
  Seq. No.
                    297265
  Seq. ID
                    LIB3137-014-Q1-K1-B6
                    BLASTX
  Method
                    g82696
  NCBI GI
                    352
  BLAST score
                    2.0e-33
  E value
                    81
  Match length
  % identity
                    glycine-rich protein - maize >gi_22293_emb_CAA43431_
  NCBI Description
                     (X61121) glycine-rich protein [Zea mays]
                    297266
  Seq. No.
                    LIB3137-014-Q1-K1-D2
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g4263509
                     164
  BLAST score
                     6.0e-17
  E value
                     112
  Match length
                     51
  % identity
                    (AC004044) hypothetical protein [Arabidopsis thaliana]
  NCBI Description
                     297267
  Seq. No.
                     LIB3137-014-Q1-K1-D7
  Seq. ID
                     BLASTX
  Method
                     g3063706
  NCBI GI
                     173
  BLAST score
                     1.0e-12
  E value
                     75
  Match length
                     44
  % identity
                     (AL022537) putative protein [Arabidopsis thaliana]
  NCBI Description
  Seq. No.
                     297268
                     LIB3137-014-Q1-K1-F1
  Seq. ID
  Method
                     BLASTX
                     g1076809
  NCBI GI
  BLAST score
                     353
                     2.0e-33
  E value
                     90
  Match length
                     76
  % identity
                     H+-transporting ATPase (EC 3.6.1.35) - maize
  NCBI Description
                     >gi 758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase
                     [Zea mays]
                     297269
  Seq. No.
  Seq. ID
                     LIB3137-014-Q1-K1-F6
                     BLASTX
  Method
  NCBI GI
                     q3789954
  BLAST score
                     461
                     3.0e-46
  E value
```



```
% identity
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
                  297270
Seq. No:
                  LIB3137-014-Q1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913182
BLAST score
                  227
                  8.0e-19
E value
Match length
                  67
% identity
                  67
NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE (CAD)
                  >qi 2239258 emb CAA74070_ (Y13733) cinnamyl alcohol
                  dehydrogenase [Zea mays]
                  297271
Seq. No.
Seq. ID
                  LIB3137-015-Q1-K1-A9
                  BLASTX
Method
                  q82696
NCBI GI
                   244
BLAST score
                   3.0e-21
E value
Match length
                   58
% identity
                   83
                  glycine-rich protein - maize >gi 22293_emb_CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
                   297272
Seq. No.
                   LIB3137-015-Q1-K1-F10
Seq. ID
                   BLASTN
Method
                   g296593
NCBI GI
                   60
BLAST score
                   4.0e-25
E value
Match length
                   76
                   95
% identity
NCBI Description H. vulgare pZE40 gene
                   297273
Seq. No.
                   LIB3137-015-Q1-K1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1654140
                   329
BLAST score
                   6.0e-31
E value
Match length
                   82
% identity
                   74
                   (U37840) lipoxygenase [Lycopersicon esculentum]
NCBI Description
                   297274
Seq. No.
                   LIB3137-016-Q1-K1-A2
Seq. ID
Method
                   BLASTX
                   g2829894
NCBI GI
                   234
BLAST score
                   9.0e-20
E value
                   84
Match length
                   51
% identity
NCBI Description (AC002311) Unknown protein [Arabidopsis thaliana]
```

Seq. ID

Method



```
297275
Seq. No.
                  LIB3137-016-Q1-K1-A5
Seq. ID
Method
                  BLASTX
                  g283038
NCBI GI
                  467
BLAST score
                  7.0e-47
E value
                  104
Match length
% identity
                  88
                  chlorophyll a/b-binding protein (cab-m7) precursor - maize
NCBI Description
                  >gi 22230 emb CAA37474 (X53398) light harvesting
                  chlorophyll a /b binding protein [Zea mays]
Seq. No.
                  297276
                  LIB3137-016-Q1-K1-B2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2921303
BLAST score
                   105
E value
                   5.0e-52
Match length
                   219
                   94
% identity
                  Zea mays herbicide safener binding protein (SBP1) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   297277
                   LIB3137-016-Q1-K1-D10
Seq. ID
Method
                   BLASTX
                   g4567232
NCBI GI
BLAST score
                   217
                   1.0e-17
E value
                   71
Match length
% identity
                   (AC007119) putative 40S ribosomal protein S25 [Arabidopsis
NCBI Description
                   thaliana]
                   297278
Seq. No.
                   LIB3137-016-Q1-K1-E6
Seq. ID
                   BLASTX
Method
                   g4539343
NCBI GI
                   208
BLAST score
E value
                   2.0e-16
                   49
Match length
                   76
% identity
                   (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                   297279
Seq. No.
Seq. ID
                   LIB3137-016-Q1-K1-F2
                   BLASTX
Method
NCBI GI
                   q4006893
                   333
BLAST score
                   2.0e-33
E value
                   97
Match length
                   75
% identity
                   (Z99708) aminopeptidase-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   297280
```

LIB3137-016-Q1-K1-H6

BLASTX



```
q266578
   NCBI GI
                      224
  BLAST score
E value
                      9.0e-21
                      57
   Match length
                      89
   % identity
                      METALLOTHIONEIN-LIKE PROTEIN 1 >gi_100898_pir_
   NCBI Description
                      metallothionein-like protein - maize >gi_236730 bbs 57629
                       (S57628) metallothionein homologue [Zea mays, Peptide, 76
                       aa] [Zea mays] >gi_559536_emb_CAA57676_ (X82186)
                      metallothionein- like protein [Zea mays]
                       >gi_228095_prf__1717215A metallothionein-like protein [Zea
                      mays]
                       297281
   Seq. No.
                       LIB3137-017-Q1-K1-E11
   Seq. ID
                       BLASTX
   Method
                       q2829275
   NCBI GI
                       161
   BLAST score
                       5.0e-11
   E value
                       99
   Match length
    % identity
                       (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis
   NCBI Description
                       thaliana] >gi_3513740 (AF080118) contains similarity to
                       nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_
                       (AL049525) nucleoside diphosphate kinase 3 (ndpk3)
                       [Arabidopsis thaliana]
                       297282
    Seq. No.
                       LIB3137-017-Q1-K1-G12
    Seq. ID
                       BLASTX
    Method
                       g2464852
    NCBI GI
    BLAST score
                       178
                       7.0e-13
    E value
    Match length
                       120
                       36
    % identity
                       (Z99707) putative protein [Arabidopsis thaliana]
    NCBI Description
                       297283
    Seq. No.
    Seq. ID
                       LIB3137-017-Q1-K1-G4
                       BLASTX
    Method
                       g2984709
    NCBI GI
                       513
    BLAST score
                       3.0e-52
    E value
    Match length
                       98
                       99
    % identity
                       (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
    NCBI Description
                       297284
    Seq. No.
                       LIB3137-018-Q1-K1-A8
    Seq. ID
    Method
                       BLASTX
                       q1418125
    NCBI GI
                       263
    BLAST score
                       5.0e-23
    E value
    Match length
                       69
                       68
    % identity
```

NCBI Description (D58404) CTP:phosphocholine cytidylyltransferase [Brassica



napus]

```
Seq. No.
                     297285
                     LIB3137-018-Q1-K1-B10
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                     g3785973
   BLAST score
                     187
                     5.0e-14
   E value
                     62
   Match length
                     65
   % identity
                     (AC005560) putative homeobox protein [Arabidopsis thaliana]
   NCBI Description
   Seq. No.
                     297286
                     LIB3137-018-Q1-K1-C5
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                      q3136311
   BLAST score
                      169
   E value
                      1.0e-16
                      71
   Match length
                      56
   % identity
                     (AF062734) soluble acid invertase [Saccharum robustum]
   NCBI Description
                      297287
   Seq. No.
                      LIB3137-018-Q1-K1-D1
   Seq. ID
                      BLASTX
   Method
                      g1155261
   NCBI GI
                      288
   BLAST score
                      7.0e-26
   E value
   Match length
                      64
                      88
   % identity
                      (U40217) eukaryotic release factor 1 homolog [Arabidopsis
   NCBI Description
                      thaliana]
                      297288
   Seq. No.
                      LIB3137-018-Q1-K1-D3
   Seq. ID
                      BLASTX
   Method
                      g112994
   NCBI GI
                      401
   BLAST score
                      3.0e-39
   E value
                      89
   Match length
                      92
   % identity
                      GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
   NCBI Description
                      >gi_82685_pir__S04536 embryonic abundant protein,
                      glycine-rich - maize >gi 22313_emb_CAA31077_ (X12564)
                      ABA-inducible gene protein [Zea mays]
                      >gi 226091 prf 1410284A abscisic acid inducible gene [Zea
                      mays]
                      297289
   Seq. No.
                      LIB3137-018-Q1-K1-E6
   Seq. ID
                      BLASTX
   Method
                      g2792238
   NCBI GI
   BLAST score
                      155
                      3.0e-10
   E value
                      88
   Match length
                      40
    % identity
                      (AF032697) NBS-LRR type resistance protein [Oryza sativa]
   NCBI Description
```

```
297290
Seq. No.
                  LIB3137-018-Q1-K1-G5
Seq. ID
                  BLASTX
Method
                  q4468048
NCBI GI
BLAST score
                  173
E value
                  2.0e-12
                  110
Match length
% identity
NCBI Description (X78703) catechol O-methyltransferase [Vanilla planifolia]
                  297291
Seq. No.
                  LIB3137-018-Q1-K1-G7
Seq. ID
                  BLASTX
Method
                  q2984709
NCBI GI
                  329
BLAST score
                  1.0e-30
E value
                  66
Match length
                  97
% identity
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                  297292
Seq. No.
                  LIB3137-019-Q1-K1-A7
Seq. ID
Method
                  BLASTX
                  q4220528
NCBI GI
                   333
BLAST score
                   4.0e-31
E value
                   111
Match length
                   59
% identity
                   (AL035356) glucose-6-phosphate isomerase [Arabidopsis
NCBI Description
                   thaliana]
                   297293
Seq. No.
                   LIB3137-019-Q1-K1-A8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2984709
BLAST score
                   532
                   2.0e-54
E value
                   101
Match length
% identity
                   99
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
```

Seq. No. 297294

Seq. ID LIB3137-019-Q1-K1-E7

Method BLASTX
NCBI GI g3861366
BLAST score 237
E value 8.0e-20
Match length 145
% identity 40

NCBI Description (AJ235273) 5-AMINOLEVULINIC ACID SYNTHASE (hemA)

[Rickettsia prowazekii]

Seq. No. 297295

Seq. ID LIB3137-019-Q1-K1-G9

Method BLASTX NCBI GI g4204912



```
BLAST score
E value
                   4.0e-11
                   53
Match length
                   58
% identity
                  (U58918) MEK kinase [Arabidopsis thaliana]
NCBI Description
                   297296
Seq. No.
                   LIB3137-019-Q1-K1-H4
Seq. ID
                   BLASTX
Method
                   q4584545
NCBI GI
BLAST score
                   492
E value
                   9.0e-50
Match length
                   142
% identity
                  (AL049608) putative protein [Arabidopsis thaliana]
NCBI Description
                   297297
Seq. No.
                   LIB3137-020-Q1-K1-C1
Seq. ID
                   BLASTN
Method
                   g550433
NCBI GI
                   85
BLAST score
                   3.0e-40
E value
                   204
Match length
                   83
% identity
NCBI Description Z.mays CYP71C1 gene for cytochrome P-450
                   297298
Seq. No.
                   LIB3137-020-Q1-K1-C2
Seq. ID
                   BLASTX
Method
                   q3687235
NCBI GI
                   340
BLAST score
                   7.0e-32
E value
                   119
Match length
% identity
                   61
                   (AC005169) putative copia-like transposable element
NCBI Description
                   [Arabidopsis thaliana]
                   297299
Seq. No.
                   LIB3137-020-Q1-K1-F1
Seq. ID
Method
                   BLASTX
                   q4586103
NCBI GI
BLAST score
                   292
                   3.0e-26
E value
                   73
Match length
                   71
 % identity
                   (ALO49638) putative protein [Arabidopsis thaliana]
NCBI Description
                   297300
 Seq. No.
                   LIB3137-020-Q1-K1-F11
 Seq. ID
 Method
                   BLASTX
                   q118104
 NCBI GI
                   662
 BLAST score
```

1.0e-69 E value 140 Match length 89 % identity

PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) NCBI Description

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)

>gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) maize >gi_168461 (M55021) cyclophilin [Zea mays]
>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

 Seq. No.
 297301

 Seq. ID
 LIB3137-020-Q1-K1-F3

 Method
 BLASTX

 NCBI GI
 g2160170

 BLAST score
 193

 E value
 1.0e-14

Match length 81 % identity 58

NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 297302

Seq. ID LIB3137-020-Q1-K1-F6

Method BLASTX
NCBI GI g2996096
BLAST score 273
E value 5.0e-24
Match length 140
% identity 42

NCBI Description (AF030517) translation elongation factor-1 alpha; EF-1

alpha [Oryza sativa]

Seq. No. 297303

Seq. ID LIB3137-020-Q1-K1-H12

Method BLASTX
NCBI GI g4097565
BLAST score 172
E value 6.0e-18
Match length 65
% identity 64

NCBI Description (U64920) ATGP3 [Arabidopsis thaliana]

Seq. No. 297304

Seq. ID LIB3137-021-Q1-K1-B10

Method BLASTX
NCBI GI g1619602
BLAST score 323
E value 5.0e-30
Match length 90
% identity 62

NCBI Description (Y08726) MtN3 [Medicago truncatula]

Seq. No. 297305

Seq. ID LIB3137-021-Q1-K1-D9

Method BLASTX
NCBI GI g4210330
BLAST score 322
E value 8.0e-30
Match length 97
% identity 65

NCBI Description (AJ223802) 2-oxoglutarate dehydrogenase, El subunit

[Arabidopsis thaliana]

Seq. No. 297306



```
LIB3137-021-Q1-K1-F11
Seq. ID
                                                             BLASTX
Method
                  g112994
NCBI GI
                  274
BLAST score
                  2.0e-24
E value
Match length
                  82
% identity
                  71
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi 22313 emb CAA31077 (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >qi 226091 prf 1410284A abscisic acid inducible gene [Zea
                  mays]
                  297307
Seq. No.
                  LIB3137-021-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g120670
                  235
BLAST score
                  7.0e-20
E value
Match length
                  81
                  59
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >qi 100879 pir S06879 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) C - maize
                  >qi 295853 emb CAA33620 (X15596) GAPDH [Zea mays]
Seq. No.
                  297308
                  LIB3137-021-Q1-K1-H1
Seq. ID
Method
                  BLASTX
                  g2190550
NCBI GI
BLAST score
                  218
E value
                  1.0e-17
                  94
Match length
% identity
                  53
                   (AC001229) ESTs gb T45673, gb N37512 come from this gene.
NCBI Description
                   [Arabidopsis thaliana]
                  297309
Seq. No.
                  LIB3137-021-Q1-K1-H8
Seq. ID
                  BLASTX
Method
                  g1346109
NCBI GI
BLAST score
                  302
                  1.0e-27
E value
                  88
Match length
                  70
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                  PROTEIN (GPB-LR) (RWD) >gi 540535_dbj_BAA07404_ (D38231)
                  RWD [Oryza sativa]
                   297310
Seq. No.
```

Seq. ID LIB3137-022-Q1-K1-B7

Method BLASTX
NCBI GI g2984709
BLAST score 522
E value 3.0e-53
Match length 99

% identity (AF053468) DnaJ-related protein ZMDJ1 [Zea mays] NCBI Description 297311 Seq. No. LIB3137-022-Q1-K1-C3 Seq. ID BLASTX Method g4512615 NCBI GI 208 BLAST score 2.0e-16 E value 52 Match length 81 % identity (AC004793) Strong similarity to gb X59970 3-isopropylmalate NCBI Description dehydrogenase (IMDH) from Brassica napus. EST gb_F14478 comes from this gene. [Arabidopsis thaliana] 297312 Seq. No. LIB3137-022-Q1-K1-C4 Seq. ID BLASTX Method g3450842 NCBI GI 296 BLAST score 8.0e-27 E value Match length 91 % identity 57 NCBI Description sativa] 297313 Seq. No. LIB3137-022-Q1-K1-C6 Seq. ID

(AF080436) mitogen activated protein kinase kinase [Oryza

BLASTN Method NCBI GI g18963 146 BLAST score E value 2.0e-76 Match length 222 91 % identity

NCBI Description Z.mays mRNA for dehydrin (dhn3)

297314 Seq. No.

LIB3137-022-Q1-K1-D12 Seq. ID

BLASTX Method g2500959 NCBI GI 449 BLAST score E value 1.0e-44 Match length 111 76 % identity

ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS) NCBI Description

>gi 1653611_dbj_BAA18523_ (D90915) alanyl-tRNA synthetase

[Synechocystis sp.]

297315 Seq. No.

Seq. ID LIB3137-022-Q1-K1-H9

BLASTX Method NCBI GI g1373209 BLAST score 174 2.0e-12 E value Match length 94 49 % identity

(U53855) prostacyclin synthase [Rattus norvegicus] NCBI Description



```
297316
Seq. No.
Seq. ID
                  LIB3137-023-Q1-K1-A12
                  BLASTX
Method
NCBI GI
                  g4337174
                  271
BLAST score
                  4.0e-24
E value
                  104
Match length
                  52
% identity
                  (AC006416) Similar to gi 1573829 HI0816 aminopeptidase P
NCBI Description
                  homolog (pepP) from Haemophilus influenzae genome
                  gb U32764. [Arabidopsis thaliana]
                  297317
Seq. No.
                  LIB3137-023-Q1-K1-C2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3334756
                  292
BLAST score
                  2.0e-26
E value
                  117
Match length
% identity
                  53
                   (Y16672) putative arginine/serine-rich splicing factor
NCBI Description
                   [Medicago sativa]
                  297318
Seq. No.
                  LIB3137-023-Q1-K1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g400578
                   214
BLAST score
                   4.0e-17
E value
                  86
Match length
                   47
% identity
                  NADH-UBIQUINONE OXIDOREDUCTASE 18 KD SUBUNIT PRECURSOR
NCBI Description
                   (COMPLEX I-18 KD) (CI-18 KD) (COMPLEX I-AQDQ) (CI-AQDQ)
                   >gi_346531_pir_ S28240 NADH dehydrogenase (ubiquinone) (EC
                   1.6.5.3) chain CI-18(IP) - bovine >gi 226 emb CAA44900
                   (X63215) NADH dehydrogenase [Bos taurus]
                   297319
Seq. No.
                   LIB3137-023-Q1-K1-C8
Seq. ID
                   BLASTN
Method
                   g342631
NCBI GI
                   46
BLAST score
                   4.0e-17
E value
                   110
Match length
                   85
% identity
                  Maize mitochondrial F-1-ATPase subunit-2 mRNA, complete cds
NCBI Description
                   297320
Seq. No.
Seq. ID
                   LIB3137-023-Q1-K1-D3
Method
                   BLASTX
NCBI GI
                   g2425066
                   237
BLAST score
                   7.0e-20
E value
                   126
Match length
```

NCBI Description (AF019147) cysteine proteinase Mir3 [Zea mays]

51

% identity

Seq. ID

Method



```
297321
Seq. No.
                  LIB3137-023-Q1-K1-D5
Seq. ID
                  BLASTX
Method
                  g633110
NCBI GI
                  256
BLAST score
                  5.0e-31
E value
                  126
Match length
% identity
                  (D31843) plasma membrane H+-ATPase [Oryza sativa]
NCBI Description
                  297322
Seq. No.
                  LIB3137-023-Q1-K1-E1
Seq. ID
                  BLASTX
Method
                  g4115379
NCBI GI
                  158
BLAST score
                  3.0e-11
E value
                   62
Match length
                   53
% identity
                   (AC005967) putative carbonyl reductase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   297323
                  LIB3137-023-Q1-K1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131772
                   197
BLAST score
E value
                   9.0e-20
                   90
Match length
                   68
% identity
                   40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
NCBI Description
                   >gi_82723_pir__A30097 ribosomal protein S14 (clone MCH1) -
                   maize
                   297324
Seq. No.
                   LIB3137-023-Q1-K1-F12
Seq. ID
                   BLASTX
Method
                   q3688398
NCBI GI
                   310
BLAST score
                   2.0e-28
E value
                   118
Match length
                   58
% identity
                  (AJ006358) ascorbate peroxidase [Hordeum vulgare]
NCBI Description
                   297325
Seq. No.
                   LIB3137-023-Q1-K1-G3
Seq. ID
                   BLASTX
Method
                   g4580461
NCBI GI
                   310
BLAST score
                   5.0e-29
E value
                   73
Match length
                   79
% identity
                  (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
                   297326
Seq. No.
```

41695

LIB3137-023-Q1-K1-H2

BLASTX



```
g1174391
NCBI GI
                  257
                                                                    BLAST score
                                                  198
                  3.0e-22
E value
                  119
Match length
                  39
% identity
                  SUPEROXIDE DISMUTASE 3.4 PRECURSOR (MN)
NCBI Description
                  >gi_539066_pir__B48684 superoxide dismutase (EC 1.15.1.1)
                   (Mn) 3.2 precursor - maize
                  297327
Seq. No.
                  LIB3137-023-Q1-K1-H3
Seq. ID
Method
                  BLASTX
                  q4186184
NCBI GI
                  148
BLAST score
                   2.0e-09
E value
                   34
Match length
% identity
                   74
NCBI Description (AF111168) unknown [Homo sapiens]
                   297328
Seq. No.
                   LIB3137-024-Q1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3264596
                   209
BLAST score
                   6.0e-17
E value
                   62
Match length
                   74
% identity
                   (AF057183) putative tonoplast aquaporin [Zea mays]
NCBI Description
                   297329
Seq. No.
                   LIB3137-024-Q1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3885882
                   191
BLAST score
                   1.0e-14
E value
Match length
                   81
                   53
% identity
NCBI Description (AF093629) inorganic pyrophosphatase [Oryza sativa]
                   297330
Seq. No.
                   LIB3137-024-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                   g3163946
NCBI GI
                   525
BLAST score
                   1.0e-53
E value
                   109
Match length
                   90
 % identity
                   (AJ005599) alpha-tubulin 1 [Eleusine indica]
 NCBI Description
                   297331
 Seq. No.
                   LIB3137-024-Q1-K1-C7
 Seq. ID
                   BLASTN
 Method
                   g2921303
 NCBI GI
                   166
 BLAST score
                   2.0e-88
 E value
                   286
 Match length
 % identity
                   90
```

Seq. ID



```
NCBI Description Zea mays herbicide safener binding protein (SBP1) mRNA,
                complete cds
                  297332
Seq. No.
                  LIB3137-024-Q1-K1-D9
Seq. ID
                  BLASTN
Method
                  g397395
NCBI GI
                  76
BLAST score
                  8.0e-35
E value
                  132
Match length
                  89
% identity
NCBI Description Z.mays MNB1b mRNA for DNA-binding protein
                  297333
Seq. No.
                  LIB3137-024-Q1-K1-F1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2832696
                  155
BLAST score
                  2.0e-10
E value
Match length
                  113
                  29
% identity
NCBI Description (AL021713) putative protein [Arabidopsis thaliana]
                  297334
Seq. No.
                  LIB3137-024-Q1-K1-F4
Seq. ID
Method
                  BLASTX
                   q729773
NCBI GI
BLAST score
                   218
                   1.0e-17
E value
Match length
                   66
                   64
% identity
                  HEAT SHOCK FACTOR PROTEIN 1 (HSF 1) (HEAT SHOCK
NCBI Description
                   TRANSCRIPTION FACTOR 1) (HSTF 1) >gi_429155_emb_CAA53761_
                   (X76167) heat shock factor [Arabidopsis thaliana]
                   297335
Seq. No.
                   LIB3137-024-Q1-K1-F6
Seq. ID
                   BLASTX
Method
                   g2911073
NCBI GI
                   454
BLAST score
                   3.0e-45
E value
                   141
Match length
                   68
% identity
                   (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                   297336
Seq. No.
                   LIB3137-024-Q1-K1-F8
Seq. ID
                   BLASTX
Method
                   q3355780
NCBI GI
                   220
BLAST score
                   6.0e-18
E value
                   83
Match length
                   57
% identity
                  (AJ004997) expansin18 [Lycopersicon esculentum]
NCBI Description
                   297337
Seq. No.
```

LIB3137-024-Q1-K1-G9

Method

BLASTX



```
BLASTX
Method
                  q1706260
NCBI GI
                  317
BLAST score
                  2.0e-29
E value
                  60
Match length
                  97
% identity
                  CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131_pir __S59597
NCBI Description
                  cysteine proteinase 1 precursor - maize
                   >gi 643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
                   mays]
Seq. No.
                   297338
                   LIB3137-024-Q1-K1-H1
Seq. ID
Method
                  BLASTX
                   g2244915
NCBI GI
                   213
BLAST score
                   5.0e-17
E value
Match length
                   122
                   35
% identity
                   (Z97339) strong homology to reverse transcriptase
NCBI Description
                   [Arabidopsis thaliana]
                   297339
Seq. No.
Seq. ID
                   LIB3137-024-Q1-K1-H3
                   BLASTX
Method
NCBI GI
                   g132724
BLAST score
                   198
                   2.0e-15
E value
Match length
                   50
                   74
% identity
                   50S RIBOSOMAL PROTEIN L18 >gi_71259 pir_ R5BS8F ribosomal
NCBI Description
                   protein L18 - Bacillus stearothermophilus
                   297340
Seq. No.
                   LIB3137-027-Q1-K1-B11
Seq. ID
                   BLASTN
Method
                   g3004949
NCBI GI
                   58
BLAST score
                   5.0e-24
E value
                   94
Match length
                   90
 % identity
                   Zea mays tonoplast intrinsic protein (ZmTIP1) mRNA,
NCBI Description
                   complete cds
                   297341
 Seq. No.
                   LIB3137-027-Q1-K1-C10
 Seq. ID
                   BLASTX
 Method
                   g1665867
 NCBI GI
                   178
 BLAST score
                   1.0e-22
 E value
                   105
 Match length
                   53
 % identity
 NCBI Description (Y09123) aspartic proteinase [Centaurea calcitrapa]
                   297342
 Seq. No.
 Seq. ID
                   LIB3137-027-Q1-K1-D3
```

Seq. No.

Seq. ID

297347

LIB3137-027-Q1-K1-H2



```
q4432856
  NCBI GI
                    183
*BLAST score
                    1.0e-13
  E value
                    95
  Match length
                    46
  % identity
                    (AC006300) putative 2A6 protein [Arabidopsis thaliana]
  NCBI Description
                    297343
  Seq. No.
                    LIB3137-027-Q1-K1-E10
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g113621
  BLAST score
                    250
                    4.0e-35
  E value
  Match length
                    100
                     82
  % identity
                    FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
  NCBI Description
                    >gi 68196_pir__ADZM fructose-bisphosphate aldolase (EC
                     4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
                     [Zea mays] >gi 295850_emb_CAA31366_ (X12872) fructose
                     bisphosphate aldolase [Zea mays] >gi 225624 prf 1307278A
                     cytoplasmic aldolase [Zea mays]
  Seq. No.
                     297344
                    LIB3137-027-Q1-K1-E3
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     q4587577
  BLAST score
                     142
  E value
                     9.0e-09
  Match length
                     54
                     46
  % identity
                    (AC006550) F1003.17 [Arabidopsis thaliana]
  NCBI Description
  Seq. No.
                     297345
                     LIB3137-027-Q1-K1-E4
  Seq. ID
                     BLASTX
  Method
                     g2598575
  NCBI GI
                     181
  BLAST score
  E value
                     2.0e-13
                     110
  Match length
                     37
  % identity
  NCBI Description (Y15293) MtN21 [Medicago truncatula]
                     297346
  Seq. No.
                     LIB3137-027-Q1-K1-G6
  Seq. ID
                     BLASTX
  Method
                     q710626
  NCBI GI
  BLAST score
                     154
                     2.0e-10
  E value
                     41
  Match length
                     59
  % identity
                     (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941
  NCBI Description
                     (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                     thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis
                     thaliana]
```



```
BLASTX
Method
                  q2182267
NCBI GI
                  407
BLAST score
                  6.0e-40
E value
                  115
Match length
                  71
% identity
                  (L37359) lipoxygenase [Hordeum vulgare]
NCBI Description
                  297348
Seq. No.
                  LIB3137-027-Q1-K1-H7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q22312
                  37
BLAST score
                  2.0e-11
E value
                  49
Match length
% identity
                  94
                  Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                  abscisic acid)
                  297349
Seq. No.
                  LIB3137-028-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4056432
                  553
BLAST score
                   6.0e-57
E value
Match length
                  142
                  70
% identity
                   (AC005990) Similar to gi 2245014 glucosyltransferase
NCBI Description
                  homolog from Arabidopsis thaliana chromosome 4 contig
                  gb Z97341. ESTs gb T20778 and gb_AA586281 come from this
                   gene. [Arabidopsis thaliana]
                   297350
Seq. No.
                  LIB3137-028-Q1-K1-A7
Seq. ID
Method
                  BLASTN
                   g11957
NCBI GI
                   221
BLAST score
                   1.0e-121
E value
                   261
Match length
                   48
% identity
NCBI Description Rice complete chloroplast genome
                   297351
Seq. No.
                   LIB3137-028-Q1-K1-C10
Seq. ID
                   BLASTX
Method
                   g2702281
NCBI GI
                   227
BLAST score
                   6.0e-19
E value
                   72
Match length
                   60
% identity
                   (AC003033) putative protein disulfide isomerase precursor
NCBI Description
                   [Arabidopsis thaliana]
                   297352
Seq. No.
Seq. ID
                   LIB3137-028-Q1-K1-E8
```

BLASTX NCBI GI g2160690

Method



```
BLAST score
                  1.0e-21
E value
                  71
Match length
                   59
% identity
                   (U73526) B' regulatory subunit of PP2A [Arabidopsis
NCBI Description
                  thaliana]
                   297353
Seq. No.
                  LIB3137-028-Q1-K1-G7
Seq. ID
Method
                  BLASTX
                  g2952328
NCBI GI
BLAST score
                   305
                   7.0e-28
E value
Match length
                   83
% identity
                   72
                   (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza
NCBI Description
                   sativa]
                   297354
Seq. No.
                   LIB3137-029-Q1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2462832
BLAST score
                   290
                   4.0e-26
E value
Match length
                   113
                   53
% identity
                  (AF000657) similar to Bacillus CotA [Arabidopsis thaliana]
NCBI Description
                   297355
Seq. No.
                   LIB3137-029-Q1-K1-B4
Seq. ID
                   BLASTX
Method
                   g3236253
NCBI GI
BLAST score
                   387
                   2.0e-37
E value
Match length
                   134
                   54
% identity
                   (AC004684) receptor-like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   297356
Seq. No.
Seq. ID
                   LIB3137-029-Q1-K1-B8
                   BLASTX
Method
                   g3337367
NCBI GI
BLAST score
                   204
E value
                   3.0e-16
                   87
Match length
                   54
% identity
                   (AC004481) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   297357
Seq. No.
                   LIB3137-029-Q1-K1-C10
Seq. ID
Method
                   BLASTX
                   q136640
NCBI GI
                   195
BLAST score
E value
                   6.0e-15
Match length
                   86
```

41701

55

% identity



```
UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_170785 (M62720)
                  ubiquitin carrier protein [Triticum aestivum]
Seq. No.
                  297358
                  LIB3137-029-Q1-K1-F11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1504051
BLAST score
                  51
E value
                  8.0e-20
Match length
                  249
% identity
                  81
                  Zea mays mRNA for Calcium-dependent protein kinase,
NCBI Description
                  complete cds
                  297359
Seq. No.
Seq. ID
                  LIB3137-029-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  g2804280
BLAST score
                  242
E value
                  2.0e-20
Match length
                  122
% identity
                  (AB003687) 6-4 photolyase [Arabidopsis thaliana]
NCBI Description
                  >qi 3929918 dbj BAA34711 (AB017331) 6-4 photolyase
                  [Arabidopsis thaliana]
Seq. No.
                  297360
                  LIB3137-029-Q1-K1-F6
Seq. ID
Method
                  BLASTX
                  g1504052
NCBI GI
                  278
BLAST score
E value
                  1.0e-24
Match length
                  113
% identity
                  (D87042) Calcium-dependent protein kinase [Zea mays]
NCBI Description
                  297361
Seq. No.
                  LIB3137-029-Q1-K1-G7
Seq. ID
                  BLASTX
Method
                  g2827619
NCBI GI
                  257
BLAST score
E value
                  2.0e-22
                  87
Match length
                  62
% identity
                  (AL021636) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  297362
Seq. No.
Seq. ID
                  LIB3137-030-Q1-K1-E6
                  BLASTX
Method
                  g4126809
NCBI GI
                  394
```

Method BLASTX
NCBI GI g4126809
BLAST score 394
E value 3.0e-38
Match length 89
% identity 46

NCBI Description (AB017042) glyoxalase I [Oryza sativa]

NCBI Description



```
297363
Seq. No.
                  LIB3137-030-Q1-K1-F7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1706965
BLAST score
                  145
                  1.0e-09
E value
                  61
Match length
                  49
% identity
                  (U60754) delta-24-sterol methyltransferase [Triticum
NCBI Description
                  aestivum]
                  297364
Seq. No.
                  LIB3137-030-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                  q115815
NCBI GI
                  468
BLAST score
                  4.0e-47
E value
                  112
Match length
                  79
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-M9) (LHCP) >gi 100866 pir_ S13098 chlorophyll
                  a/b-binding protein precursor - maize
                  >qi 22355 emb CAA39376 (X55892) light-harvesting
                  chlorophyll a/b binding protein [Zea mays]
                  297365
Seq. No.
Seq. ID
                  LIB3137-032-Q1-K1-A9
Method
                  BLASTX
                  g2673947
NCBI GI
                  259
BLAST score
                   2.0e-22
E value
Match length
                  119
                   27
% identity
                   (U62931) multidrug resistance protein 1 [Aspergillus
NCBI Description
                   flavus] >qi 2673949 (U62932) multidrug resistance protein 1
                   [Aspergillus flavus]
Seq. No.
                   297366
Seq. ID
                  LIB3137-032-Q1-K1-C9
                   BLASTX
Method
NCBI GI
                   g3522937
                   354
BLAST score
                   1.0e-33
E value
Match length
                   116
% identity
                  (AC004411) unknown protein [Arabidopsis thaliana]
NCBI Description
                   297367
Seq. No.
                   LIB3137-033-Q1-K1-A10
Seq. ID
Method
                   BLASTX
                   g1574938
NCBI GI
BLAST score
                   209
                   6.0e-17
E value
                   68
Match length
% identity
```

(U34726) superoxide dismutase 4 [Zea mays]



```
297368
Seq. No.
                  LIB3137-033-Q1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115786
BLAST score
                  390
                  6.0e-38
E value
Match length
                  92
                  83
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB) (LHCP) >gi 82680 pir A29119 chlorophyll a/b-binding
                  protein - maize >gi 22357 emb CAA68451 (Y00379) LHCP [Zea
                  297369
Seq. No.
Seq. ID
                  LIB3137-033-Q1-K1-B2
                  BLASTN
Method
                  q3955072
NCBI GI
BLAST score
                  105
                  5.0e-52
E value
                  235
Match length
% identity
NCBI Description Zea mays PHYT II gene for acidic phytase
Seq. No.
                  297370
Seq. ID
                  LIB3137-033-Q1-K1-C1
                  BLASTX
Method
                  q542157
NCBI GI
                  141
BLAST score
E value
                  9.0e-09
Match length
                   31
                  84
% identity
NCBI Description ribosomal 5S RNA-binding protein - Rice
Seq. No.
                   297371
                   LIB3137-033-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1519249
BLAST score
                   157
E value
                   4.0e-11
Match length
                   58
% identity
                   62
NCBI Description (U65956) GF14-b protein [Oryza sativa]
Seq. No.
                   297372
                   LIB3137-033-Q1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1346735
BLAST score
                   169
                   5.0e-12
E value
                   73
Match length
```

48 % identity

2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE NCBI Description

(PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi 1076562_pir__S49647 phosphoglycerate mutase (EC 5.4.2.1) - castor bean >gi_474170_emb_CAA49995_ (X70652)

phosphoglycerate mutase [Ricinus communis]

Method

NCBI GI

BLASTX q4539422



```
297373
Seq. No.
                  LIB3137-033-Q1-K1-F11
Seq. ID
                  BLASTX
Method
                  g2668742
NCBI GI
                  378
BLAST score
                  2.0e-36
E value
                  85
Match length
                  88
% identity
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                  297374
Seq. No.
                  LIB3137-033-Q1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g66009
                   235
BLAST score
                   8.0e-22
E value
Match length
                   68
                   82
% identity
                   glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C,
NCBI Description
                   cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH
                   (AA 1-337) [Zea mays]
Seq. No.
                   297375
                   LIB3137-033-Q1-K1-G9
Seq. ID
Method
                   BLASTX
                   q170033
NCBI GI
                   383
BLAST score
E value
                   5.0e-37
                   108
Match length
% identity
                   64
                  (L00353) uricase II subunit [Glycine max]
NCBI Description
                   297376
Seq. No.
                   LIB3137-035-Q1-K1-A12
Seq. ID
                   BLASTN
Method
                   g22354
NCBI GI
BLAST score
                   42
                   1.0e-14
E value
                   70
Match length
                   91
% identity
                   Zea mays L. mRNA for light-harvesting chlorophyll a/b
NCBI Description
                   binding protein
                   297377
Seq. No.
Seq. ID
                   LIB3137-035-Q1-K1-B9
                   BLASTN
Method
                   g3135542
NCBI GI
BLAST score
                   71
                   1.0e-31
E value
                   87
Match length
                   95
% identity
                   Oryza sativa aquaporin (PIP2a) mRNA, complete cds
NCBI Description
                   297378
Seq. No.
Seq. ID
                   LIB3137-035-Q1-K1-C1
```

BLAST score

Match length

E value

446 2.0e-44

84



```
BLAST score
                  7.0e-09
E value
Match length
                  67
                  46
% identity
                  (AL049171) putative protein [Arabidopsis thaliana]
NCBI Description
                  297379
Seq. No.
                  LIB3137-035-Q1-K1-C7
Seq. ID
Method
                  BLASTX
                  g121631
NCBI GI
BLAST score
                  225
E value
                  1.0e-18
Match length
                  69
% identity
                  GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR
NCBI Description
                  >gi_72323_pir_KNNT2S glycine-rich protein 2 - wood tobacco
                   >gi 19743 emb CAA42622 (X60007) nsGRP-2 [Nicotiana
                   sylvestris]
                   297380
Seq. No.
                   LIB3137-035-Q1-K1-D11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2921304
BLAST score
                   328
                   8.0e-31
E value
Match length
                   91
% identity
                   (AF033496) herbicide safener binding protein [Zea mays]
NCBI Description
                   297381
Seq. No.
                   LIB3137-035-Q1-K1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3080439
BLAST score
                   161
E value
                   5.0e-11
                   54
Match length
% identity
                   (AL022605) putative protein [Arabidopsis thaliana]
NCBI Description
                   297382
Seq. No.
                   LIB3137-035-Q1-K1-E4
Seq. ID
                   BLASTN
Method
                   g2655030
NCBI GI
                   241
BLAST score
                   1.0e-133
E value
                   269
Match length
                   97
 % identity
                   Zea mays starch synthase isoform zSTSII-2 (zSSIIb) mRNA,
NCBI Description
                   complete cds
                   297383
 Seq. No.
                   LIB3137-035-Q1-K1-F6
 Seq. ID
                   BLASTX
Method
                   g134598
NCBI GI
```

Method

NCBI GI

BLASTN

g3452297



```
% identity
NCBI Description SUPEROXIDE DISMUTASE-4AP (CU-ZN)
                  297384
Seq. No.
                  LIB3137-035-Q1-K1-H2
Seq. ID
                  BLASTX
Method
                  g3128206
NCBI GI
                  423
BLAST score
                  8.0e-42
E value
                  108
Match length
                  70
% identity
NCBI Description (AC004077) unknown protein [Arabidopsis thaliana]
                  297385
Seq. No.
                  LIB3137-035-Q1-K1-H3
Seq. ID
                  BLASTX
Method
                  g2431769
NCBI GI
                  178
BLAST score
                  3.0e-13
E value
                  68
Match length
                  59
% identity
NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays]
                  297386
Seq. No.
                  LIB3137-035-Q1-K1-H5
Seq. ID
                  BLASTX
Method
                   q2425066
NCBI GI
                   155
BLAST score
                   4.0e-15
E value
                   73
Match length
                   66
% identity
NCBI Description (AF019147) cysteine proteinase Mir3 [Zea mays]
                   297387
Seq. No.
                   LIB3137-035-Q1-K1-H8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1498597
                   228
BLAST score
                   4.0e-19
E value
                   75
Match length
                   64
% identity
                   (U66105) phospholipid transfer protein [Zea mays]
NCBI Description
                   297388
Seq. No.
Seq. ID
                   LIB3137-036-Q1-K1-A11
                   BLASTX
Method
NCBI GI
                   q2244749
                   395
BLAST score
                   2.0e-38
E value
                   107
Match length
% identity
                   (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   297389
                   LIB3137-036-Q1-K1-B11
Seq. ID
```



```
BLAST score
                  3.0e-23
E value
                  138
Match length
                  88
% identity
NCBI Description Zea mays retrotransposon Ji-4 5' LTR, partial sequence
                  297390
Seq. No.
                  LIB3137-036-Q1-K1-D12
Seq. ID
Method
                  BLASTX
                  q1653626
NCBI GI
BLAST score
                  153
E value
                  4.0e-10
Match length
                  90
                  36
% identity
NCBI Description (D90915) hypothetical protein [Synechocystis sp.]
                  297391
Seq. No.
                  LIB3137-036-Q1-K1-G10
Seq. ID
                  BLASTX
Method
                  q134598
NCBI GI
                  207
BLAST score
E value
                   1.0e-16
Match length
                   64
% identity
                   70
NCBI Description SUPEROXIDE DISMUTASE-4AP (CU-ZN)
                   297392
Seq. No.
                  LIB3137-038-Q1-K1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4335745
BLAST score
                   214
E value
                   3.0e-17
Match length
                   115
% identity
                   42
                   (AC006284) putative hydrolase (contains an
NCBI Description
                   esterase/lipase/thioesterase active site serine domain
                   (prosite: PS50187) [Arabidopsis thaliana]
Seq. No.
                   297393
                   LIB3137-038-Q1-K1-B2
Seq. ID
                   BLASTX
Method
                   g479386
NCBI GI
                   150
BLAST score
E value
                   3.0e-12
Match length
                   65
                   63
% identity
NCBI Description isocitrate dehydrogenase - soybean
                   297394
Seq. No.
                   LIB3137-038-Q1-K1-C1
Seq. ID
                   BLASTX
Method
                   g2499608
NCBI GI
BLAST score
                   260
                   2.0e-27
E value
                   105
Match length
                   64
% identity
```

41708

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 4 (MAP KINASE 4)



(ATMPK4) >gi_2129645_pir__S40470 mitogen-activated protein kinase 4 (EC 2.7.1.-) - Arabidopsis thaliana >gi 457400 dbj_BAA04867_ (D21840) MAP kinase [Arabidopsis thaliana]

297395 Seq. No. LIB3137-038-Q1-K1-D3 Seq. ID BLASTX Method NCBI GI g1655637 BLAST score 166 1.0e-11 E value Match length 82 % identity 48

(Z54179) orf [Mus musculus] NCBI Description

297396 Seq. No.

Seq. ID LIB3137-038-Q1-K1-E1

Method BLASTN NCBI GI g2668739 BLAST score 96 2.0e-46 E value Match length 180 % identity 88

Zea mays translation initiation factor GOS2 (TIF) mRNA, NCBI Description

complete cds

297397 Seq. No.

LIB3137-038-Q1-K1-E2 Seq. ID

Method BLASTX g1086833 NCBI GI 144 BLAST score 5.0e-09 E value Match length 96

31 % identity

(U41264) coded for by C. elegans cDNA CEESN26F; coded for NCBI Description

by C. elegans cDNA CEESI89F; similar to 60S acidic ribosomal protein Po (L10) [Caenorhabditis elegans]

297398 Seq. No.

Seq. ID LIB3137-038-Q1-K1-G10

BLASTX Method g1203832 NCBI GI 176 BLAST score 6.0e-13 E value 98 Match length 41 % identity

(U46003) beta-D-glucan exohydrolase, isoenzyme ExoII NCBI Description

[Hordeum vulgare] >gi_1588407_prf_ 2208395A beta-D-glucan

exohydrolase [Hordeum vulgare]

297399 Seq. No.

Seq. ID LIB3137-038-Q1-K1-G6

BLASTN Method NCBI GI g18963 BLAST score 219 1.0e-120 E value 246 Match length



```
% identity
NCBI Description Z.mays mRNA for dehydrin (dhn3)
                  297400
Seq. No.
                  LIB3137-038-Q1-K1-H11
Seq. ID
                  BLASTX
Method
                  g2293566
NCBI GI
                  386
BLAST score
                  2.0e-37
E value
Match length
                  109
                  72
% identity
NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
                  297401
Seq. No.
                  LIB3137-039-Q1-K1-C8
Seq. ID
                  BLASTX
Method
                  g2984709
NCBI GI
                  278
BLAST score
                  9.0e-25
E value
                  78
Match length
                  74
% identity
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                   297402
Seq. No.
                  LIB3137-039-Q1-K1-D4
Seq. ID
                  BLASTX
Method
                   q4337179
NCBI GI
                   188
BLAST score
                   3.0e-14
E value
                   54
Match length
                   63
% identity
                   (AC006416) This gene is continued on the 5' end of BAC
NCBI Description
                   T12M14. [Arabidopsis thaliana]
                   297403
Seq. No.
                   LIB3137-040-Q1-K1-A11
Seq. ID
                   BLASTN
Method
                   g2921303
NCBI GI
                   207
BLAST score
                   1.0e-113
E value
                   309
Match length
                   100
% identity
                   Zea mays herbicide safener binding protein (SBP1) mRNA,
NCBI Description
                   complete cds
                   297404
Seq. No.
Seq. ID
                   LIB3137-040-Q1-K1-A8
                   BLASTX
Method
                   q2623307
NCBI GI
                   403
BLAST score
                   3.0e-39
E value
Match length
                   97
                   73
% identity
                   (AC002409) putative ubiquitin protease [Arabidopsis
NCBI Description
                   thaliana]
```

41710

297405

Seq. No.



```
LIB3137-040-Q1-K1-B10
Seq. ID
                  BLASTX
Method
                  g1403675
NCBI GI
                  493
BLAST score
                  7.0e-50
E value
                  136
Match length
                  74
% identity
NCBI Description (U41323) beta-1,3-glucanase [Glycine max]
Seq. No.
                  297406
                  LIB3137-040-Q1-K1-B12
Seq. ID
Method
                  BLASTX
                  g585963
NCBI GI
                  260
BLAST score
                  1.0e-22
E value
                   69
Match length
% identity
                  77
NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT
                  297407
Seq. No.
                  LIB3137-040-Q1-K1-B8
Seq. ID
Method
                  BLASTX
                   g3337356
NCBI GI
                   206
BLAST score
                   2.0e-16
E value
Match length
                   71
                   56
% identity
                   (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
                   297408
Seq. No.
Seq. ID
                   LIB3137-040-Q1-K1-B9
                   BLASTX
Method
                   g4097880
NCBI GI
                   154
BLAST score
                   4.0e-21
E value
                   115
Match length
                   57
% identity
NCBI Description (U70866) polyprotein [Bean pod mottle virus]
                   297409
Seq. No.
Seq. ID
                   LIB3137-040-Q1-K1-C11
                   BLASTX
Method
NCBI GI
                   q4097880
BLAST score
                   265
                   2.0e-23
E value
                   92
Match length
                   61
% identity
                   (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   297410
Seq. No.
Seq. ID
                   LIB3137-040-Q1-K1-C8
                   BLASTN
Method
                   g2773153
NCBI GI
BLAST score
                   99
E value
                   3.0e-48
```

41711

219

Match length



% identity Oryza sativa abscisic acid- and stress-inducible protein NCBI Description (Asr1) mRNA, complete cds 297411 Seq. No. LIB3137-040-Q1-K1-F11 Seq. ID BLASTX Method q2239083 NCBI GI BLAST score 166 2.0e-11 E value 108 Match length % identity 40 (Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase NCBI Description [Dianthus caryophyllus] >gi_2239087_emb_CAB06429_ (Z84385) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] Seq. No. 297412 LIB3137-040-Q1-K1-G12 Seq. ID Method BLASTX g541943 NCBI GI 202 BLAST score E value 9.0e-16 39 Match length 90 % identity metallothionein - soybean >gi 228682 prf 1808316A NCBI Description metallothionein-like protein [Glycine max] Seq. No. 297413 LIB3137-040-Q1-K1-H10 Seq. ID Method BLASTX g4262183 NCBI GI BLAST score 158 9.0e-11 E value 61 Match length % identity 51 (AC005508) 51434 [Arabidopsis thaliana] NCBI Description 297414 Seq. No. LIB3137-041-Q1-K1-C2 Seq. ID BLASTX Method g2829912 NCBI GI BLAST score 222 3.0e-18 E value 57 Match length 74 % identity (AC002291) Similar ATP-dependent RNA Helicase [Arabidopsis NCBI Description

thaliana]

297415

Seq. No.

LIB3137-041-Q1-K1-C5 Seq. ID

BLASTX Method NCBI GI q4008159 274 BLAST score 3.0e-24 E value 70 Match length 76 % identity



NCBI Description (AB015601) DnaJ homolog [Salix gilgiana] 297416 Seq. No. LIB3137-041-Q1-K1-C9 Seq. ID BLASTX Method g4325282 NCBI GI 186 BLAST score 3.0e-14 E value 69 Match length 52 % identity (AF123310) NAC domain protein NAM [Arabidopsis thaliana] NCBI Description >gi 4325286 gb AAD17314_ (AF123311) NAC domain protein NAM [Arabidopsis thaliana] 297417 Seq. No. Seq. ID LIB3137-041-Q1-K1-D12 Method BLASTX NCBI GI g1524115 BLAST score 285 E value 1.0e-25 Match length 111 49 % identity (X95270) subtilisin-like endoprotease [Lycopersicon NCBI Description esculentum] >gi_4200334_emb_CAA76724_ (Y17275) P69A protein [Lycopersicon esculentum] 297418 Seq. No. LIB3137-041-Q1-K1-E7 Seq. ID BLASTX Method g2655888 NCBI GI 268 BLAST score 9.0e-24 E value 94 Match length 50 % identity NCBI Description (AL009171) 62D9.a [Drosophila melanogaster] 297419 Seq. No. LIB3137-041-Q1-K1-H9 Seq. ID BLASTX Method g1708236 NCBI GI 259 BLAST score 1.0e-22 E value 65 Match length 75 % identity HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) NCBI Description (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)

>gi_2129617_pir JC4567 hydroxymethylglutaryl-CoA synthase

(EC 4.1.3.5) - Arabidopsis thaliana >gi 1143390 emb CAA58763 (X83882)

hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]

>qi 1586548 prf 2204245A hydroxy methylglutaryl CoA

synthase [Arabidopsis thaliana]

297420 Seq. No.

Seq. ID LIB3137-042-Q1-K1-H10

Method BLASTX NCBI GI q626042

Seq. ID



```
BLAST score
                  2.0e-38
E value
                  97
Match length
                  80
% identity
                  beta-glucosidase, root meristem (EC 3.2.1.-) precursor -
NCBI Description
                  maize >gi 435313 emb CAA52293 (X74217) beta-glucosidase
                   [Zea mays]
                  297421
Seq. No.
                  LIB3137-043-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115771
                   530
BLAST score
                   3.0e-54
E value
Match length
                  117
% identity
                   86
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll
                   a/b-binding protein precursor - maize
                   >gi 22224 emb CAA32900 (X14794) chlorophyll a/b-binding
                   preprotein (AA 1 - 262) [Zea mays]
Seq. No.
                   297422
                   LIB3137-043-Q1-K1-D8
Seq. ID
Method
                  BLASTX
                   q517500
NCBI GI
BLAST score
                   144
E value
                   1.0e-10
                   69
Match length
                   71
% identity
                   (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                   protein [Zea mays] >gi 444338 prf 1906386A photosystem II
                   OE17 protein [Pisum sativum]
                   297423
Seq. No.
                   LIB3137-043-Q1-K1-E11
Seq. ID
                   BLASTX
Method
                   q1619300
NCBI GI
                   170
BLAST score
E value
                   3.0e-12
                   74
Match length
                   51
% identity
                  (X95269) LRR protein [Lycopersicon esculentum]
NCBI Description
                   297424
Seq. No.
Seq. ID
                   LIB3137-043-Q1-K1-E2
                   BLASTX
Method
NCBI GI
                   g3403236
BLAST score
                   382
                   6.0e-37
E value
Match length
                   128
                   58
% identity
                   (AF071544) ribulose-1,5-bisphosphate carboxylase/oxygenase
NCBI Description
                   small subunit N-methyltransferase I [Spinacia oleracea]
Seq. No.
                   297425
```

LIB3137-043-Q1-K1-F4



```
BLASTX
Method
                  q4336747
NCBI GI
                  322
BLAST score
                  8.0e-30
E value
                  130
Match length
                  55
% identity
                  (AF104924) unconventional myosin heavy chain [Zea mays]
NCBI Description
                  297426
Seq. No.
                  LIB3137-043-Q1-K1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4584548
                  430
BLAST score
                   4.0e-43
E value
                  104
Match length
                   83
% identity
                  (AL049608) putative protein [Arabidopsis thaliana]
NCBI Description
                   297427
Seq. No.
                  LIB3137-044-Q1-K1-B7
Seq. ID
                  BLASTN
Method
NCBI GI
                   q1518674
BLAST score
                   193
                   1.0e-104
E value
                   264
Match length
                   93
% identity
                  Zea mays beta D-glucosidase (glu1) gene, intron 10
NCBI Description
                   transposon 2, complete sequence
                   297428
Seq. No.
                   LIB3137-044-Q1-K1-B9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2668742
BLAST score
                   349
                   3.0e-33
E value
                   81
Match length
                   85
% identity
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                   297429
Seq. No.
Seq. ID
                   LIB3137-044-Q1-K1-C3
Method
                   BLASTX
                   g100918
NCBI GI
BLAST score
                   219
                   6.0e-18
E value
                   80
Match length
                   57
% identity
                   RAB-17 protein - maize >gi 239236 bbs 66621 RAB-17
NCBI Description
                   protein=substrate for casein kinase 2 [Zea mays L.=maize,
                   line W64 A, Peptide, 168 aa]
Seq. No.
                   297430
                   LIB3137-044-Q1-K1-D7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2109457
BLAST score
                   152
```

·* '

41715

4.0e-10

E value



Match length 94 % identity 47

NCBI Description (AF001501) chitinase [Oryza sativa]

Seq. No.

297431

Seq. ID

LIB3137-044-Q1-K1-D9

Method NCBI GI BLAST score BLASTX g481031 148 7.0e-10

45

E value Match length % identity

% identity 60
NCBI Description transcription factor SF3 - common sunflower

Seq. No.

297432

Seq. ID

LIB3137-044-Q1-K1-E9

Method BLASTX
NCBI GI g464707
BLAST score 186
E value 4.0e-14
Match length 76
% identity 51

NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal

protein S18.A - Arabidopsis thaliana

>gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
[Arabidopsis thaliana] >gi 434343 emb CAA82273_ (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)

S18 ribosomal protein [Arabidopsis thaliana]

>gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal

protein [Arabidopsis thaliana]

Seq. No. 297433

Seq. ID LIB3137-044-Q1-K1-F1

Method BLASTX
NCBI GI g3647355
BLAST score 314
E value 6.0e-29
Match length 115
% identity 54

NCBI Description (Z97348) predicted using hexExon; MAL3P1.12 (PFC0150w),

Human hypothetical protein KIAA0249-related protein len: 1160 aa; Similarity to 2 human and an yeast hypothetical gene. Human hypothetical protein KIAA0249 (SW:Y249 HUMA

Seq. No. 297434

Seq. ID LIB3137-044-Q1-K1-H5

Method BLASTX
NCBI GI g2827709
BLAST score 235
E value 5.0e-20



```
Match length
                  58
% identity
                  (AL021684) predicted protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  297435
Seq. ID
                  LIB3137-045-Q1-K1-C1
                  BLASTX
Method
NCBI GI
                  g3549681
                  334
BLAST score
                  3.0e-31
E value
Match length
                  140
% identity
                  46
                  (AL031394) male sterility 2-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  297436
                  LIB3137-045-Q1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3080427
                  206
BLAST score
E value
                  3.0e-16
Match length
                  102
% identity
                  45
                  (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
                  297437
Seq. No.
                  LIB3137-045-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2109457
                  385
BLAST score
                  4.0e-37
E value
Match length
                  115
% identity
                  66
NCBI Description (AF001501) chitinase [Oryza sativa]
Seq. No.
                  297438
                  LIB3137-045-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q464987
BLAST score
                  204
E value
                  3.0e-16
                  57
Match length
% identity
NCBI Description
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN
                  LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)
                  >gi 421858 pir S32672 ubiquitin--protein ligase (EC
                  6.3.2.19) UBC10 - Arabidopsis thaliana
                  >qi 297878 emb CAA78715 (Z14991) ubiquitin conjugating
```

enzyme [Arabidopsis thaliana] >qi 349213 (L00640) ubiquitin

conjugating enzyme [Arabidopsis thaliana]

Seq. No. 297439

Seq. ID LIB3137-047-Q1-K1-C7

Method BLASTX NCBI GI g2668742 BLAST score 431 E value 1.0e-42



```
Match length
                  99
% identity
                   (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                  297440
Seq. No.
                  LIB3137-047-Q1-K1-F4
Seq. ID
                  BLASTX
Method
                  q477226
NCBI GI
                   448
BLAST score
                   6.0e-45
E value
                  87
Match length
                   97
% identity
                  heat shock protein HSP82 - maize >gi_300083 bbs 130886
NCBI Description
                   (S59780) HSP82=82 kda heat shock protein [Zea mays,
                   seedling, leaves, Peptide, 715 aa] [Zea mays]
Seq. No.
                   297441
                  LIB3137-047-Q1-K1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4539423
BLAST score
                   432
E value
                   7.0e-43
Match length
                   112
% identity
                   73
                   (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   297442
                   LIB3137-047-Q1-K1-H6
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2921303
BLAST score
                   195
E value
                   1.0e-106
                   283
Match length
% identity
                   Zea mays herbicide safener binding protein (SBP1) mRNA,
NCBI Description
                   complete cds
                   297443
Seq. No.
Seq. ID
                   LIB3137-049-Q1-K1-A11
                   {\tt BLASTX}
Method
                   g3551954
NCBI GI
BLAST score
                   172
E value
                   2.0e-12
                   93
Match length
                   40
% identity
                   (AF082030) senescence-associated protein 5 [Hemerocallis
NCBI Description
                   hybrid cultivar]
                   297444
Seq. No.
                   LIB3137-049-Q1-K1-D2
Seq. ID
Method
                   BLASTX
                   g3024122
NCBI GI
BLAST score
                   487
E value
                   3.0e-49
Match length
                   121
```

79

% identity

Seq. ID



```
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
                  ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi 1778821
                  (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]
                  297445
Seq. No.
                  LIB3137-049-Q1-K1-G1
Seq. ID
                  BLASTX
Method
                  g3258635
NCBI GI
                  158
BLAST score
                  1.0e-10
E value
                  112
Match length
% identity
                  30
NCBI Description (AF041049) 4-coumarate: CoA ligase [Populus tremuloides]
Seq. No.
                  297446
                  LIB3137-049-Q1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g67529
BLAST score
                  164
                   2.0e-11
E value
Match length
                  95
                   41
% identity
                  membrane alanyl aminopeptidase (EC 3.4.11.2) - Escherichia
NCBI Description
                   coli
                   297447
Seq. No.
Seq. ID
                   LIB3137-050-Q1-K1-B10
Method
                   BLASTX
                   g729671
NCBI GI
                   221
BLAST score
                   3.0e-25
E value
                   78
Match length
% identity
                   83
NCBI Description HISTONE H2A >gi_473603 (U08225) histone H2A [Zea mays]
                   297448
Seq. No.
Seq. ID
                   LIB3137-050-Q1-K1-C2
                   BLASTN
Method
                   g1177368
NCBI GI
                   55
BLAST score
                   2.0e-22
E value
Match length
                   95
                   89
% identity
NCBI Description Z.mays mRNA for ribosomal protein L39
                   297449
Seq. No.
Seq. ID
                   LIB3137-050-Q1-K1-F9
Method
                   BLASTX
                   q2673918
NCBI GI
BLAST score
                   198
                   1.0e-15
E value
Match length
                   57
 % identity
                   (AC002561) unknwon protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                   297450
```

41719

LIB3137-050-Q1-K1-H12

BLAST score

E value

152 7.0e-10



```
BLASTX
Method
                  q2668742
NCBI GI
                  421
BLAST score
                  2.0e-41
E value
                  85
Match length
                  95
% identity
                   (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                   297451
Seq. No.
                  LIB3137-050-Q1-K1-H7
Seq. ID
                  BLASTX
Method
                   g3414817
NCBI GI
                   206
BLAST score
                   8.0e-21
E value
                   95
Match length
                   57
% identity
                   (AF064212) globulin-1 [Zea mays subsp. mays]
NCBI Description
Seq. No.
                   297452
                   LIB3137-056-Q1-K1-B9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g20266
BLAST score
                   54
                   1.0e-21
E value
Match length
                   82
                   91
% identity
                   O.sativa mRNA for lipoxygenase L-2
NCBI Description
                   >gi_2171696_dbj_E03480_E03480 cDNA encoding rice
                   lipoxygenase L-3
                   297453
Seq. No.
                   LIB3137-056-Q1-K1-D10
Seq. ID
Method
                   BLASTX
                   g3702351
NCBI GI
                   242
BLAST score
                   2.0e-20
E value
                   95
Match length
                   49
% identity
                   (AC005397) putative desiccation protectant protein
NCBI Description
                   [Arabidopsis thaliana]
                   297454
Seq. No.
Seq. ID
                   LIB3137-057-Q1-K1-A12
                   BLASTX
Method
                   g4406759
NCBI GI
                   171
BLAST score
                   1.0e-12
E value
Match length
                   75
                   51
% identity
                   (ACO06836) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   297455
 Seq. No.
                   LIB3137-057-Q1-K1-B11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3025299
```



```
Match length
                  30
% identity
                  HYPOTHETICAL 62.3 KD PROTEIN T29M21.25 >gi 2088660
NCBI Description
                  (AF002109) ABC1 isolog [Arabidopsis thaliana]
                  297456
Seq. No.
                  LIB3137-057-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2984709
                  179
BLAST score
                  3.0e-13
E value
                  40
Match length
% identity
                  88
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                  297457
Seq. No.
                  LIB3137-057-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2498077
BLAST score
                  184
                  7.0e-14
E value
                  96
Match length
% identity
                   47
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                   (PP18) >gi_1777930 (U55019) nucleoside diphosphate kinase
                   [Saccharum officinarum]
                   297458
Seq. No.
                  LIB3137-058-Q1-K1-B12
Seq. ID
                   BLASTX
Method
                   g123617
NCBI GI
                   137
BLAST score
E value
                   1.0e-08
Match length
                   45
                   64
% identity
                  HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi 99707 pir JA0170
NCBI Description
                   heat shock protein 70-2 - Arabidopsis thaliana (fragment)
                   >gi_166766 (M23106) heat shock protein HSP70-2 [Arabidopsis
                   thaliana]
                   297459
Seq. No.
                   LIB3137-058-Q1-K1-B7
Seq. ID
                   BLASTX
Method
                   g2127458
NCBI GI
BLAST score
                   210
                   1.0e-16
E value
Match length
                   118
                   37
% identity
                   abc1 protein - Mycobacterium leprae >gi 466965 (U00016)
NCBI Description
                   abc1; B1937 C3 233 [Mycobacterium leprae]
```

297460 Seq. No.

LIB3137-058-Q1-K1-D5 Seq. ID

BLASTX Method g3367593 NCBI GI 165 BLAST score 2.0e-11 E value



```
Match length
                  52
% identity
                   (AL031135) putative protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3805841_emb_CAA21461_ (AL031986) putative protein
                   [Arabidopsis thaliana]
                  297461
Seq. No.
                  LIB3137-058-Q1-K1-E12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g741983
                   221
BLAST scorè
                   3.0e-18
E value
                   73
Match length
                   67
% identity
NCBI Description sucrose synthase: ISOTYPE=2 [Zea mays]
                   297462
Seq. No.
                   LIB3137-058-Q1-K1-E5
Seq. ID
                   BLASTX
Method
                   q4335745
NCBI GI
                   366
BLAST score
E value
                   5.0e-35
Match length
                   131
                   50
% identity
                   (AC006284) putative hydrolase (contains an
NCBI Description
                   esterase/lipase/thioesterase active site serine domain
                   (prosite: PS50187) [Arabidopsis thaliana]
                   297463
Seq. No.
                   LIB3137-058-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   g1351136
NCBI GI
                   150
BLAST score
                   5.0e-11
E value
                   62
Match length
                   66
% identity
                   SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
NCBI Description
                   >gi 514946 (L22296) UDP-glucose:D-fructose
                   2-glucosyl-transferase [Zea mays] >gi_533252 (L33244)
                   sucrose synthase 2 [Zea mays]
                   297464
 Seq. No.
                   LIB3137-058-Q1-K1-F4
 Seq. ID
                   BLASTX
Method
                   g3047111
NCBI GI
                   276
BLAST score
                   1.0e-24
E value
                   69
Match length
                   57
 % identity
```

(AF058919) No definition line found [Arabidopsis thaliana] NCBI Description

Seq. No.

LIB3137-058-Q1-K1-G4 Seq. ID

297465

BLASTX Method NCBI GI q4158230 BLAST score 218 4.0e-18 E value



```
Match length
                  88
% identity
                  (Y18625) amylogenin [Triticum aestivum]
NCBI Description
                  297466
Seq. No.
                  LIB3137-059-Q1-K1-A1
Seq. ID
                  BLASTX
Method
                  g1169383
NCBI GI
                  232
BLAST score
                  2.0e-23
E value
                  63
Match length
                  85
% identity
                  DNAJ PROTEIN HOMOLOG ATJ >gi_535588 (L36113) putative
NCBI Description
                  [Arabidopsis thaliana] >gi 1582356 prf 2118338A AtJ2
                  protein [Arabidopsis thaliana]
                  297467
Seq. No.
                  LIB3137-059-Q1-K1-C12
Seq. ID
                  BLASTX
Method
                  g283038
NCBI GI
                  337
BLAST score
E value
                  5.0e-36
                  101
Match length
                  79
% identity
                  chlorophyll a/b-binding protein (cab-m7) precursor - maize
NCBI Description
                  >gi 22230 emb_CAA37474 (X53398) light harvesting
                  chlorophyll a /b binding protein [Zea mays]
                  297468
Seq. No.
                  LIB3137-059-Q1-K1-D11
Seq. ID
                  BLASTX
Method
                   g710626
NCBI GI
                   154
BLAST score
                   4.0e-10
E value
                   68
Match length
                   49
% identity
                   (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941
NCBI Description
                   (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                   thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis
                   thaliana]
                   297469
Seq. No.
Seq. ID
                   LIB3137-059-Q1-K1-D3
Method
                   BLASTN
NCBI GI
                   q236729
                   105
BLAST score
                   8.0e-52
E value
                   133
Match length
                   97
% identity
                  metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]
NCBI Description
Seq. No.
                   297470
```

Seq. ID LIB3137-059-Q1-K1-F7

Method BLASTN
NCBI GI g4140643
BLAST score 45
E value 4.0e-16



```
Match length
                  87
% identity
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                  complete sequence
                   297471
Seq. No.
                   LIB3137-059-Q1-K1-G2
Seq. ID
                  BLASTX
Method
                   q135411
NCBI GI
                   401
BLAST score
                   4.0e-52
E value
Match length
                   111
% identity
                   92
                  TUBULIN ALPHA-2 CHAIN >gi_82732_pir__S15772 tubulin alpha-2
NCBI Description
                   chain - maize >gi_22148_emb_CAA33733_ (X15704)
                   alpha2-tubulin [Zea mays]
                   297472
Seq. No.
                   LIB3137-059-Q1-K1-H11
Seq. ID
                   BLASTX
Method
                   g2494280
NCBI GI
                   145
BLAST score
                   3.0e-09
E value
Match length
                   59
% identity
                   47
                   ELONGATION FACTOR TS (EF-TS) >gi_1653231_dbj_BAA18146_
NCBI Description
                   (D90912) elongation factor TS [Synechocystis sp.]
                   297473
Seq. No.
                   LIB3137-059-Q1-K1-H3
Seq. ID
                   BLASTX
Method
                   g2832700
NCBI GI
                   191
BLAST score
                   3.0e-18
E value
Match length
                   93
 % identity
                   61
                   (AL021713) unknown protein [Arabidopsis thaliana]
NCBI Description
                   297474
 Seq. No.
                   LIB3137-060-Q1-K1-E11
 Seq. ID
                   BLASTX
 Method
                   g3452497
 NCBI GI
                   139
 BLAST score
                   1.0e-08
 E value
                   87
 Match length
                    37
 % identity
                   (Y17796) ketol-acid reductoisomerase [Pisum sativum]
 NCBI Description
                    297475
 Seq. No.
                    LIB3137-060-Q1-K1-F5
 Seq. ID
                    BLASTX
 Method
                    g1039332
 NCBI GI
                    158
 BLAST score
                    1.0e-10
 E value
                    98
 Match length
```

NCBI Description (X86101) glutamyl tRNA reductase [Hordeum vulgare]

41

% identity

BLAST score

Match length

E value

165 7.0e-12

78



```
297476
Seq. No.
                   LIB3137-060-Q1-K1-F7
Seq. ID
                   BLASTX
Method
                   g116380
NCBI GI
                   208
BLAST score
                   2.0e-16
E value
                   43
Match length
                   91
% identity
                   CHALCONE SYNTHASE C2 (NARINGENIN-CHALCONE SYNTHASE C2)
NCBI Description
                   >gi_66554_pir__SYZMCC naringenin-chalcone synthase (EC
                   2.3.1.74) c2 - maize >gi_22218_emb_CAA42764_ (X60205)
                   chalcone synthase [Zea mays]
                   297477
Seq. No.
                   LIB3137-061-Q1-K1-D9
Seq. ID
Method
                   BLASTX
                   g2499614
NCBI GI
                   195
BLAST score
                   1.0e-15
E value
                   49
Match length
                   82
% identity
                   MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG NTF3 (P43)
NCBI Description
                   >gi_481830_pir__S39559 mitogen-activated protein kinase 3
homolog ntf3 - common tobacco >gi_406751_emb_CAA49592_
                    (X69971) NTF3 [Nicotiana tabacum]
                   297478
Seq. No.
                   LIB3137-061-Q1-K1-E6
Seq. ID
                   BLASTX
Method
                   g548770
NCBI GI
                   194
BLAST score
                   3.0e-25
E value
                   108
Match length
                    61
% identity
                   60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
NCBI Description
                   protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                    ribosomal protein L3 [Oryza sativa]
                    297479
Seq. No.
Seq. ID
                    LIB3137-061-Q1-K1-E7
                    BLASTN
Method
                    g3004949
NCBI GI
BLAST score
                    116
                    1.0e-58
E value
                    255
Match length
 % identity
                    Zea mays tonoplast intrinsic protein (ZmTIP1) mRNA,
NCBI Description
                    complete cds
                    297480
 Seq. No.
 Seq. ID
                    LIB3137-061-Q1-K1-F8
                    BLASTX
Method
                    q2326947
NCBI GI
```

```
% identity 49
NCBI Description (Z50801) Chlorophyll a/b-binding protein CP29 precursor [Zea mays]

Seq. No. 297481
Seq. ID LIB3137-061-Q1-K1-G12
Method BLASTX
NCBI GI g2979555
BLAST score 205
```

% identity 44
NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]

 Seq. No.
 297482

 Seq. ID
 LIB3137-061-Q1-K1-H12

 Method
 BLASTX

 NCBI GI
 64585873

3.0e-16

85

NCBI GI g4585873
BLAST score 198
E value 1.0e-15
Match length 54
% identity 69

E value Match length

NCBI Description (AC005850) Putative protein kinase [Arabidopsis thaliana]

Seq. No. 297483

Seq. ID LIB3137-062-Q1-K1-A11

Method BLASTX | NCBI GI g1321661 BLAST score 317 E value 1.0e-29 Match length 83 % identity 75

NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

Seq. No. 297484

Seq. ID LIB3137-062-Q1-K1-B3

Method BLASTX
NCBI GI g3914468
BLAST score 244
E value 6.0e-21
Match length 89
% identity 55

NCBI Description 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)

>gi_478411_pir__JQ2257 nuclear antigen 21D7 - carrot
>gi_217911_dbj_BAA02696_ (D13434) 21D7 antigen [Daucus

carota]

Seq. No. 297485

Seq. ID LIB3137-062-Q1-K1-B6

Method BLASTX
NCBI GI g2829688
BLAST score 164
E value 2.0e-11
Match length 61
% identity 66

NCBI Description CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE)

(O-ACETYLSERINE (THIOL)-LYASE) (CSASE)



>gi_1076798_pir__S52738 cysteine synthase (EC 4.2.99.8)
precursor - maize >gi_758353_emb_CAA59798_ (X85803)
cysteine synthase [Zea mays]

297486 Seq. No. LIB3137-062-Q1-K1-D2 Seq. ID Method BLASTX NCBI GI g3550985 BLAST score 157 2.0e-13 E value 65 Match length % identity 66

NCBI Description (AB010740) OsS5a [Oryza sativa]

Seq. No. 297487 Seq. ID LIB3137-062-Q1-K1-D6

Method BLASTN
NCBT GI 920248

NCBI GI g20248
BLAST score 38
E value 5.0e-12
Match length 106
% identity 84

NCBI Description O.sativa gt-2 gene

Seq. No. 297488

Seq. ID LIB3137-062-Q1-K1-E4

Method BLASTX
NCBI GI g82696
BLAST score 253
E value 5.0e-22
Match length 60
% identity 82

NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_

(X61121) glycine-rich protein [Zea mays]

Seq. No. 297489

Seq. ID LIB3137-062-Q1-K1-E8

Method BLASTX
NCBI GI g123620
BLAST score 476
E value 5.0e-48
Match length 101
% identity 94

NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi_100224_pir__S14950

heat shock cognate protein 70 - tomato

>gi 19258 emb_CAA37971_ (X54030) heat shock protein cognate

70 [Lycopersicon esculentum]

Seq. No. 297490

Seq. ID LIB3137-062-Q1-K1-E9

Method BLASTX
NCBI GI g4587611
BLAST score 337
E value 7.0e-32
Match length 91
% identity 75

NCBI Description (AC006951) putative 40S ribosomal protein S17 [Arabidopsis

% identity

NCBI Description

61



thaliana]

```
Seq. No.
                  297491
                  LIB3137-062-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112994
BLAST score
                  270
                  3.0e-24
E value
                  63
Match length
                  86
% identity
NCBI Description
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >qi 226091 prf 1410284A abscisic acid inducible gene [Zea
                  mays]
Seq. No.
                  297492
Seq. ID
                  LIB3137-062-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g3915826
BLAST score
                  239
                  2.0e-20
E value
Match length
                  65
                  74
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L5
                  297493
Seq. No.
                  LIB3137-062-Q1-K1-G6
Seq. ID
Method
                  BLASTX
                  q3719211
NCBI GI
BLAST score
                  195
E value
                  2.0e-15
Match length
                  51
% identity
                  75
NCBI Description (U97021) UIP2 [Arabidopsis thaliana]
                  297494
Seq. No.
                  LIB3150-001-Q1-N1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4454032
BLAST score
                  222
                  4.0e-18
E value
Match length
                  137
% identity
                  34
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                  297495
Seq. ID
                  LIB3150-001-Q1-N1-C2
Method
                  BLASTX
NCBI GI
                  q4584548
BLAST score
                  199
E value
                  2.0e-15
Match length
                  62
```

(AL049608) putative protein [Arabidopsis thaliana]

Method

NCBI GI

BLASTX

g123549



```
297496
Seq. No.
Seq. ID
                  LIB3150-001-Q1-N1-D7
                  BLASTX
Method
NCBI GI
                  g1184776
BLAST score
                  633
                  2.0e-66
E value
                  135
Match length
                  90
% identity
                  (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC4 [Zea mays]
Seq. No.
                  297497
Seq. ID
                  LIB3150-001-Q1-N1-E3
                  BLASTX
Method
                  g4079800
NCBI GI
BLAST score
                  251
                  7.0e-24
E value
                  87
Match length
                  75
% identity
                   (AF052503) S-phase-specific ribosomal protein [Oryza
NCBI Description
                  sativa]
                  297498
Seq. No.
Seq. ID
                  LIB3150-001-Q1-N1-E5
                  BLASTX
Method
                  q1321661
NCBI GI
                  164
BLAST score
                  2.0e-11
E value
                  82
Match length
                  48
% identity
NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]
                  297499
Seq. No.
Seq. ID
                  LIB3150-001-Q1-N1-F10
                  BLASTX
Method
NCBI GI
                  g1184776
BLAST score
                  370
E value
                  1.0e-35
                  85
Match length
                  86
% identity
                  (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC4 [Zea mays]
                  297500
Seq. No.
Seq. ID
                  LIB3150-001-Q1-N1-G3
Method
                  BLASTX
NCBI GI
                  q4522007
BLAST score
                   256
                   4.0e-22
E value
Match length
                   66
% identity
NCBI Description
                  (AC007069) unknown protein [Arabidopsis thaliana]
Seq. No.
                   297501
                  LIB3150-001-Q1-N1-H1
Seq. ID
```

Method

NCBI GI

BLASTX

g480450



BLAST score E value 3.0e-19 Match length 53 85 % identity 17.5 KD CLASS II HEAT SHOCK PROTEIN >gi 100885 pir S14998 NCBI Description heat shock protein, 18K - maize >gi 22339 emb CAA38013_ (X54076) 18kDa heat shock protein [Zea mays] Seq. No. 297502 Seq. ID LIB3150-002-Q1-N1-C10 Method BLASTX NCBI GI g462234 BLAST score 243 6.0e-21 E value Match length 63 81 % identity HISTONE H2A >gi 419741 pir S30155 histone H2A - Norway NCBI Description spruce >gi_297871_emb_CAA48030_ (X67819) histone H2A [Picea abies] Seq. No. 297503 Seq. ID LIB3150-002-Q1-N1-D12 Method BLASTX NCBI GI q4519539 BLAST score 150 5.0e-10 E value Match length 53 58 % identity NCBI Description (AB016256) NAD-dependent sorbitol dehydrogenase [Malus domestica] Seq. No. 297504 LIB3150-002-Q1-N1-D2 Seq. ID Method BLASTX NCBI GI g4049534 BLAST score 266 E value 1.0e-23 Match length 69 % identity 68 NCBI Description (AL034564) 40s ribosomal protein [Schizosaccharomyces pombe] >gi_4481957_emb_CAB38515.1_ (AL035637) ribosomal protein subunit s18. [Schizosaccharomyces pombe] Seq. No. 297505 Seq. ID LIB3150-002-Q1-N1-D7 Method BLASTX NCBI GI g3452497 BLAST score 223 E value 1.0e-18 Match length 64 67 % identity NCBI Description (Y17796) ketol-acid reductoisomerase [Pisum sativum] Seq. No. 297506 LIB3150-002-Q1-N1-E1 Seq. ID

```
BLAST score
                  6.0e-42
E value
Match length
                  114
                  77
% identity
                  ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
NCBI Description
                  thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid
                  reductoisomerase [Arabidopsis thaliana]
                   297507
Seq. No.
                   LIB3150-002-Q1-N1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4079809
BLAST score
                   180
E value
                   2.0e-13
                   114
Match length
% identity
                  (AF071172) HERC2 [Homo sapiens]
NCBI Description
                   297508
Seq. No.
                   LIB3150-002-Q1-N1-G5
Seq. ID
                   BLASTX
Method
                   q3892056
NCBI GI
BLAST score
                   241
E value
                   1.0e-20
                   62
Match length
                   76
% identity
                   (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   297509
                   LIB3150-002-Q1-N1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2811031
BLAST score
                   155
E value
                   5.0e-12
Match length
                   112
% identity
                   41
                   BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (BADH)
NCBI Description
                   >gi 2109299 gb AAB58165.1_ (AF000132) betaine aldehyde
                   dehydrogenase [Amaranthus hypochondriacus]
                   297510
Seq. No.
                   LIB3150-003-Q1-N1-C1
Seq. ID
                   BLASTX
Method
                   g3236242
NCBI GI
                   205
BLAST score
                   1.0e-16
E value
                   72
Match length
                   64
 % identity
                   (AC004684) putative ribosomal protein L36 [Arabidopsis
NCBI Description
                   thaliana]
                   297511
 Seq. No.
                   LIB3150-003-Q1-N1-D2
 Seq. ID
                   BLASTX
 Method
```

41731

g118104

1.0e-26

290

NCBI GI

E value

BLAST score

Seq. No.

Seq. ID

297516

LIB3150-004-Q1-N1-B1



```
Match length
                  74
                  77
% identity
NCBI Description
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
                  (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi 68408 pir CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi_168461 (M55021) cyclophilin [Zea mays]
                  >gi 829148 emb_CAA48638_ (X68678) cyclophilin [Zea mays]
Seq. No.
                  297512
                  LIB3150-003-Q1-N1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3805954
BLAST score
                  207
E value
                  2.0e-16
Match length
                  72
% identity
                  53
NCBI Description
                  (Y10414) stress protein [Rhizopus stolonifer]
Seq. No.
                  297513
Seq. ID
                  LIB3150-003-Q1-N1-E4
Method
                  BLASTN
NCBI GI
                  g22119
BLAST score
                  43
E value
                  5.0e-15
                  66
Match length
                  91
% identity
NCBI Description Maize Adhl-F mRNA for alcohol dehydrogenase
Seq. No.
                  297514
Seq. ID
                  LIB3150-003-Q1-N1-E6
Method
                  BLASTX
NCBI GI
                  q266346
BLAST score
                  198
E value
                  5.0e-22
Match length
                  91
                  67
% identity
NCBI Description
                  KETOL-ACID REDUCTOISOMERASE PRECURSOR (ACETOHYDROXY-ACID
                  REDUCTOISOMERASE) (ALPHA-KETO-BETA-HYDROXYLACIL
                  REDUCTOISOMERASE) >gi_81509_pir__S17180 ketol-acid
                  reductoisomerase (EC \overline{1.1.1.86}) \overline{precursor} - spinach
                  >gi_21234_emb_CAA40356_ (X57073) ketol-acid
                  reductoisomerase [Spinacia oleracea]
                  297515
Seq. No.
Seq. ID
                  LIB3150-004-Q1-N1-A7
Method
                  BLASTX
NCBI GI
                  q548851
BLAST score
                  224
E value
                  2.0e-18
Match length
                  62
                  73
% identity
                  40S RIBOSOMAL PROTEIN S20 >gi 481226 pir S38356 ribosomal
NCBI Description
                  protein S20 - rice >gi 391875 dbj BAA02157 (D12632) 40S
                  subunit ribosomal protein [Oryza sativa]
```



```
BLASTX
Method
                  g119355
NCBI GI
BLAST score
                  170
                  2.0e-12
E value
                  61
Match length
                  59
% identity
                  ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                  >gi_100869_pir__S16257 phosphopyruvate hydratase (EC
                  4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
                  [Zea mays]
Seq. No.
                  297517
Seq. ID
                  LIB3150-004-Q1-N1-B2
                  BLASTX
Method
NCBI GI
                  q2499932
BLAST score
                  296
                  7.0e-27
E value
                  111
Match length
                  59
% identity
NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_726305
                  (U22442) adenine phosphoribosyltransferase form 1 [Triticum
                  aestivum]
                  297518
Seq. No.
                  LIB3150-004-Q1-N1-B3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2499932
BLAST score
                  345
                  1.0e-32
E value
                  113
Match length
                  60
% identity
                  ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_726305
NCBI Description
                   (U22442) adenine phosphoribosyltransferase form 1 [Triticum
                  aestivum]
                  297519
Seq. No.
                  LIB3150-004-Q1-N1-B5
Seq. ID
Method
                  BLASTX
                  g112994
NCBI GI
                  258
BLAST score
                  9.0e-29
E value
                  87
Match length
% identity
                  79
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >gi 82685_pir__S04536 embryonic abundant protein,
                   glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi 226091_prf 1410284A abscisic acid inducible gene [Zea
                  mays]
                   297520
Seq. No.
Seq. ID
                  LIB3150-004-Q1-N1-C4
                  BLASTX
Method
```

41733

g560150

7.0e-10

152

NCBI GI

E value

BLAST score



```
Match length
                  38
% identity
                  (X74772) SF16 protein [Helianthus annuus]
NCBI Description
                  297521
Seq. No.
                  LIB3150-004-Q1-N1-D4
Seq. ID
                  BLASTX
Method
                  q4191778
NCBI GI
                  265
BLAST score
                  4.0e-23
E value
                  75
Match length
                  72
% identity
                  (AC005917) putative nucleosome assembly protein I
NCBI Description
                   [Arabidopsis thaliana]
                  297522
Seq. No.
                  LIB3150-004-Q1-N1-F9
Seq. ID
                  BLASTN
Method
                  g21796
NCBI GI
                  33
BLAST score
                  3.0e-09
E value
Match length
                  65
                  88
% identity
                  Wheat histone H3 gene
NCBI Description
                   297523
Seq. No.
                  LIB3150-005-Q1-N1-A1
Seq. ID
                  BLASTX
Method
                   g1168811
NCBI GI
                   506
BLAST score
                   2.0e-51
E value
                   113
Match length
% identity
                   85
                   CELL DIVISION CONTROL PROTEIN 2 HOMOLOG B
NCBI Description
                   >gi_282864_pir__S23096 protein kinase (EC 2.7.1.37) cdc2
                   homolog B - Arabidopsis thaliana >gi_217851_dbj_BAA01624_
                   (D10851) p32 protein serine/threonine kinase-related
                   protein [Arabidopsis thaliana]
                   297524
Seq. No.
Seq. ID
                   LIB3150-005-Q1-N1-A3
                   BLASTX
Method
                   g4588906
NCBI GI
BLAST score
                   175
                   8.0e-13
E value
                   50
Match length
                   72
% identity
                   (AF118149) ribosomal protein S7 [Secale cereale]
NCBI Description
                   297525
Seq. No.
```

Seq. ID LIB3150-005-Q1-N1-C6

Method BLASTX
NCBI GI g1575130
BLAST score 161
E value 4.0e-11
Match length 47
% identity 72



```
NCBI Description (U58209) lumenal binding protein cBiPe3 [Zea mays]
                  297526
Seq. No.
                  LIB3150-005-Q1-N1-D5
Seq. ID
                  BLASTX
Method
                  q1561577
NCBI GI
BLAST score
                  233
E value
                  1.0e-19
                  77
Match length
                  61
% identity
NCBI Description (Y08252) spermine synthase 1 [Datura stramonium]
                  297527
Seq. No.
                  LIB3150-005-Q1-N1-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                   a4467096
                   217
BLAST score
                   1.0e-17
E value
Match length
                   121
                   43
% identity
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]
                   297528
Seq. No.
                   LIB3150-005-Q1-N1-E11
Seq. ID
Method
                   BLASTX
                   q4056494
NCBI GI
                   235
BLAST score
                   8.0e-20
E value
                   108
Match length
% identity
                   66
                   (AC005896) putative protein translocase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   297529
                   LIB3150-005-Q1-N1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q629843
BLAST score
                   268
E value
                   1.0e-23
Match length
                   75
                   68
 % identity
                   heat shock protein hsp70-4 - maize (fragment)
NCBI Description
                   >gi 498773_emb_CAA55183_ (X78414) heat shock protein 70 kDa
                   [Zea mays]
                   297530
 Seq. No.
                   LIB3150-005-Q1-N1-H6
 Seq. ID
 Method
                   BLASTX
                   q119355
 NCBI GI
 BLAST score
                   194
                   4.0e-15
 E value
                   77
 Match length
                   56
 % identity
                   ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
 NCBI Description
                    (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                   >gi_100869_pir__S16257 phosphopyruvate hydratase (EC
```

4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase

NCBI Description



[Zea mays]

```
3
                  297531
Seq. No.
                  LIB3150-006-Q1-N1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2342685
                  236
BLAST score
                   4.0e-27
E value
                  109
Match length
                   59
% identity
                   (AC000106) Contains similarity to Rhodococcus amidase
NCBI Description
                   (gb_D16207). ESTs gb_T20504, gb_H36650, gb_N97423, gb_H36595
                   come from this gene. [Arabidopsis thaliana]
                   297532
Seq. No.
                   LIB3150-006-Q1-N1-D7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4406816
                   394
BLAST score
                   2.0e-38
E value
                   113
Match length
                   72
% identity
NCBI Description (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]
                   297533
Seq. No.
                   LIB3150-006-Q1-N1-E1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1184775
                   77
BLAST score
                   1.0e-35
E value
                   97
Match length
                   95
% identity
                   Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC4
NCBI Description
                   (gpc4) mRNA, complete cds
                   297534
Seq. No.
                   LIB3150-006-Q1-N1-F6
Seq. ID
                   BLASTN
Method
                   g1658192
NCBI GI
                   67
BLAST score
                   3.0e-29
E value
                   255
Match length
                   82
% identity
                   Sorghum bicolor obtusifoliol 14-alpha demethylase CYP51
NCBI Description
                   (CYP51) mRNA, complete cds
                   297535
Seq. No.
                   LIB3150-006-Q1-N1-G8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2493147
                   363
BLAST score
                   1.0e-34
E value
                   87
Match length
                   84
% identity
```

(U27098) H+-ATPase [Oryza sativa]

VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_857574

NCBI Description



```
297536
Seq. No.
Seq. ID
                  LIB3150-007-Q1-N1-B11
                  BLASTX
Method
NCBI GI
                  q4586588
                  336
BLAST score
                  1.0e-31
E value
                  102
Match length
                  69
% identity
                  (AB024998) translation elongation factor [Cicer arietinum]
NCBI Description
                  297537
Seq. No.
                  LIB3150-007-Q1-N1-D3
Seq. ID
                  BLASTX
Method
                  g1350783
NCBI GI
                  236
BLAST score
                  5.0e-20
E value
                  91
Match length
                  30
% identity
                  RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR
NCBI Description
                  >gi 282883 pir S27756 receptor-like protein kinase
                  precursor - Arabidopsis thaliana >gi 166850 (M84660)
                  receptor-like protein kinase [Arabidopsis thaliana]
                  >gi 2842492 emb CAA16889 (AL021749) receptor-like protein
                  kinase 5 precursor (RLK5) [Arabidopsis thaliana]
                  297538
Seq. No.
                  LIB3150-007-Q1-N1-H2
Seq. ID
                  BLASTX
Method
                  g135398
NCBI GI
                  485
BLAST score
                   5.0e-49
E value
Match length
                   90
% identity
                  TUBULIN ALPHA-1 CHAIN >gi_82731_pir__S15773 tubulin alpha-1
NCBI Description
                   chain - maize >gi 22147 emb CAA33734 (X15704)
                   alpha1-tubulin [Zea mays]
                   297539
Seq. No.
                   LIB3150-008-Q1-N1-B10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3334320
                   456
BLAST score
                   1.0e-45
E value
Match length
                   92
% identity
                   40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
NCBI Description
                   ribosome-associated protein p40 [Glycine max]
                   297540
Seq. No.
Seq. ID
                   LIB3150-008-Q1-N1-D1
                   BLASTX
Method
NCBI GI
                   q3201541
                   208
BLAST score
                   1.0e-32
E value
Match length
                   74
% identity
                   89
                  (AJ005077) TCTR2 protein [Lycopersicon esculentum]
```



```
297541
Seq. No.
Seq. ID
                  LIB3150-008-Q1-N1-D12
                  BLASTX
Method
                  g2583129
NCBI GI
                  264
BLAST score
                  6.0e-23
E value
                  72
Match length
% identity
                   (AC002387) putative methionine aminopeptidase [Arabidopsis
NCBI Description
                  thaliana]
                   297542
Seq. No.
Seq. ID
                  LIB3150-008-Q1-N1-D7
                  BLASTX
Method
                   g1841502
NCBI GI
                   219
BLAST score
                   6.0e-18
E value
                   81
Match length
                   58
% identity
                   (Y11029) glutothione-dependent formaldehyde dehydrogenase
NCBI Description
                   [Zea mays]
                   297543
Seq. No.
                   LIB3150-008-Q1-N1-G9
Seq. ID
                   BLASTX
Method
                   g4206112
NCBI GI
                   185
BLAST score
                   2.0e-14
E value
                   49
Match length
                   76
% identity
                   (AF097662) alpha tubulin [Mesembryanthemum crystallinum]
NCBI Description
                   297544
Seq. No.
                   LIB3150-009-Q1-N1-A9
Seq. ID
Method
                   BLASTN
                   q168675
NCBI GI
                   85
BLAST score
                   5.0e-40
E value
                   117
Match length
% identity
                   93
                   Maize mutant zein (zE19) gene, complete cds
NCBI Description
                   297545
Seq. No.
Seq. ID
                   LIB3150-009-Q1-N1-B8
                   BLASTX
Method
NCBI GI
                   g231683
BLAST score
                   229
                   4.0e-19
E value
Match length
                   81
                   62
 % identity
                   CALNEXIN HOMOLOG PRECURSOR >gi_421825_pir__JN0597
NCBI Description
                   calnexin-like protein - Arabidopsis thaliana
                   >gi_16211_emb_CAA79144_ (Z18242) calnexin homolog
                   [Arabidopsis thaliana]
```

41738

297546

Seq. No.



```
LIB3150-009-Q1-N1-C10
Seq. ID
                  BLASTX
Method
                  q168691
NCBI GI
                  169
BLAST score
                  4.0e-20
E value
                  106
Match length
                  59
% identity
NCBI Description (M29628) zein [Zea mays]
                  297547
Seq. No.
                  LIB3150-009-Q1-N1-C12
Seq. ID
                  BLASTX
Method
                  q141617
NCBI GI
                  273
BLAST score
                  1.0e-24
E value
                  73
Match length
                   67
% identity
                  ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                   >gi_100941_pir__S12140 zein Zc1 - maize
                   >gi_100945_pir__B29017 zein 2 - maize
                   >gi_22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                   >gi^{-}16866^{-}6 (M^{-}16460) 16^{-}kDa zein protein [Zea mays]
                   297548
Seq. No.
                   LIB3150-009-Q1-N1-C5
Seq. ID
                   BLASTX
Method
                   g141617
NCBI GI
                   283
BLAST score
                   3.0e-25
E value
                   105
Match length
                   52
% identity
                   ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                   >gi 100941 pir S12140 zein Zc1 - maize
                   >gi 100945 pir B29017 zein 2 - maize
                   >qi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                   >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
                   297549
Seq. No.
                   LIB3150-009-Q1-N1-D1
Seq. ID
                   BLASTX
Method
                   g118104
NCBI GI
                   283
BLAST score
                   2.0e-25
E value
                   74
Match length
                   76
% identity
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                   >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                   maize >gi 168461 (M55021) cyclophilin [Zea mays]
                   >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]
                   297550
 Seq. No.
                   LIB3150-009-Q1-N1-D10
 Seq. ID
                   BLASTN
Method
 NCBI GI
                   q22514
 BLAST score
                   35
```

41739

3.0e-10

E value



Match length % identity

NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No.

297551 Seq. ID

LIB3150-009-Q1-N1-D12

Method BLASTN NCBI GI q168425 BLAST score 79

E value 2.0e-36 Match length 267 % identity 83

NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds

Seq. No. 297552

Seq. ID LIB3150-009-Q1-N1-D4

Method BLASTX NCBI GI g114420 BLAST score 183 E value 1.0e-13 Match length 73 % identity 56

ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR NCBI Description

>gi 100882 pir S11491 H+-transporting ATP synthase (EC

3.6.1.34) beta chain, mitochondrial - maize

>gi 22173 emb CAA38140 (X54233) ATPase Fl subunit protein [Zea mays] >gi 897618 (M36087) F-1-ATPase subunit 2 [Zea

mays]

Seq. No. 297553

Seq. ID LIB3150-009-Q1-N1-E1

Method BLASTX NCBI GI q2286153 BLAST score 236 E value 4.0e-20 59 Match length % identity 81

NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No. 297554

LIB3150-009-Q1-N1-E11 Seq. ID

Method BLASTX NCBI GI g141603 BLAST score 446 E value 2.0e-44 Match length 110 % identity

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)

>gi_72311_pir__ZIZM2 19K zein precursor (clone A20) - maize

>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 297555

Seq. ID LIB3150-009-Q1-N1-E3

Method BLASTX NCBI GI g3123264 BLAST score 239 E value 2.0e-20

1,5



```
Match length
                  68
% identity
                  72
                  60S RIBOSOMAL PROTEIN L27 >gi 2244857 emb CAB10279
NCBI Description
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
                  297556
Seq. No.
                  LIB3150-009-Q1-N1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4185308
BLAST score
                  183
E value
                  1.0e-13
                  103
Match length
% identity
                  47
NCBI Description
                  (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
                  297557
Seq. No.
                  LIB3150-009-Q1-N1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22528
BLAST score
                  35
                  3.0e-10
E value
Match length
                  75
% identity
                  87
NCBI Description Zea mays mRNA encoding a zein (clone A20)
Seq. No.
                  297558
                  LIB3150-009-Q1-N1-G9
Seg. ID
Method
                  BLASTX
NCBI GI
                  g141599
BLAST score
                  155
                  2.0e-10
E value
Match length
                  55
                  58
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19A2)
NCBI Description
                  >gi 72316 pir ZIZMA2 19K zein precursor (clone cZ19A2) -
                  maize (fragment) >gi_168670 (M12142) 19 kDa zein protein
                  [Zea mays]
Seq. No.
                  297559
Seq. ID
                  LIB3150-009-Q1-N1-H10
Method
                  BLASTX
NCBI GI
                  g141604
BLAST score
                  408
E value
                  7.0e-40
Match length
                  116
                  76
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)
                  >gi_72310 pir _ZIZM91 19K zein precursor (clone cZ19C1) -
                  maize >gi 168678 (M12146) 19 kDa zein protein [Zea mays]
Seq. No.
                  297560
Seq. ID
                  LIB3150-009-Q1-N1-H11
```

Method BLASTX
NCBI GI g82654
BLAST score 273
E value 4.0e-24
Match length 77

```
% identity
NCBI Description 10K zein precursor - maize >gi_22541_emb_CAA30409_ (X07535)
                  10kDa zein (AA 1 - 150) [Zea mays]
                  297561
Seq. No.
                  LIB3150-010-Q1-N1-A5
Seq. ID
                  BLASTN
Method
                  q22312
NCBI GI
                  73
BLAST score
                   4.0e-33
E value
                  176
Match length
% identity
                   86
                  Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                   abscisic acid)
                   297562
Seq. No.
                   LIB3150-010-Q1-N1-B7
Seq. ID
Method
                   BLASTX
                   g1184774
NCBI GI
                   431
BLAST score
                   7.0e-43
E value
                   94
Match length
% identity
                   (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC3 [Zea mays]
                   297563
Seq. No.
                   LIB3150-010-Q1-N1-D5
Seq. ID
Method
                   BLASTN
                   g22326
NCBI GI
                   156
BLAST score
                   1.0e-82
E value
Match length
                   160
                   99
% identity
NCBI Description Z.mays gene for Hageman factor inhibitor
                   297564
Seq. No.
                   LIB3150-010-Q1-N1-F10
Seq. ID
                   BLASTX
Method
                   g141605
NCBI GI
                   528
BLAST score
                   6.0e-54
E value
                   121
Match length
                   88
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                   >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                   maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
                   297565
Seq. No.
                   LIB3150-010-Q1-N1-G1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g625147
BLAST score
                   123
                   6.0e-63
E value
Match length
                   231
                   88
 % identity
NCBI Description Zea mays protein disulfide isomerase (pdi) mRNA, complete
```



cds

```
Seq. No.
                  297566
                  LIB3150-010-Q1-N1-H9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4191782
BLAST score
                  185
                  7.0e-14
E value
                  63
Match length
                  54
% identity
                  (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  LIB3150-011-Q1-N1-B10
Seq. ID
                  BLASTX
Method
                  q82696
NCBI GI
                   301
BLAST score
E value
                   1.0e-27
                   74
Match length
                   78
% identity
                  glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
Seq. No.
                   297568
                   LIB3150-011-Q1-N1-B12
Seq. ID
                   BLASTX
Method
                   g1172836
NCBI GI
                   378
BLAST score
E value
                   2.0e-36
                   95
Match length
                   75
% identity
                   GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi_496272 (L16787)
NCBI Description
                   small ras-related protein [Nicotiana tabacum]
Seq. No.
                   297569
                   LIB3150-012-Q1-N1-A4
Seq. ID
                   BLASTX
Method
                   q1184776
NCBI GI
                   503
BLAST score
                   3.0e-51
E value
                   101
Match length
                   95
% identity
                   (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC4 [Zea mays]
                   297570
Seq. No.
                   LIB3150-012-Q1-N1-A5
Seq. ID
                   BLASTX
Method
                   g82696
NCBI GI
                   178
BLAST score
                   1.0e-13
E value
                   39
Match length
                   87
 % identity
                   glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
```

297571

Seq. No.

Seq. ID

Method NCBI GI



```
LIB3150-012-Q1-N1-B11
Seq. ID
Method
                  BLASTX
                  q131772
NCBI GI
                  151
BLAST score
                  5.0e-10
E value
                  67
Match length
                  55
% identity
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
NCBI Description
                  >gi 82723_pir__A30097 ribosomal protein S14 (clone MCH1) -
                  297572
Seq. No.
                  LIB3150-012-Q1-N1-C10
Seq. ID
                  BLASTX
Method
                  q3915465
NCBI GI
                  204
BLAST score
                  4.0e-16
E value
                  104
Match length
% identity
                  HYPOTHETICAL GTP-BINDING PROTEIN IN XSEA-HISS INTERGENIC
NCBI Description
                   REGION >gi_1788858 (AE000337) putative GTP-binding factor
                   [Escherichia coli] >gi 1805570 dbj_BAA16397_ (D90880)
                   similar to [SwissProt Accession Number P44536] [Escherichia
                   colil
                   297573
Seq. No.
                   LIB3150-012-Q1-N1-D3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q118390
                   307
BLAST score
                   2.0e-28
E value
                   80
Match length
                   80
% identity
                   PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC)
NCBI Description
                   >gi 2144526 pir__DCZMP pyruvate decarboxylase (EC 4.1.1.1)
                   - maize >gi 22395 emb CAA42120_ (X59546) pyruvate
                   decarboxylase [Zea mays]
                   297574
Seq. No.
                   LIB3150-012-Q1-N1-F7
Seq. ID
                   BLASTX
Method
                   g132736
NCBI GI
                   161
BLAST score
                   3.0e-11
E value
                   69
Match length
                   49
 % identity
                   60S RIBOSOMAL PROTEIN L19 (VEGETATIVE SPECIFIC PROTEIN V14)
NCBI Description
                   (22 KD CALMODULIN-BINDING PROTEIN) >gi 71266_pir__R5D09E
                   ribosomal protein L19.e - slime mold (Dictyostelium
                   discoideum) >gi_295737 emb_CAA33443 (X15383) V14
                   [Dictyostelium discoideum] >gi 443591 (L27657) ribosomal
                   protein [Dictyostelium discoideum]
                   297575
 Seq. No.
```

41744

LIB3150-012-Q1-N1-H6

BLASTN

q2431766



```
BLAST score
                  46
                  3.0e-17
E value
                  98
Match length
                  87
% identity
                  Zea mays acidic ribosomal protein P3a (rpp3a) mRNA,
NCBI Description
                  complete cds
                  297576
Seq. No.
                  LIB3150-013-Q1-N1-B10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1848210
BLAST score
                  152
E value
                  5.0e-10
                  37
Match length
                  81
% identity
NCBI Description (Y11208) histone H2B1 [Nicotiana tabacum]
                   297577
Seq. No.
                  LIB3150-013-Q1-N1-F12
Seq. ID
                  BLASTX
Method
                  g3122053
NCBI GI
                   176
BLAST score
                   7.0e-13
E value
Match length
                   110
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                   >gi_1235582_emb_CAA65391_ (X96555) elongation factor
                   1-alpha [Pisum sativum]
                   297578
Seq. No.
                   LIB3150-013-Q1-N1-G5
Seq. ID
Method
                   BLASTN
                   g22516
NCBI GI
BLAST score
                   189
                   1.0e-102
E value
Match length
                   217
% identity
                   97
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                   297579
Seq. No.
                   LIB3150-014-Q1-N1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2281647
BLAST score
                   148
                   1.0e-09
E value
                   36
Match length
                   75
 % identity
                   (AF003104) AP2 domain containing protein RAP2.11
NCBI Description
                   [Arabidopsis thaliana]
                   297580
 Seq. No.
                   LIB3150-014-Q1-N1-C2
 Seq. ID
                   BLASTX
 Method
                   g1658313
 NCBI GI
                   250
 BLAST score
```

41745

1.0e-21

72

E value

Match length

```
% identity
NCBI Description (Y08987) osr40g2 [Oryza sativa]
                  297581
Seq. No.
                  LIB3150-014-Q1-N1-C9
Seq. ID
                  BLASTX
Method
                  g1184776
NCBI GI
                  162
BLAST score
                  2.0e-11
E value
                  48
Match length
                  71
% identity
                  (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC4 [Zea mays]
                  297582
Seq. No.
                  LIB3150-014-Q1-N1-D10
Seq. ID
                  BLASTN
Method
                   g3747049
NCBI GI
BLAST score
                   57
                   1.0e-23
E value
                   145
Match length
                   85
% identity
NCBI Description Zea mays ribosomal protein L26 mRNA, partial cds
                   297583
Seq. No.
                   LIB3150-014-Q1-N1-D8
Seq. ID
                   BLASTN
Method
                   g168484
NCBI GI
                   209
BLAST score
                   1.0e-114
E value
                   328
Match length
                   91
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                   297584
Seq. No.
                   LIB3150-014-Q1-N1-D9
Seq. ID
Method
                   BLASTX
                   q585876
NCBI GI
                   188
BLAST score
E value
                   2.0e-14
                   67
Match length
                   63
% identity
                   60S RIBOSOMAL PROTEIN L23A (L25) >gi_1084424_pir__S48026
NCBI Description
                   ribosomal protein L25 - common tobacco >gi_310935 (L18908)
                   60S ribosomal protein L25 [Nicotiana tabacum]
```

Seq. No. 297585

Seq. ID LIB3150-014-Q1-N1-G2

Method BLASTX
NCBI GI g2230757
BLAST score 347
E value 9.0e-33
Match length 92
% identity 70

NCBI Description (Y11969) dnaJ-like protein [Arabidopsis thaliana]

Seq. No. 297586

```
LIB3150-014-Q1-N1-H1
Seq. ID
                  BLASTX
Method
                  a629767
NCBI GI
                  250
BLAST score
                  1.0e-21
E value
                  114
Match length
                  47
% identity
NCBI Description 11S globulin - oat >gi_472867_emb_CAA52764_ (X74741) 11S
                  globulin [Avena sativa]
                  297587
Seq. No.
                  LIB3150-015-Q1-N1-A3
Seq. ID
Method
                  BLASTX
                   q1350680
NCBI GI
                   300
BLAST score
                   2.0e-27
E value
                   102
Match length
                   60
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L1
                   297588
Seq. No.
                   LIB3150-015-Q1-N1-A4
Seq. ID
                   BLASTX
Method
                   q4582468
NCBI GI
                   351
BLAST score
                   1.0e-33
E value
                   82
Match length
                   87
% identity
NCBI Description (AC007071) putative 40S ribosomal protein; contains
                   C-terminal domain [Arabidopsis thaliana]
                   297589
Seq. No.
                   LIB3150-015-Q1-N1-B1
Seq. ID
Method
                   BLASTX
                   g121569
NCBI GI
BLAST score
                   373
E value
                   5.0e-36
                   104
Match length
                   70
 % identity
                   IMMUNOGLOBULIN BINDING PROTEIN HOMOLOG B70 (HEAT SHOCK
 NCBI Description
                   PROTEIN 70 HOMOLOG) (B-70) >gi_484510_pir__JQ0966
                   immunoglobulin-binding protein homolog b70 - maize
                   (fragment)
                   297590
 Seq. No.
                   LIB3150-015-Q1-N1-C3
 Seq. ID
```

Method BLASTX
NCBI GI g2267597
BLAST score 189
E value 2.0e-14
Match length 75
% identity 59

NCBI Description (AF009413) 10 kDa chaperonin [Oryza sativa]

Seq. No. 297591

Seq. ID LIB3150-015-Q1-N1-D12

Method BLASTX



```
NCBI GI
                   g3776564
BLAST score
                   253
                   1.0e-21
E value
Match length
                   66
% identity
                   68
                   (AC005388) Similar to hypothetical protein T1D16.16
NCBI Description
                   gi 3075397 from A. thaliana BAC gb AC004484. [Arabidopsis
                   thaliana]
                   297592
Seq. No.
                   LIB3150-015-Q1-N1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1084457
BLAST score
                   259
E value
                   1.0e-22
Match length
                   80
                   66
% identity
NCBI Description
                  elongation factor 1-beta - Rice >gi 432368 dbj BAA04903
                   (D23674) elongation factor 1 beta [Oryza sativa]
Seq. No.
                   297593
Seq. ID
                   LIB3150-015-Q1-N1-D9
Method
                   BLASTX
NCBI GI
                   g1222552
BLAST score
                   607
                   3.0e-63
E value
Match-length
                   141
                   78
% identity
NCBI Description (U49330) pectin methylesterase [Lycopersicon esculentum]
Seq. No.
                   297594
                   LIB3150-015-Q1-N1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1710551
BLAST score
                   281
                   5.0e-25
E value
Match length
                   51
                   100
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L39 >qi 1177369 emb CAA64728
                   (X95458) ribosomal protein L39 [Zea mays]
                   297595
Seq. No.
Seq. ID
                   LIB3150-015-Q1-N1-E3
Method
                   BLASTN
NCBI GI
                   q450548
BLAST score
                   68
E value
                   5.0e-30
Match length
                   168
% identity
                   86
                   O.sativa (pRSAM-1) gene for S-adenosyl methionine
NCBI Description
                   synthetase
```

297596 Seq. No.

LIB3150-015-Q1-N1-G2 Seq. ID

Method BLASTN NCBI GI g22324 BLAST score 38

Method

NCBI GI

E value

BLAST score

g4454464

7.0e-17

```
3.0e-12
E value
                   46
Match length
 % identity
                   96
NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)
                   297597
 Seq. No.
                   LIB3150-016-Q1-N1-A6
 Seq. ID
                   BLASTX
 Method
                   g131772
 NCBI GI
                   147
 BLAST score
                   2.0e-09
 E value
 Match length
                   31
 % identity
                   97
                   40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
 NCBI Description
                   >gi 82723 pir_A30097 ribosomal protein S14 (clone MCH1) -
                   297598
 Seq. No.
                   LIB3150-016-Q1-N1-D10
 Seq. ID
                   BLASTX
 Method
                   q3746060
 NCBI GI
                   415
BLAST score
 E value
                   9.0e-41
 Match length
                   86
 % identity
 NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]
                   297599
 Seq. No.
                   LIB3150-016-Q1-N1-D2
 Seq. ID
                   BLASTX
 Method
                   g419803
 NCBI GI
                    361
 BLAST score
                    1.0e-34
 E value
 Match length
                    79
                    87
 % identity
                   zein protein - maize >gi_168705 (M72708) zein protein [Zea
 NCBI Description
                    mays]
                    297600
 Seq. No.
                    LIB3150-016-Q1-N1-D7
 Seq. ID
                    BLASTX
 Method
                    g3915031
 NCBI GI
                    178
 BLAST score
                    4.0e-13
 E value
                    42
 Match length
                    71
  % identity
 NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
                    (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232
                    (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase
                    [Gossypium hirsutum]
                    297601
  Seq. No.
                    LIB3150-016-Q1-N1-E1
  Seq. ID
                    BLASTX
```

```
Match length 64
% identity 59
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
Seq. No. 297602
```

Seq. ID LIB3150-016-Q1-N1-G3
Method BLASTX
NCBI GI g122022
BLAST score 301
E value 2.0e-27
Match length 85
% identity 74

% identity 74

NCBI Description HISTONE H2B >gi_283025_pir__S22323 histone H2B - wheat >gi_21801 emb CAA42530_ (X59873) histone H2B [Triticum]

aestivum]

 Seq. No.
 297603

 Seq. ID
 LIB3150-016-Q1-N1-G4

 Method
 BLASTX

 NCBI GI
 g1814403

NCBI GI g1814403 BLAST score 186 E value 2.0e-14 Match length 57 % identity 67

NCBI Description (U84889) methionine synthase [Mesembryanthemum

crystallinum]

Seq. No. 297604

Seq. ID LIB3150-016-Q1-N1-H4

Method BLASTX
NCBI GI g1922246
BLAST score 166
E value 9.0e-13
Match length 75
% identity 61

NCBI Description (Y10086) putative dehydrogenase [Arabidopsis thaliana]

Seq. No. 297605

Seq. ID LIB3150-017-Q1-N1-B11

Method BLASTX
NCBI GI g543711
BLAST score 170
E value 4.0e-13
Match length 97
% identity 49

NCBI Description 14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3

protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140)

brain specific protein [Oryza sativa]

Seq. No. 297606

Seq. ID LIB3150-017-Q1-N1-D6

Method BLASTX
NCBI GI g3914423
BLAST score 374
E value 4.0e-36
Match length 74
% identity 95



```
NCBI Description PROFILIN 4 >gi_2642324 (AF032370) profilin [Zea mays]
                  297607
Seq. No.
                  LIB3150-017-Q1-N1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1498382
                  158
BLAST score
                  3.0e-11
E value
                   65
Match length
% identity
                   55
                  (U60507) actin [Zea mays]
NCBI Description
Seq. No.
                   297608
                   LIB3150-017-Q1-N1-F10
Seq. ID
                   BLASTN
Method
                   g1550813
NCBI GI
                   67
BLAST score
                   8.0e-30
E value
                   119
Match length
                   89
% identity
NCBI Description Z.mays mRNA for acidic ribosomal protein PO
                   297609
Seq. No.
                   LIB3150-017-Q1-N1-H11
Seq. ID
                   BLASTX
Method
                   q2668742
NCBI GI
                   250
BLAST score
E value
                   1.0e-21
Match length
                   69
                   72
% identity
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]
                   297610
Seq. No.
                   LIB3150-017-Q1-N1-H6
Seq. ID
Method
                   BLASTX
                   q4455207
NCBI GI
                   293
BLAST score
                   1.0e-26
E value
                   88
Match length
                   72
 % identity
                   (AL035440) ubiquitin-like protein [Arabidopsis thaliana]
 NCBI Description
                   297611
 Seq. No.
                   LIB3150-018-Q1-N1-A1
 Seq. ID
                   BLASTN
 Method
                   g496267
 NCBI GI
                   41
 BLAST score
                   5.0e-14
 E value
                   81
 Match length
                   88
 % identity
                   Nicotiana tabacum GTP-binding protein (Ran-A1) mRNA,
 NCBI Description
                   complete cds
```

Seq. No. 297612

Seq. ID LIB3150-018-Q1-N1-A7 Method BLASTX

Method BLASTX NCBI GI g4154352

BLAST score

E value

430

9.0e-43



```
BLAST score
E value
                  2.0e-14
Match length
                  78
                  53
% identity
                  (AF110333) PrMC3 [Pinus radiata]
NCBI Description
Seq. No.
                  297613
                  LIB3150-018-Q1-N1-B4
Seq. ID
Method
                  BLASTX
                  g2865175
NCBI GI
BLAST score
                  229
E value
                  4.0e-19
Match length
                  94
% identity
                  54
                  (AB010945) AtRer1A [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  297614
Seq. ID
                  LIB3150-018-Q1-N1-F10
Method
                  BLASTX
NCBI GI
                  g995714
BLAST score
                  271
E value
                  6.0e-24
Match length
                  104
                  52
% identity
NCBI Description (X91258) L3177 [Saccharomyces cerevisiae]
                  297615
Seq. No.
                  LIB3150-019-Q1-N1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q133867
BLAST score
                  259
                  1.0e-22
E value
Match length
                  72
% identity
                  72
NCBI Description
                  40S RIBOSOMAL PROTEIN S11 >qi 82722 pir S16577 ribosomal
                  protein S11 - maize >gi 22470 emb CAA39438 (X55967)
                  ribosomal protein S11 [Zea mays]
Seq. No.
                  297616
Seq. ID
                  LIB3150-019-Q1-N1-A12
Method
                  BLASTX
NCBI GI
                  g82718
BLAST score
                  309
E value
                  2.0e-28
Match length
                  88
% identity
                  68
                  pyruvate, orthophosphate dikinase (EC 2.7.9.1) 2, cytosolic
NCBI Description
                  - maize (fragment) >gi_257810_bbs_117087 (S46967)
                  orthophosphate dikinase, PPDK {N-terminal} [maize, Peptide
                  Partial, 90 aa] [Zea mays]
Seq. No.
                  297617
Seq. ID
                  LIB3150-019-Q1-N1-A3
Method
                  BLASTX
NCBI GI
                  g66009
```



```
Match length
                  93
                  86
% identity
NCBI Description
                  glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C,
                  cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH
                   (AA 1-337) [Zea mays]
Seq. No.
                  297618
Seq. ID
                  LIB3150-019-Q1-N1-B4
Method
                  BLASTN
NCBI GI
                  q444046
BLAST score
                  66
E value
                  9.0e-29
Match length
                  293
% identity
                  83
NCBI Description Z.mays OBF1 mRNA for ocs-element binding factor
Seq. No.
                  297619
Seq. ID
                  LIB3150-019-Q1-N1-C4
Method
                  BLASTX
                  g2827143
NCBI GI
BLAST score
                  700
E value
                  3.0e-74
                  137
Match length
                  91
% identity
                   (AF027174) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                  297620
Seq. No.
                  LIB3150-019-Q1-N1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2996096
BLAST score
                  429
                  2.0e-42
E value
Match length
                  105
% identity
                  80
                  (AF030517) translation elongation factor-1 alpha; EF-1
NCBI Description
                  alpha [Oryza sativa]
Seq. No.
                  297621
                  LIB3150-019-Q1-N1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q66615
BLAST score
                  237
E value
                   4.0e-20
Match length
                  79
% identity
                  65
NCBI Description glutathione transferase (EC 2.5.1.18) I - maize
Seq. No.
                  297622
Seq. ID
                  LIB3150-019-Q1-N1-E12
Method
                  BLASTX
```

NCBI GI g3318613 BLAST score 375 E value 4.0e-36 Match length 105 % identity

NCBI Description (AB016064) mitochondrial phosphate transporter [Zea mays]

NCBI GI

BLAST score



```
Seq. No.
                  297623
Seq. ID
                  LIB3150-019-Q1-N1-E6
Method
                  BLASTX
NCBI GI
                  q1184776
                  278
BLAST score
E value
                  9.0e-25
                  101
Match length
                   54
% identity
                   (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC4 [Zea mays]
Seq. No.
                   297624
Seq. ID
                  LIB3150-019-Q1-N1-G12
Method
                  BLASTX
NCBI GI
                   g3036805
BLAST score
                   209
                   1.0e-16
E value
                   67
Match length
                   54
% identity
                  (AL022373) thaumatin-like protein [Arabidopsis thaliana]
NCBI Description
                   297625
Seq. No.
Seq. ID
                  LIB3150-019-Q1-N1-H11
                  BLASTX
Method
NCBI GI
                   g3868758
BLAST score
                   314
                   6.0e-29
E value
Match length
                   84
                   71
% identity
NCBI Description
                  (D89802) elongation factor 1B gamma [Oryza sativa]
                   297626
Seq. No.
Seq. ID
                   LIB3150-020-Q1-N1-A2
Method
                   BLASTX
NCBI GI
                   g4006868
BLAST score
                   219
                   6.0e-18
E value
Match length
                   80
% identity
                   59
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
                   297627
Seq. No.
Seq. ID
                  LIB3150-020-Q1-N1-A8
Method
                   BLASTN
NCBI GI
                   g22549
BLAST score
                   155
E value
                   5.0e-82
Match length
                   239
% identity
                   91
NCBI Description Maize gene for a 27kDa storage protein, zein
Seq. No.
                   297628
Seq. ID
                  LIB3150-020-Q1-N1-C3
                  BLASTX
Method
```

41754

g3163946

```
8.0e-52
E value
                   94
Match length
                   100
% identity
                   (AJ005599) alpha-tubulin 1 [Eleusine indica]
NCBI Description
                   297629
Seq. No.
                   LIB3150-020-Q1-N1-D12
Seq. ID
                   BLASTN
Method
                   g829147
NCBI GI
                   94
BLAST score
                   8.0e-46
E value
Match length
                   142
                   92
% identity
NCBI Description Z.mays gene for cyclophilin
                    297630
Seq. No.
                   LIB3150-020-Q1-N1-D6
Seq. ID
Method
                   BLASTX
                    g119150
NCBI GI
                    206
BLAST score
E value
                    5.0e-27
                    111
Match length
% identity
                    ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                    >gi_82081_pir__S10507 translation elongation factor eEF-1
alpha chain - tomato >gi_19273_emb_CAA32618_ (X14449) EF
                    1-alpha (AA 1-448) [Lycopersicon esculentum]
                    >gi_295810_emb_CAA37212_ (X53043) elongation factor 1-alpha
                    [Lycopersicon esculentum]
                    297631
Seq. No.
                    LIB3150-020-Q1-N1-E11
Seq. ID
                    BLASTN
Method
                    g829147
NCBI GI
BLAST score
                    37
                    9.0e-12
E value
                    97
Match length
                    85
 % identity
 NCBI Description Z.mays gene for cyclophilin
                    297632
 Seq. No.
                    LIB3150-020-Q1-N1-G9
 Seq. ID
                    BLASTN
 Method
                    g2331300
 NCBI GI
                    52
 BLAST score
                    9.0e-21
 E value
                    140
 Match length
                    85
 % identity
                    Zea mays ribosomal protein S4 type I (rps4) mRNA, complete
 NCBI Description
                    297633
 Seq. No.
                    LIB3150-021-Q1-N1-C11
 Seq. ID
                    BLASTX
 Method
```

g100525

2.0e-47

470

NCBI GI

E value

BLAST score



```
Match length
                  23
% identity
                  ubiquitin precursor UbB2 - common sunflower (fragment)
NCBI Description
                  >gi 18803 emb CAA40323 (X57003) polyubiquitin protein
                  [Helianthus annuus]
                  297634
Seq. No.
                  LIB3150-021-Q1-N1-C9
Seq. ID
                  BLASTN
Method
NCBI GI
                  q1864000
BLAST score
                  40
                  3.0e-13
E value
Match length
                  52
                   94
% identity
NCBI Description Maize DNA for Fd III, complete cds
                   297635
Seq. No.
                  LIB3150-021-Q1-N1-E1
Seq. ID
Method
                  BLASTN
                   g3747049
NCBI GI
                   44
BLAST score
                   6.0e-16
E value
Match length
                   84
% identity
                   89
NCBI Description Zea mays ribosomal protein L26 mRNA, partial cds
                   297636
Seq. No.
                   LIB3150-021-Q1-N1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3023812
BLAST score
                   176
                   4.0e-13
E value
                   48
Match length
% identity
                   73
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_435046 (L26924) glyceraldehyde-phosphate dehydrogenase
                   [Ginkgo biloba]
Seq. No.
                   297637
                   LIB3150-021-Q1-N1-H12
 Seq. ID
                   BLASTN
Method
                   g1184773
NCBI GI
                   34
BLAST score
                   4.0e-10
 E value
                   62
 Match length
                   89
 % identity
                   Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC3
 NCBI Description
                   (gpc3) mRNA, complete cds
                   297638
 Seq. No.
                   LIB3150-021-Q1-N1-H6
 Seq. ID
                   BLASTN
 Method
```

Method BLASTN
NCBI GI g22338
BLAST score 64
E value 1.0e-27
Match length 155
% identity 86



```
NCBI Description Maize mRNA for an 18kDa heat shock protein
                  297639
Seq. No.
Seq. ID
                  LIB3150-022-Q1-N1-A3
Method
                  BLASTX
NCBI GI
                  q602958
BLAST score
                  231
E value
                  1.0e-19
Match length
                  81
% identity
                  58
                  (U18102) Phalaenopsis sp. 'hybrid SM9108' actin
NCBI Description
                   [Phalaenopsis sp. 'hybrid SM9108']
                  297640
Seq. No.
Seq. ID
                  LIB3150-022-Q1-N1-D10
Method
                  BLASTX
NCBI GI
                  g2369714
BLAST score
                  272
                  1.0e-24
E value
Match length
                  67
% identity
                  75
                  (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                  297641
Seq. No.
Seq. ID
                  LIB3150-022-Q1-N1-E12
Method
                  BLASTX
NCBI GI
                  g2499489
BLAST score
                  212
E value
                  5.0e-17
Match length
                  118
% identity
                  48
                  PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
NCBI Description
                  BETA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                  (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                  (PPI-PFK) >gi 483536 emb CAA83683 (Z32850)
                  pyrophosphate-dependent phosphofructokinase beta subunit
                   [Ricinus communis]
Seq. No.
                  297642
                  LIB3150-022-Q1-N1-E5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2811133
BLAST score
                  222
E value
                  1.0e-122
Match length
                  257
% identity
                  97
NCBI Description
                  Zea mays starch synthase isoform zSTSII-1 (zSSIIa) mRNA,
                  partial cds
Seq. No.
                  297643
```

Seq. ID LIB3150-022-Q1-N1-E9

Method BLASTN
NCBI GI g1498052
BLAST score 64
E value 2.0e-27
Match length 152
% identity 86



95

thaliana]

% identity

NCBI Description

NCBI Description Zea mays ribosomal protein S8 mRNA, complete cds

Seq. No. 297644 Seq. ID LIB3150-022-Q1-N1-F6 Method BLASTX NCBI GI q4176535 BLAST score 149 1.0e-09 E value Match length 93 37 % identity (AL035263) putative TFIIH subunit (transcription-repair fac NCBI Description tor) [Schizosaccharomyces pombe] Seq. No. 297645 LIB3150-022-Q1-N1-H4 Seq. ID Method BLASTX NCBI GI q2613143 BLAST score 231 2.0e-19 E value Match length 82 % identity 61 NCBI Description (AF030548) tubulin [Oryza sativa] Seq. No. 297646 LIB3150-022-Q1-N1-H9 Seq. ID Method BLASTX NCBI GI g2833460 BLAST score 201 E value 1.0e-15 Match length 73 51 % identity RIBOFLAVIN-SPECIFIC DEAMINASE >qi 1001153 dbj BAA10295 NCBI Description (D64001) riboflavin biosynthesis protein [Synechocystis sp.] Seq. No. 297647 Seq. ID LIB3150-023-Q1-N1-A11 Method BLASTX NCBI GI g1169528 BLAST score 156 1.0e-10 E value Match length 44 73 % identity ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2) NCBI Description (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi_602253 (U17973) enolase [Zea mays] Seq. No. 297648 Seq. ID LIB3150-023-Q1-N1-A6 Method BLASTX NCBI GI q4263519 BLAST score 272 E value 5.0e-24 Match length 55

41758

(AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis



```
297649
Seq. No.
Seq. ID
                  LIB3150-023-Q1-N1-C8
Method
                  BLASTX
                  g135060
NCBI GI
BLAST score
                  370
                  8.0e-36
E value
Match length
                  76
% identity
                  97
                  SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
NCBI Description
                  (SHRUNKEN-1) >gi_66570_pir__YUZMS sucrose synthase (EC
                  2.4.1.13) - maize >gi_22486_emb_CAA26247_ (X02400) sucrose
                  synthase [Zea mays] >gi_22488_emb_CAA26229_ (X02382)
                  sucrose synthase [Zea mays]
                  297650
Seq. No.
Seq. ID
                  LIB3150-023-Q1-N1-D4
Method
                  BLASTX
NCBI GI
                  g4589852
BLAST score
                  270
                  5.0e-24
E value
Match length
                  97
% identity
                  52
                  (AB025968) cycloartenol synthase [Glycyrrhiza glabra]
NCBI Description
                  297651
Seq. No.
Seq. ID
                  LIB3150-023-Q1-N1-E3
Method
                  BLASTX
NCBI GI
                  g4588012
BLAST score
                  162
                  1.0e-11
E value
Match length
                  40
% identity
                   (AF085717) putative callose synthase catalytic subunit
NCBI Description
                   [Gossypium hirsutum]
                  297652
Seq. No.
Seq. ID
                  LIB3150-023-Q1-N1-F1
Method
                  BLASTX
NCBI GI
                  q731707
BLAST score
                  277
E value
                  1.0e-24
Match length
                  115
% identity
                  47
                  SET1 PROTEIN >gi 626647 pir S48961 hypothetical protein
NCBI Description
                  YHR119w - yeast (Saccharomyces cerevisiae) >gi 529135
                   (U00059) Setlp [Saccharomyces cerevisiae]
Seq. No.
                  297653
Seq. ID
                  LIB3150-023-Q1-N1-F6
Method
                  BLASTN
NCBI GI
                  g22549
BLAST score
                  159
E value
                  2.0e-84
```

41759

NCBI Description Maize gene for a 27kDa storage protein, zein

203

95

Match length % identity

Seq. ID

```
297654
Seq. No.
                  LIB3150-023-Q1-N1-G6
Seq. ID
                  BLASTX
Method
                  g1519251
NCBI GI
                  591
BLAST score
                  2.0e-61
E value
                  131
Match length
% identity
NCBI Description (U65957) GF14-c protein [Oryza sativa]
                  297655
Seq. No.
                  LIB3150-023-Q1-N1-H11
Seq. ID
                  BLASTN
Method
                   q22272
NCBI GI
                   57
BLAST score
                   9.0e-24
E value
Match length
                   73
                   95
% identity
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
                   297656
Seq. No.
                   LIB3150-025-Q1-N1-A9
Seq. ID
Method
                   BLASTX
                   q3355468
NCBI GI
                   153
BLAST score
                   3.0e-10
E value
                   109
Match length
% identity
                   (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                   thaliana]
                   297657
Seq. No.
                   LIB3150-025-Q1-N1-C11
Seq. ID
                   BLASTX
Method
                   g3834321
NCBI GI
                   302
BLAST score
                   1.0e-27
E value
Match length
                   98
                   59
 % identity
                   (AC005679) Strong similarity to F13P17.9 gi 3337356
NCBI Description
                   transport protein SEC61 alpha subunit homolog from
                   Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis
                   thaliana]
                   297658
 Seq. No.
                   LIB3150-025-Q1-N1-F9
 Seq. ID
 Method
                   BLASTX
                   g3043428
 NCBI GI
                   252
 BLAST score
                   5.0e-22
 E value
                   77
 Match length
                   68
 % identity
                   (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
 NCBI Description
                   297659
 Seq. No.
```

41760

LIB3150-026-Q1-N1-C10



```
BLASTX
Method
                  g2369714
NCBI GI
                  168
BLAST score
                  5.0e-13
E value
                  90
Match length
                  51
% identity
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]
                  297660
Seq. No.
                  LIB3150-026-Q1-N1-E7
Seq. ID
                  BLASTN
Method
NCBI GI
                  q22119
                  58
BLAST score
                  5.0e-24
E value
                  173
Match length
                   84
% identity
NCBI Description Maize Adhl-F mRNA for alcohol dehydrogenase
                   297661
Seq. No.
                   LIB3150-026-Q1-N1-F1
Seq. ID
                   BLASTX
Method
                   g1172977
NCBI GI
BLAST score
                   146
                   9.0e-10
E value
                   32
Match length
                   88
% identity
                   60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic
NCBI Description
                   ribosomal protein L18 [Arabidopsis thaliana]
                   297662
Seq. No.
                   LIB3150-026-Q1-N1-F5
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1519250
                   37
BLAST score
                   1.0e-11
E value
                   73
Match length
                   88
 % identity
NCBI Description Oryza sativa GF14-c protein mRNA, complete cds
                   297663
Seq. No.
                   LIB3150-026-Q1-N1-F9
 Seq. ID
                   BLASTN
Method
                   g22338
NCBI GI
                   70
BLAST score
                   2.0e-31
 E value
                   110
Match length
                   92
 % identity
                   Maize mRNA for an 18kDa heat shock protein
 NCBI Description
                   297664
 Seq. No.
                   LIB3150-026-Q1-N1-G1
 Seq. ID
                   BLASTX
 Method
                   q1706253
 NCBI GI
                   165
 BLAST score
                   1.0e-11
 E value
                   83
 Match length
```

43

% identity



NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 7 (PPIASE) (ROTAMASE) (CYCLOPHILIN-7) >gi 863016 (U27559) cyclophilin

[Caenorhabditis elegans]

Seq. No. 297665

Seq. ID LIB3150-026-Q1-N1-G4

Method BLASTX
NCBI GI g113621
BLAST score 432
E value 8.0e-43
Match length 91
% identity 90

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A

cytoplasmic aldolase [Zea mays]

Seq. No. 297666

Seq. ID LIB3150-026-Q1-N1-G5

Method BLASTX
NCBI GI 94467125
BLAST score 441
E value 7.0e-44
Match length 106
% identity 74

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 297667

Seq. ID LIB3150-026-Q1-N1-G8

Method BLASTN
NCBI GI g22312
BLAST score 96
E value 9.0e-47
Match length 244
% identity 88

NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA =

abscisic acid)

Seq. No. 297668

Seq. ID LIB3150-026-Q1-N1-H8

Method BLASTX
NCBI GI g2443388
BLAST score 248
E value 2.0e-21
Match length 85
% identity 66

NCBI Description (D38452) calcium-dependent protein kinase-related kinase

[Zea mays]

Seq. No. 297669

Seq. ID LIB3150-027-Q1-N1-A12

Method BLASTX
NCBI GI g2130032
BLAST score 261
E value 1.0e-22



```
Match length
% identity
                  49
                  catechol O-methyltransferase (EC 2.1.1.6) - barley
NCBI Description
                  297670
Seq. No.
                  LIB3150-027-Q1-N1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q602605
BLAST score
                  44
E value
                  1.0e-15
Match length
                  56
% identity
                  95
                  Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin
NCBI Description
                  297671
Seq. No.
Seq. ID
                  LIB3150-027-Q1-N1-A7
Method
                  BLASTX
                  g2384758
NCBI GI
BLAST score
                  330
                  4.0e-31
E value
Match length
                  92
                  72
% identity
                  (AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza
NCBI Description
                  sativa]
                  297672
Seq. No.
Seq. ID
                  LIB3150-027-Q1-N1-B10
                  BLASTX
Method
NCBI GI
                  g1350986
BLAST score
                  291
E value
                  2.0e-26
Match length
                  83
                  72
% identity
                  40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
NCBI Description
                  >qi 483431 dbj BAA05059 (D26060) cyc07 [Oryza sativa]
                  297673
Seq. No.
                  LIB3150-027-Q1-N1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4033424
                  301
BLAST score
E value
                  2.0e-27
Match length
                  100
% identity
                  68
                  SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
NCBI Description
                  PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic
                  pyrophosphatase [Zea mays]
Seq. No.
                  297674
                  LIB3150-027-Q1-N1-C1
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g4587553
BLAST score 214
E value 3.0e-17
Match length 79
% identity 54

NCBI Description (AC006577) F15I1.20 [Arabidopsis thaliana]

```
297675
Seq. No.
                  LIB3150-027-Q1-N1-C2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g556685
BLAST score
                  57
                  1.0e-23
E value
Match length
                  89
% identity
                  91
NCBI Description Z.mays mRNA for ADP-ribosylation factor
                  297676
Seq. No.
Seq. ID
                  LIB3150-027-Q1-N1-E11
Method
                  BLASTX
                  g320130
NCBI GI
BLAST score
                  221
E value
                  4.0e-18
Match length
                  87
                  53
% identity
NCBI Description
                  acetolactate synthase (EC 4.1.3.18) (clone pSOG109) - maize
                  >gi_22141_emb_CAA45117_ (X63554) acetohydroxyacid synthase
                   [Zea mays]
                  297677
Seq. No.
Seq. ID
                  LIB3150-027-Q1-N1-E2
Method
                  BLASTX
NCBI GI
                  g4587553
BLAST score
                  192
                  1.0e-14
E value
Match length
                  66
% identity
                  58
NCBI Description
                  (AC006577) F15I1.20 [Arabidopsis thaliana]
Seq. No.
                  297678
Seq. ID
                  LIB3150-027-Q1-N1-F6
Method
                  BLASTX
NCBI GI
                  g3986695
BLAST score
                  165
E value
                  9.0e-12
                  61
Match length
% identity
                  61
NCBI Description
                 (AF101423) ribosomal protein L12 [Cichorium intybus]
                  297679
Seq. No.
Seq. ID
                  LIB3150-028-Q1-N1-A4
Method
                  BLASTX
NCBI GI
                  g2244797
BLAST score
                  167
E value
                  7.0e-12
                  94
Match length
```

Seq. No. 297680

% identity

Seq. ID LIB3150-028-Q1-N1-C8

43

Method BLASTN NCBI GI q4416300

NCBI Description (297336) hypothetical protein [Arabidopsis thaliana]



BLAST score 8.0e-42 E value 235 Match length 58 % identity

Zea mays chromosome 4 22 kDa zein-associated intercluster NCBI Description

region, complete sequence

297681 Seq. No.

Seq. ID LIB3150-028-Q1-N1-D11

BLASTX Method g113621 NCBI GI 340 BLAST score 3.0e-32 E value 80 Match length 86 % identity

FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME NCBI Description >gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase

[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A

cytoplasmic aldolase [Zea mays]

297682 Seq. No.

LIB3150-028-Q1-N1-E11 Seq. ID

BLASTX Method g3747046 NCBI GI 358 BLAST score 4.0e-34 E value 77 Match length 91 % identity

(AF093538) voltage-dependent anion-selective channel NCBI Description

protein [Zea mays]

297683 Seq. No.

Seq. ID LIB3150-028-Q1-N1-E9

BLASTN Method g485376 NCBI GI 35 BLAST score 1.0e-10 E value 71 Match length 87 % identity

Zea mays alpha-3-tubulin gene, complete cds NCBI Description

297684 Seq. No.

Seq. ID LIB3150-028-Q1-N1-F10

BLASTX Method NCBI GI q2832648 138 BLAST score 6.0e-09 E value 80 Match length % identity

(AL021710) membrane-bound small GTP-binding - like protein NCBI Description

[Arabidopsis thaliana]

297685 Seq. No.

LIB3150-028-Q1-N1-F2 Seq. ID

Method BLASTN

Seq. ID



```
g22312
NCBI GI
                  226
BLAST score
                  1.0e-124
E value
                  374
Match length
                  90
% identity
                  Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                  abscisic acid)
                  297686
Seq. No.
Seq. ID
                  LIB3150-028-Q1-N1-G5
                  BLASTX
Method
NCBI GI
                  q2342678
                  137
BLAST score
                  9.0e-09
E value
                  57
Match length
                   53
% identity
                   (AC000106) Similar to Arabidopsis luminal binding protein
NCBI Description
                   (gb_D89342). [Arabidopsis thaliana]
                   297687
Seq. No.
                   LIB3150-028-Q1-N1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2511531
                   220
BLAST score
                   4.0e-18
E value
                   82
Match length
                   57
% identity
                   (AF008120) alpha tubulin 1 [Eleusine indica]
NCBI Description
                   >gi 3163944 emb_CAA06618_ (AJ005598) alpha-tubulin 1
                   [Eleusine indica]
                   297688
Seq. No.
                   LIB3150-028-Q1-N1-H9
Seq. ID
                   BLASTX
Method
                   g4646206
NCBI GI
                   247
BLAST score
                   4.0e-21
E value
                   119
Match length
% identity
                   (AC007230) Contains similarity to gb_D13630 KIAA0005 gene
NCBI Description
                   from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360,
                   gb_T20468, gb_T45191 and gb_AI100459 come from this gene.
                   [Arabidopsis thaliana]
                   297689
 Seq. No.
                   LIB3150-029-Q1-N1-A4
 Seq. ID
                   BLASTX
Method
                   q1703380
 NCBI GI
                   298
 BLAST score
                   4.0e-27
 E value
                   67
Match length
                   88
 % identity
                   ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760)
 NCBI Description
                   ADP-ribosylation factor [Oryza sativa]
 Seq. No.
                   297690
```

LIB3150-029-Q1-N1-A6

Seq. No.

Seq. ID



```
BLASTX
Method
                  q3915826
NCBI GI
                  375
BLAST score
                  4.0e-36
E value
                  96
Match length
                  76
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L5
                  297691
Seq. No.
                  LIB3150-029-Q1-N1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q266567
BLAST score
                  198
                  1.0e-20
E value
Match length
                  111
                  53
% identity
                  MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR
NCBI Description
                   (ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II)
                  >gi_421956_pir__$23558 mitochondrial processing peptidase
                   (EC 3.4.99.41) alpha chain precursor - potato
                   >gi 21493 emb_CAA46990_ (X66284) mitochondrial processing
                   peptidase [Solanum tuberosum]
Seq. No.
                   297692
                   LIB3150-029-Q1-N1-F9
Seq. ID
                   BLASTX
Method
                   q542125
NCBI GI
                   149
BLAST score
                   6.0e-10
E value
                   53
Match length
                   62
% identity
                   translation elongation factor eEF-1 alpha chain - barley
NCBI Description
                   >gi_396134_emb_CAA80666 (Z23130) protein synthesis
                   elongation factor-1 alpha [Hordeum vulgare]
                   297693
Seq. No.
                   LIB3150-029-Q1-N1-G1
 Seq. ID
                   BLASTN
Method
                   q1550813
NCBI GI
                   59
 BLAST score
                   1.0e-24
 E value
                   107
Match length
                   89
 % identity
                   Z.mays mRNA for acidic ribosomal protein PO
 NCBI Description
                   297694
 Seq. No.
                   LIB3150-030-Q1-N1-A4
 Seq. ID
                   BLASTN
 Method
                   q22514
 NCBI GI
                   121
 BLAST score
                   1.0e-61
 E value
                   249
 Match length
                   87
 % identity
                   Maize Zcl gene for Zein Zcl (14 kD zein-2)
 NCBI Description
                   297695
```

41767

LIB3150-030-Q1-N1-B4

```
BLASTN
Method
NCBI GI
                  g22312
                  121
BLAST score
                  7.0e-62
E value
                  165
Match length
                  93
% identity
                  Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                  abscisic acid)
                  297696
Seq. No.
                  LIB3150-030-Q1-N1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4033424
                   297
BLAST score
E value
                   3.0e-27
                   62
Match length
% identity
                   SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
NCBI Description
                   PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic
                   pyrophosphatase [Zea mays]
                   297697
Seq. No.
Seq. ID
                   LIB3150-030-Q1-N1-C6
Method
                   BLASTX
                   q1732511
NCBI GI
                   506
BLAST score
                   2.0e-51
E value
                   116
Match length
% identity
                   (U62742) Ran binding protein 1 homolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   297698
                   LIB3150-030-Q1-N1-D1
Seq. ID
                   BLASTX
Method
                   q113621
NCBI GI
                   155
BLAST score
                   7.0e-11
E value
                   36
Match length
                   89
 % identity
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
NCBI Description
                   >gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
                   4.1.2.13), cytosolic - maize >gi 168420 (M16220) aldolase
                   [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
                   bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A
                   cytoplasmic aldolase [Zea mays]
                   297699
 Seq. No.
```

Seq. ID LIB3150-030-Q1-N1-D2

Method BLASTX
NCBI GI g2654208
BLAST score 163
E value 8.0e-12
Match length 60
% identity 63

NCBI Description (AF035456) heat shock 70 protein [Spinacia oleracea] >gi_2773050 (AF039083) heat shock 70 protein [Spinacia

% identity

96



oleracea]

```
Seq. No.
                  297700
Seq. ID
                  LIB3150-030-Q1-N1-E2
Method
                  BLASTN
NCBI GI
                  q1658312
BLAST score
                  47
                  1.0e-17
E value
                  99
Match length
                  88
% identity
NCBI Description O.sativa osr40g2 gene
Seq. No.
                  297701
Seq. ID
                  LIB3150-030-Q1-N1-E4
Method
                  BLASTN
NCBI GI
                  q829147
BLAST score
                  72
                  2.0e-32
E value
Match length
                  96
                  94
% identity
NCBI Description Z.mays gene for cyclophilin
Seq. No.
                  297702
Seq. ID
                  LIB3150-030-Q1-N1-F2
Method
                  BLASTX
NCBI GI
                  g1709920
BLAST score
                  240
                  2.0e-20
E value
Match length
                  72
                  62
% identity
NCBI Description
                  PHOSPHORIBOSYLAMINE--GLYCINE LIGASE PRECURSOR (GARS)
                  (GLYCINAMIDE RIBONUCLEOTIDE SYNTHETASE)
                  (PHOSPHORIBOSYLGLYCINAMIDE SYNTHETASE)
                  >gi 1019915 emb CAA52778 (X74766) glycinamide
                  ribonucleotide synthetase [Arabidopsis thaliana]
                  297703
Seq. No.
                  LIB3150-030-Q1-N1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g120670
BLAST score
                  381
                  4.0e-37
E value
Match length
                  84
% identity
                  87
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi_100879_pir__S06879 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) C - maize
                  >gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]
Seq. No.
                  297704
Seq. ID
                  LIB3150-030-Q1-N1-G3
Method
                  BLASTN
NCBI GI
                  g1895083
BLAST score
                  43
E value
                  2.0e-15
Match length
                  51
```



NCBI Description Zea mays golgi associated protein se-wap41 mRNA, complete cds 297705 Seq. No. LIB3150-030-Q1-N1-H6 Seq. ID BLASTX Method

g4467128 NCBI GI 320 BLAST score 7.0e-31 E value Match length 96 71 % identity

(AL035538) putative protein [Arabidopsis thaliana] NCBI Description

297706 Seq. No.

LIB3150-031-Q1-N1-A11 Seq. ID

BLASTN Method g747916 NCBI GI 62 BLAST score 1.0e-26 E value 110 Match length 89 % identity

NCBI Description Z.mays CaM2 mRNA for calmodulin

297707 Seq. No.

LIB3150-031-Q1-N1-A7 Seq. ID

BLASTX Method g113621 NCBI GI 268 BLAST score 1.0e-23 E value 95 Match length 93 % identity

FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME NCBI Description

>gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi 168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A

cytoplasmic aldolase [Zea mays]

297708 Seq. No.

LIB3150-031-Q1-N1-B4 Seq. ID

BLASTX Method q2909846 NCBI GI 181 BLAST score 2.0e-13 E value 55 Match length 65 % identity

(AF045570) (S)-adenosyl-L-methionine:delta 24-sterol NCBI Description

methyltransferase [Zea mays]

297709 Seq. No.

LIB3150-031-Q1-N1-D10 Seq. ID

BLASTX Method q1685091 NCBI GI 337 BLAST score 1.0e-31 E value 98 Match length 68 % identity

Seq. No.

Seq. ID

Method

297715

BLASTX

LIB3150-032-Q1-N1-D6



```
(U45243) diphenol oxidase [Nicotiana tabacum]
NCBI Description
Seq. No.
                  297710
Seq. ID
                  LIB3150-031-Q1-N1-D12
Method
                  BLASTX
NCBI GI
                  q3163946
BLAST score
                  261
E value
                  5.0e-38
Match length
                  102
                  72
% identity
                  (AJ005599) alpha-tubulin 1 [Eleusine indica]
NCBI Description
                  297711
Seq. No.
Seq. ID
                  LIB3150-031-Q1-N1-F1
Method
                  BLASTX
NCBI GI
                  q1076626
BLAST score
                  491
                  1.0e-49
E value
                  97
Match length
                  93
% identity
                  glycine rich protein - common tobacco
NCBI Description
                  >gi_790473_emb_CAA58702_ (X83731) soluble, glycine rich
                  protein [Nicotiana tabacum]
Seq. No.
                  297712
Seq. ID
                  LIB3150-031-Q1-N1-H5
Method
                  BLASTX
NCBI GI
                  q4588003
BLAST score
                  238
                  7.0e-20
E value
                  65
Match length
                  74
% identity
                  (AF085279) hypothetical EIF-2-Alpha [Arabidopsis thaliana]
NCBI Description
                  297713
Seq. No.
Seq. ID
                  LIB3150-031-Q1-N1-H9
Method
                  BLASTX
NCBI GI
                  g4455293
BLAST score
                  213
E value
                  4.0e-17
Match length
                  88
% identity
                  61
NCBI Description
                  (AL035528) putative protein [Arabidopsis thaliana]
Seq. No.
                  297714
                  LIB3150-032-Q1-N1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3402679
BLAST score
                  184
E value
                  3.0e-14
Match length
                  81
% identity
                  52
NCBI Description
                  (AC004697) unknown protein [Arabidopsis thaliana]
```



```
q118104
NCBI GI
                  566
BLAST score
                  2.0e-58
E value
                  125
Match length
% identity
                  86
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi 168461 (M55021) cyclophilin [Zea mays]
                  >qi 829148 emb_CAA48638_ (X68678) cyclophilin [Zea mays]
                   297716
Seq. No.
                   LIB3150-032-Q1-N1-F4
Seq. ID
                   BLASTX
Method
                   q1174583
NCBI GI
                   201
BLAST score
E value
                   1.0e-15
Match length
                   104
% identity
                   TRANSALDOLASE >gi 1074653 pir__D64167 hypothetical protein
NCBI Description
                   HI1125 - Haemophilus influenzae (strain Rd KW20)
                   >gi_1574680 (U32792) transaldolase B (talB) [Haemophilus
                   influenzae Rd]
                   297717
Seq. No.
                   LIB3150-032-Q1-N1-G3
Seq. ID
                   BLASTX
Method
                   q2407800
NCBI GI
BLAST score
                   308
                   4.0e-28
E value
                   98
Match length
                   62
% identity
                   (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
NCBI Description
                   297718
Seq. No.
                   LIB3150-032-Q1-N1-H1
Seq. ID
                   BLASTX
Method
                   q1172811
NCBI GI
                   285
BLAST score
                   4.0e-26
E value
                   59
Match length
                   83
% identity
                   60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34)
NCBI Description
                   >gi 1076751 pir__S49575 ribosomal protein L10.e, cytosolic
                    - \overline{\text{rice}} >gi \overline{575355} emb CAA57339_ (X81691) putative tumor
                   suppresser [Oryza sativa]
                   297719
Seq. No.
                   LIB3150-033-Q1-N1-D10
 Seq. ID
                   BLASTX
Method
                    g2253583
NCBI GI
                    151
BLAST score
                    6.0e-10
E value
                    46
Match length
```

(U78721) hypothetical protein [Arabidopsis thaliana]

74

% identity

, NCBI Description

```
297720
Seq. No.
                  LIB3150-033-Q1-N1-D2
Seq. ID
Method
                  BLASTX
                  g2832700
NCBI GI
                  174
BLAST score
E value
                  8.0e-13
Match length
                  81
                  42
% identity
                  (AL021713) unknown protein [Arabidopsis thaliana]
NCBI Description
                  297721
Seq. No.
                  LIB3150-033-Q1-N1-F3
Seq. ID
Method
                  BLASTX
                  q861170
NCBI GI
                   176
BLAST score
                   3.0e-13
E value
                   48
Match length
                   77
% identity
                  (X03697) heat shock protein 70 [Zea mays]
NCBI Description
                   297722
Seq. No.
                   LIB3150-033-Q1-N1-F6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3183094
                   238
BLAST score
                   3.0e-20
E value
                   94
Match length
                   47
% identity
                   ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR (OTCASE)
NCBI Description
                   (ORNITHINE TRANSCARBAMYLASE) >gi_971168 (U13684) ornithine
                   carbamoyltransferase [Pisum sativum]
Seq. No.
                   297723
                   LIB3150-033-Q1-N1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2459421
BLAST score
                   426
                   4.0e-42
E value
                   118
Match length
% identity
                   64
                   (AC002332) putative calcium-binding EF-hand protein
NCBI Description
                   [Arabidopsis thaliana]
                   297724
 Seq. No.
                   LIB3150-033-Q1-N1-G5
 Seq. ID
                   BLASTX
Method
                   g1184774
NCBI GI
BLAST score
                   484
                   6.0e-49
E value
                   95
Match length
                   98
 % identity
                   (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC3 [Zea mays]
                   297725
 Seq. No.
                   LIB3150-033-Q1-N1-G8
 Seq. ID
                   BLASTN
 Method
```

Method

NCBI GI

BLASTX

g2081612



```
g3015620
NCBI GI
BLAST score
                  120
E value
                  5.0e-61
Match length
                  240
% identity
                  88
                  Zea mays low molecular weight heat shock protein precursor
NCBI Description
                   (hsp22) mRNA, nuclear gene encoding mitochondrial protein,
                  complete cds
                  297726
Seq. No.
                  LIB3150-034-Q1-N1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82696
                  207
BLAST score
                  9.0e-17
E value
Match length
                  57
                  75
% identity
                  glycine-rich protein - maize >gi_22293_emb_CAA43431 _
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
                  297727
Seq. No.
                  LIB3150-034-Q1-N1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1184774
BLAST score
                  149
E value
                  5.0e-15
Match length
                  94
% identity
                  51
                  (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC3 [Zea mays]
Seq. No.
                   297728
Seq. ID
                  LIB3150-034-Q1-N1-G5
                  BLASTX
Method
NCBI GI
                  q2792208
BLAST score
                   272
                   5.0e-24
E value
Match length
                  124
% identity
                  (AF032682) NBS-LRR type resistance protein [Hordeum
NCBI Description
                  vulgare]
                  297729
Seq. No.
                  LIB3150-034-Q1-N1-G7
Seq. ID
Method
                  BLASTX
                  g418777
NCBI GI
                   269
BLAST score
                   8.0e-24
E value
Match length
                  101
                   57
% identity
NCBI Description
                  phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic
                  chain (clone EP7) - Arabidopsis thaliana (fragment)
Seq. No.
                   297730
Seq. ID
                   LIB3150-035-Q1-N1-B4
```

```
289
BLAST score
                   5.0e-26
. E value
Match length
                   68
                   81
 % identity
                   (D49714) deltal-pyrroline-5-carboxylate synthetase [Oryza
 NCBI Description
                   297731
 Seq. No.
                   LIB3150-035-Q1-N1-B8
 Seq. ID
                   BLASTX
 Method
                   q231536
 NCBI GI
                   378
 BLAST score
                   2.0e-36
 E value
                   128
 Match length
 % identity
                   CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP)
 NCBI Description
                    (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL
                   AMINOPEPTIDASE) >gi_99683_pir__S22399 leucyl aminopeptidase
                    (EC 3.4.11.1) - Arabidopsis thaliana
                   >gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase
                    [Arabidopsis thaliana] >gi_4115380 (AC005967) putative
                    leucine aminopeptidase [Arabidopsis thaliana]
                    297732
 Seq. No.
                    LIB3150-035-Q1-N1-B9
 Seq. ID
                    BLASTN
 Method
                    q998429
 NCBI GI
                    45
 BLAST score
                    4.0e-16
 E value
                    126
 Match length
 % identity
                    GRF1=general regulatory factor [Zea mays, XL80, Genomic,
 NCBI Description
                    5348 nt]
                    297733
 Seq. No.
                    LIB3150-035-Q1-N1-D9
 Seq. ID
 Method
                    BLASTX
                    g4510346
 NCBI GI
                    273
  BLAST score
                    4.0e-24
 E value
                    73
 Match length
                    71
  % identity
                    (AC006921) hypothetical protein [Arabidopsis thaliana]
  NCBI Description
                    297734
  Seq. No.
                    LIB3150-035-Q1-N1-E12
  Seq. ID
                    BLASTX
  Method
  NCBI GI
                    q1708777
                    148
  BLAST score
                    1.0e-09
  E value
                    101
  Match length
                    37
  % identity
                    (Z83202) potassium channel [Arabidopsis thaliana]
  NCBI Description
                    >gi_3063705_emb_CAA18596.1_ (AL022537) potassium channel
                    protein [Arabidopsis thaliana] >gi_4090537 (U73325) K+
```

inward rectifying channel protein [Arabidopsis thaliana]

>gi 4098949 (U81239) K+ inward rectifying channel



[Arabidopsis thaliana]

```
297735
Seq. No.
                  LIB3150-035-Q1-N1-E3
Seq. ID
                  BLASTN
Method
                  q1296954
NCBI GI
                  48
BLAST score
                  5.0e-18
E value
                  83
Match length
                  89
% identity
NCBI Description O.sativa mRNA for novel protein, osr40c1
                   297736
Seq. No.
                   LIB3150-035-Q1-N1-E4
Seq. ID
Method
                   BLASTX
                   g1658313
NCBI GI
BLAST score
                   227
                   7.0e-19
E value
                   86
Match length
                   41
% identity
NCBI Description (Y08987) osr40g2 [Oryza sativa]
Seq. No.
                   297737
                   LIB3150-035-Q1-N1-E9
Seq. ID
Method
                   BLASTX
                   g118104
NCBI GI
                   283
BLAST score
                   3.0e-25
E value
                   109
Match length
                   56
% identity
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                   >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                   maize > gi 168461  (M55021) cyclophilin [Zea mays]
                   >gi 82914\overline{8} emb CAA48638 (X68678) cyclophilin [Zea mays]
                   297738
Seq. No.
                   LIB3150-035-Q1-N1-F10
Seq. ID
                   BLASTX
Method
                   g2828012
NCBI GI
                   255
BLAST score
                   3.0e-22
E value
                    67
Match length
                    67
 % identity
                   (AF036891) starch synthase I precursor [Zea mays]
NCBI Description
                    297739
 Seq. No.
                   LIB3150-035-Q1-N1-G3
 Seq. ID
                    BLASTN
Method
                    g168704
 NCBI GI
                    59
 BLAST score
                    9.0e-25
 E value
                    86
 Match length
                    95
 % identity
                   Zea mays zein protein gene, complete cds
 NCBI Description
```

297740

Seq. No.



```
LIB3150-036-Q1-N1-A8
Seq. ID
                  BLASTX
Method
                  q2668742
NCBI GI
                  239
BLAST score
                  9.0e-26
E value
                  70
Match length
                  91
% identity
                 (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                  297741
Seq. No.
                  LIB3150-036-Q1-N1-B1
Seq. ID
                  BLASTX
Method
                  a1666234
NCBI GI
                  157
BLAST score
                  1.0e-10
E value
                  40
Match length
                  80
% identity
NCBI Description (U76193) actin [Pisum sativum] >gi_1724143 (U81049) actin
                   [Pisum sativum]
                  297742
Seq. No.
                  LIB3150-036-Q1-N1-E6
Seq. ID
                  BLASTX
Method
                   q4558664
NCBI GI
BLAST score
                   441
                   7.0e-44
E value
                   122
Match length
                   63
% identity
NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]
                   297743
Seq. No.
                   LIB3150-036-Q1-N1-G12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4160346
                   218
BLAST score
E value
                   1.0e-17
Match length
                  . 84
% identity
                   51
NCBI Description (AL035216) nucleolar protein involved in pre-rRNA
                   processing [Schizosaccharomyces pombe]
                   297744
 Seq. No.
                   LIB3150-037-Q1-N1-A6
 Seq. ID
                   BLASTX
Method
 NCBI GI
                   g135535
 BLAST score
                   452
                   2.0e-45
 E value
                   110
 Match length
 % identity
                   82
                   T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)
 NCBI Description
                   (CCT-ALPHA) >gi 322602 pir JN0448 t-complex polypeptide
                   Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955
                   (D11351) t-complex polypeptide 1 homologue [Arabidopsis
                   thaliana] >gi_2326265 dbj_BAA21772_ (D11352) CCT
                   alpha/TCP-1 [Arabidopsis thaliana]
```

BLAST score

326



```
LIB3150-037-Q1-N1-B4
Seq. ID
                  BLASTN
Method
                  g2645165
NCBI GI
                  69
BLAST score
                  1.0e-30
E value
                  85
Match length
                  95
% identity
NCBI Description Oryza sativa mRNA, similar to ribosomal protein
                  297746
Seq. No.
                  LIB3150-037-Q1-N1-B5
Seq. ID
                  BLASTX
Method
                  q3395430
NCBI GI
                  154
BLAST score
                  2.0e-10
E value
                   87
Match length
% identity
                   34
                  (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   297747
Seq. No.
                   LIB3150-037-Q1-N1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4512659
                   409
BLAST score
                   4.0e-40
E value
                   116
Match length
                   70
% identity
                   (AC006931) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   >gi 4544465 gb_AAD22372.1_AC006580_4 (AC006580) putative
                   protein kinase [Arabidopsis thaliana]
                   297748
Seq. No.
                   LIB3150-037-Q1-N1-H1
Seq. ID
                   BLASTX
Method
                   g2624328
NCBI GI
                   150
BLAST score
                   6.0e-10
E value
                   65
Match length
                   45
% identity
                   (AJ002894) OsGRP2 [Oryza sativa]
NCBI Description
                   297749
Seq. No.
                   LIB3150-037-Q1-N1-H8
Seq. ID
Method
                   BLASTX
                   q1184774
NCBI GI
                   199
BLAST score
                   6.0e-16
E value
Match length
                   55
 % identity
                   (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC3 [Zea mays]
                   297750
 Seq. No.
                   LIB3150-038-Q1-N1-A7
 Seq. ID
 Method
                   BLASTX
                   g1351974
 NCBI GI
```



```
2.0e-30
E value
Match length
                  89
                  76
% identity
                  ADP-RIBOSYLATION FACTOR >gi 1076788 pir S49325
NCBI Description
                  ADP-ribosylation factor - maize >gi_1076789_pir__$53486
                  ADP-ribosylation factor - maize >gi_556686_emb CAA56351
                  (X80042) ADP-ribosylation factor [Zea mays]
Seq. No.
                  LIB3150-038-Q1-N1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q462243
BLAST score
                  325
                  4.0e-30
E value
                  88
Match length
                  77
% identity
                  HISTONE H4 >gi_421921_pir__S32769 histone H4 - tomato
NCBI Description
                  >gi 297150_emb_CAA48923_ (X69179) histone H4 [Lycopersicon
                  esculentum] >gi_297152_emb_CAA48924_ (X69180) histone H4
                   [Lycopersicon esculentum] >gi_2746721 (AF038387) histone H4
                   [Capsicum annuum]
                  297752
Seq. No.
Seq. ID
                  LIB3150-038-Q1-N1-C6
                  BLASTX
Method
                  q140496
NCBI GI
BLAST score
                   152
                   6.0e-10
E value
Match length
                   117
                   30
% identity
                  HYPOTHETICAL 42.5 KD PROTEIN IN TSM1-ARE1 INTERGENIC REGION
NCBI Description
                   >gi 83226 pir S19457 probable membrane protein YCR044c -
                   yeast (Saccharomyces cerevisiae) >gi_1907186_emb_CAA42292_
                   (X59720) YCR044c, len:357 [Saccharomyces cerevisiae]
                   297753
Seq. No.
                   LIB3150-038-Q1-N1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3914423
                   207
BLAST score
                   6.0e-17
E value
                   54
Match length
 % identity
                   PROFILIN 4 >gi_2642324 (AF032370) profilin [Zea mays]
NCBI Description
                   297754
```

LIB3150-038-Q1-N1-F3 Seq. ID

BLASTX Method g2642159 NCBI GI 191 BLAST score 9.0e-15 E value 86 Match length 49 % identity

(AC003000) putative mannose-1-phosphate guanyltransferase NCBI Description [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose

pyrophosphorylase [Arabidopsis thaliana] >gi_4151925

(AF108660) CYT1 protein [Arabidopsis thaliana]

```
297755
Seq. No.
                  LIB3150-038-Q1-N1-F5
Seq. ID
                  BLASTX
Method
                  g4581156
NCBI GI
                  192
BLAST score
                  2.0e-17
E value
                  109
Match length
                  52
% identity
                  (AC006919) putative pyruvate kinase [Arabidopsis thaliana]
NCBI Description
                   297756
Seq. No.
                  LIB3150-038-Q1-N1-F8
Seq. ID
                  BLASTX
Method
                   g533082
NCBI GI
                   288
BLAST score
                   6.0e-26
E value
Match length
                   103
                   56
% identity
                   (U07552) delta-9 stearoyl-acyl carrier protein desaturase
NCBI Description
                   [Thunbergia alata]
                   297757
Seq. No.
                   LIB3150-038-Q1-N1-H9
Seq. ID
                   BLASTX
Method
                   q3413717
NCBI GI
                                                                     ۶.,
                   160
BLAST score
                   5.0e-11
E value
                   65
Match length
                   46
% identity
                   (AC004747) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3643590 (AC005395) unknown protein [Arabidopsis
                   thaliana]
                   297758
Seq. No.
                   LIB3150-039-Q1-N1-A12
Seq. ID
                   BLASTX
Method
                   q2668742
NCBI GI
                   330
BLAST score
                   5.0e-31
E value
                   79
Match length
                   86
 % identity
                   (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                   297759
 Seq. No.
                   LIB3150-039-Q1-N1-B6
 Seq. ID
                   BLASTN
 Method
                   g22272
 NCBI GI
                   63
 BLAST score
                   4.0e-27
 E value
                   175
 Match length
                   84
 % identity
 NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
                   297760
 Seq. No.
 Seq. ID
                   LIB3150-039-Q1-N1-E10
                   BLASTX
 Method
```



```
g2459445
NCBI GI
BLAST score
                  168
E value
                  7.0e-12
                  66
Match length
% identity
                  41
                  (AC002332) putative ribonucleoprotein [Arabidopsis
NCBI Description
                  thaliana]
                  297761
Seq. No.
Seq. ID
                  LIB3150-039-Q1-N1-E11
Method
                  BLASTX
NCBI GI
                  q1184776
BLAST score
                  530
                  3.0e-54
E value
                  132
Match length
                  79
% identity
                  (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC4 [Zea mays]
Seq. No.
                  297762
Seq. ID
                  LIB3150-039-Q1-N1-E2
Method
                  BLASTX
                  g3249113
NCBI GI
BLAST score
                  157
                  6.0e-11
E value
Match length
                  66
                  52
% identity
                   (AC003114) Strong similarity to kinesin homolog IG002P16.12
NCBI Description
                  gb_2191180 from A. thaliana BAC gb_AF007270. [Arabidopsis
                  thaliana]
                  297763
Seq. No.
Seq. ID
                  LIB3150-039-Q1-N1-F1
Method
                  BLASTX
NCBI GI
                  q4104321
BLAST score
                  168
E value
                  5.0e-12
Match length
                  101
% identity
                  34
NCBI Description
                  (AF034582) vesicle associated protein [Rattus norvegicus]
                  297764
Seq. No.
                  LIB3150-040-Q1-N1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913804
BLAST score
                  274
E value
                  3.0e-24
Match length
                  105
% identity
                  58
```

NCBI Description HISTONE H2B.3 >gi 577825 emb CAA49584 (X69960) H2B histone

[Zea mays]

Seq. No. 297765

Seq. ID LIB3150-040-Q1-N1-B9

Method BLASTX NCBI GI g2827524 BLAST score 198

E value

Match length

% identity

2.0e-25

127 54



```
2.0e-15
E value
Match length
                  51
                  67
% identity
                  (AL021633) predicted protein [Arabidopsis thaliana]
NCBI Description
                  297766
Seq. No.
                  LIB3150-040-Q1-N1-D8
Seq. ID
                  BLASTX
Method
                  g3341685
NCBI GI
BLAST score
                  191
E value
                  1.0e-14
Match length
                  95
% identity
                  48
                  (AC003672) unknown protein [Arabidopsis thaliana]
NCBI Description
                  297767
Seq. No.
                  LIB3150-040-Q1-N1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1143864
BLAST score
                  193
E value
                  1.0e-14
Match length
                  108
% identity
                  43
                  (U28047) beta glucosidase [Oryza sativa]
NCBI Description
                  297768
Seq. No.
Seq. ID
                  LIB3150-041-Q1-N1-A4
Method
                  BLASTX
                  g1345588
NCBI GI
                  222
BLAST score
E value
                  1.0e-31
Match length
                  127
                  61
% identity
                  14-3-3-LIKE PROTEIN GF14-12 >gi 998432 bbs 164524
NCBI Description
                  GF14-12=GRF2 product/14-3-3 protein homolog [Zea mays,
                  XL80, Peptide, 261 aa]
                  297769
Seq. No.
                  LIB3150-041-Q1-N1-B9
Seq. ID
Method
                  BLASTN
                  g2511540
NCBI GI
                  50
BLAST score
                  2.0e-19
E value
Match length
                  130
% identity
                  85
                  Oryza sativa DNA-binding protein GBP16 (Rgbp16) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  297770
Seq. ID
                  LIB3150-041-Q1-N1-D7
Method
                  BLASTX
NCBI GI
                  q3335336
BLAST score
                  266
```

41782

NCBI Description (AC004512) Contains similarity to DnaJ gene YM8520.10

% identity

NCBI Description

gb 825566 from from S. cerevisiae cosmid gb Z49705. ESTs gb_Z47720 and gb_Z29879 come from this gene. [Arabidopsis thaliana]

```
297771
Seq. No.
Seq. ID
                  LIB3150-041-Q1-N1-H8
Method
                  BLASTX
                  g3915826
NCBI GI
                  166
BLAST score
                   1.0e-11
E value
                   33
Match length
% identity
                   94
                  60S RIBOSOMAL PROTEIN L5
NCBI Description
                   297772
Seq. No.
                   LIB3150-042-Q1-N1-B2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3024738
                   277
BLAST score
                   2.0e-24
E value
                   135
Match length
                   43
% identity
                   TYPE II DNA TOPOISOMERASE VI SUBUNIT A
NCBI Description
                   >gi_1926404_emb_CAA71605_ (Y10582) type II DNA
                   topoisomerase subunit A [Sulfolobus shibatae]
                   297773
Seq. No.
                   LIB3150-042-Q1-N1-B9
Seq. ID
Method
                   BLASTX
                   g3080437
NCBI GI
BLAST score
                   176
                   1.0e-12
E value
                   112
Match length
                   43
% identity
                   (AL022605) putative protein [Arabidopsis thaliana]
NCBI Description
                   297774
Seq. No.
                   LIB3150-042-Q1-N1-C10
Seq. ID
                   BLASTX
Method
                   g4519539
NCBI GI
                   320
BLAST score
                   8.0e-30
E value
                   98
Match length
                    64
 % identity
                    (AB016256) NAD-dependent sorbitol dehydrogenase [Malus
NCBI Description
                   domestica]
                    297775
 Seq. No.
                   LIB3150-042-Q1-N1-C11
 Seq. ID
                   BLASTX
Method
                    g82694
NCBI GI
                    336
BLAST score
                    1.0e-31
E value
                    106
Match length
                    69
```

maize (fragment) >gi_293889 (L13432)

glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) 2 -



glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

```
297776
Seq. No.
                  LIB3150-042-Q1-N1-C8
Seq. ID
                  BLASTX
Method
                  g2459420
NCBI GI
                  200
BLAST score
                  5.0e-16
E value
                  53
Match length
                  79
% identity
                  (AC002332) putative ribosomal protein L17 [Arabidopsis
NCBI Description
                  thaliana]
                  297777
Seq. No.
                  LIB3150-042-Q1-N1-D4
Seq. ID
                  BLASTX
Method
                  g3201611
NCBI GI
BLAST score
                  145
                  5.0e-09
E value
                   42
Match length
% identity
                   (AC004669) unknown protein [Arabidopsis thaliana]
NCBI Description
                   297778
Seq. No.
                   LIB3150-042-Q1-N1-E2
Seq. ID
                   BLASTX
Method
                   q135411
NCBI GI
                   305
BLAST score
E value
                   2.0e-52
                   106
Match length
                   98
% identity
                   TUBULIN ALPHA-2 CHAIN >gi 82732 pir S15772 tubulin alpha-2
NCBI Description
                   chain - maize >gi_22148_emb_CAA33733_ (X15704)
                   alpha2-tubulin [Zea mays]
                   297779
Seq. No.
                   LIB3150-042-Q1-N1-E3
Seq. ID
                   BLASTX
Method
                   q141616
NCBI GI
                   254
BLAST score
                   6.0e-22
E value
                   88
Match length
                   57
% identity
                   ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
NCBI Description
                   >gi 168662 (M12147) 15 kDa zein protein [Zea mays]
                   297780
Seq. No.
                   LIB3150-042-Q1-N1-E4
 Seq. ID
                   BLASTX
Method
                   g100925
NCBI GI
                   155
BLAST score
                   9.0e-11
E value
                   49
Match length
                   59
 % identity
                   zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_
 NCBI Description
                   (X58197) 27kDa storage protein, zein [Zea mays]
```



```
297781
Seq. No.
                   LIB3150-042-Q1-N1-E9
Seq. ID
                   BLASTX
Method
                   g1346109
NCBI GI
                   254
BLAST score
E value
                   4.0e-22
Match length
                   91
                   59
% identity
                   GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                   PROTEIN (GPB-LR) (RWD) >gi_540535_dbj_BAA07404_ (D38231)
                   RWD [Oryza sativa]
Seq. No.
                   297782
                   LIB3150-042-Q1-N1-G10
Seq. ID
                   BLASTX
Method
                   g310317
NCBI GI
                   330
BLAST score
                   8.0e-31
E value
                   110
Match length
                   59
% identity
NCBI Description (L19598) beta-tubulin [Oryza sativa]
                   297783
Seq. No.
                   LIB3150-042-Q1-N1-G11
Seq. ID
                   BLASTX
Method
                   q4415992
NCBI GI
                   182
BLAST score
                   1.0e-24
E value
                   99
Match length
                   65
% identity
NCBI Description (AF059288) beta-tubulin 2 [Eleusine indica]
                   297784
Seq. No.
                   LIB3150-042-Q1-N1-H9
Seq. ID
Method
                   BLASTN
                   q2773153
NCBI GI
                   62
BLAST score
                   2.0e-26
E value
Match length
                    90
                    92
 % identity
                   Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                    (Asr1) mRNA, complete cds
                    297785
 Seq. No.
                    LIB3150-043-Q1-N1-C10
 Seq. ID
                    BLASTX
 Method
                    g122070
 NCBI GI
                    388
 BLAST score
                    9.0e-38
 E value
                    82
 Match length
                    95
 % identity
                    HISTONE H3 >gi 82483 pir A25564 histone H3 - rice
 NCBI Description
                    >gi 169793 (M1\overline{5}664) histone 3 [Oryza sativa] >gi_940018
                    (U2\overline{5}664) histone H3 [Oryza sativa]
```

297786

LIB3150-043-Q1-N1-E10

Seq. No.

Seq. ID



Method BLASTX
NCBI GI g2554835
BLAST score 277
E value 3.0e-25
Match length 65
% identity 80

NCBI Description Chain I, Acetohydroxy Acid Isomeroreductase Complexed With

Nadph, Magnesium And Inhibitor Ipoha (N-Hydroxy-N-Isopropyloxamate) >gi_2554836_pdb_1YVE_J Chain J,

Acetohydroxy Acid Isomeroreductase Complexed With Nadph,

Magnesium And Inhibitor Ipoha (N-Hydroxy-N-

Isopropyloxamate) >gi_2554837_pdb_1YVE_K Chain K,

Acetohydroxy Acid Isomeroreductase Complexed With Nadph,

Magnesium And Inhibitor Ipoha (N-Hydroxy-N-

Isopropyloxamate) >gi_2554838_pdb_1YVE_L Chain L,

Acetohydroxy Acid Isomeroreductase Complexed With Nadph,

Magnesium And Inhibitor Ipoha (N-Hydroxy-N-

Isopropyloxamate)

Seq. No. 297787 Seq. ID LIB315

LIB3150-043-Q1-N1-E5

Method BLASTX
NCBI GI g121472
BLAST score 225
E value 1.0e-18
Match length 104
% identity 44

NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)

(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)

>gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea

mays] >gi 168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 297788

Seq. ID LIB3150-043-Q1-N1-F3

Method BLASTX
NCBI GI g3927831
BLAST score 281
E value 5.0e-25
Match length 91
% identity 55

NCBI Description (AC005727) similar to mouse ankyrin 3 [Arabidopsis

thaliana]

Seq. No. 297789

Seq. ID LIB3150-043-Q1-N1-G10

Method BLASTX
NCBI GI g1711567
BLAST score 194
E value 7.0e-25
Match length 92
% identity 62

NCBI Description ELONGATION FACTOR 1-ALPHA 2 (EF-1-ALPHA-2) (STATIN S1)

>gi_112321_pir__A40389 translation elongation factor eEF-1
alpha chain (clone pS1) - rat >gi_1083500_pir__JC2445
translation elongation factor eEF-1 alpha-like protein S1 -



mouse >gi_206438 (M62751) statin-related protein [Rattus norvegicus] >gi_1220410 (L26479) elongation factor-1 alpha [Mus musculus]

Seq. No. 297790

Seq. ID LIB3150-043-Q1-N1-G7

Method BLASTX
NCBI GI g135411
BLAST score 441
E value 5.0e-44
Match length 106
% identity 82

NCBI Description TUBULIN ALPHA-2 CHAIN >gi 82732 pir_ S15772 tubulin alpha-2

chain - maize >gi_22148_emb_CAA33733_ (X15704)

alpha2-tubulin [Zea mays]

Seq. No. 297791

Seq. ID LIB3150-044-Q1-N1-B10

Method BLASTN
NCBI GI g2104711
BLAST score 307
E value 1.0e-172
Match length 323
% identity 99

NCBI Description Zea mays endosperm specific protein mRNA, complete cds

Seq. No. 297792

Seq. ID LIB3150-044-Q1-N1-B11

Method BLASTN
NCBI GI g2104711
BLAST score 126
E value 1.0e-64
Match length 194
% identity 92

NCBI Description Zea mays endosperm specific protein mRNA, complete cds

Seq. No. 297793

Seq. ID LIB3150-044-Q1-N1-D11

Method BLASTX
NCBI GI g3163946
BLAST score 383
E value 7.0e-40
Match length 81
% identity 91

NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]

Seq. No. 297794

Seq. ID LIB3150-044-Q1-N1-E5

Method BLASTX
NCBI GI g1173218
BLAST score 196
E value 1.0e-21
Match length 81
% identity 71

NCBI Description 40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal

protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]



```
297795
Seq. No.
                  LIB3150-044-Q1-N1-E7
Seq. ID
                  BLASTN
Method
                  g168484
NCBI GI
BLAST score
                  212
                  1.0e-116
E value
                  300
Match length
                  93
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
Seq. No.
                  297796
                  LIB3150-044-Q1-N1-F3
Seq. ID
Method
                  BLASTX
                  g606751
NCBI GI
                  172
BLAST score
                  3.0e-12
E value
Match length
                  60
                  57
% identity
NCBI Description (L34934) RNA binding protein [Drosophila melanogaster]
                   297797
Seq. No.
                  LIB3150-044-Q1-N1-F7
Seq. ID
Method
                  BLASTX
                   q129916
NCBI GI
                   164
BLAST score
                   1.0e-17
E value
                   64
Match length
% identity
                   PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi 66911 pir TVWTGY
NCBI Description
                   phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                   >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                   (AA 1 - 401) [Triticum aestivum]
Seq. No.
                   297798
                   LIB3150-045-Q1-N1-B1
Seq. ID
                   BLASTN
Method
                   q531057
NCBI GI
BLAST score
                   41
                   8.0e-14
E value
                   85
Match length
                   87
% identity
                   Wheat mRNA for protein H2B-8, complete cds
NCBI Description
                   297799
Seq. No.
                   LIB3150-045-Q1-N1-D2
Seq. ID
Method
                   BLASTX
                   g113621
NCBI GI
                   150
BLAST score
                   3.0e-10
E value
                   45
Match length
                   69
 % identity
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
 NCBI Description
                   >gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
                   4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
```

[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A



cytoplasmic aldolase [Zea mays]

```
297800
Seq. No.
                  LIB3150-045-Q1-N1-D3
Seg. ID
                  BLASTX
Method
                  g3024506
NCBI GI
                  200
BLAST score
                  1.0e-15
E value
                  79
Match length
                  54
% identity
                  RAS-RELATED PROTEIN RAB11A >gi_623582 (L29271) Nt-Rab11a
NCBI Description
                  gene product [Nicotiana tabacum]
                  297801
Seq. No.
                  LIB3150-045-Q1-N1-F1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2345153
BLAST score
                  36
                  6.0e-11
E value
                  88
Match length
                  86
% identity
NCBI Description Zea mays ribsomal protein S4 (rps4) mRNA, complete cds
                   297802
Seq. No.
                  LIB3150-045-Q1-N1-F7
Seq. ID
Method
                  BLASTN
                   g434325
NCBI GI
BLAST score
                   60
                   3.0e-25
E value
Match length
                   152
                   85
% identity
NCBI Description Z.mays mRNA gs1-2 for glutamine synthetase
                   297803
Seq. No.
                   LIB3150-045-Q1-N1-H2
Seq. ID
                   BLASTN
Method
                   q168425
NCBI GI
                   35
BLAST score
                   1.0e-10
E value
                   59
Match length
                   90
% identity
                   Zea mays brittle-1 protein (bt1) mRNA, complete cds
NCBI Description
                   297804
Seq. No.
                   LIB3150-045-Q1-N1-H9
Seq. ID
                   BLASTX
Method
                   g1946355
NCBI GI
                   210
BLAST score
                   7.0e-30
E value
                   122
Match length
                   57
 % identity
                   (U93215) maize transposon MuDR mudrA protein isolog
NCBI Description
                   [Arabidopsis thaliana] >gi_2880040 (AC002340) maize
                   transposon MuDR mudrA-like protein [Arabidopsis thaliana]
                   297805
 Seq. No.
 Seq. ID
                   LIB3150-046-Q1-N1-A6
```



```
Method
NCBI GI
                  g118104
                  188
BLAST score
                  1.0e-14
E value
                  37
Match length
                   97
% identity
NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi_168461 (M55021) cyclophilin [Zea mays]
                   >gi 82914\overline{8} emb_CAA48638_ (X68678) cyclophilin [Zea mays]
                   297806
Seq. No.
                   LIB3150-046-Q1-N1-A9
Seq. ID
                   BLASTX
Method
                   q3845207
NCBI GI
                   147
BLAST score
                   2.0e-09
E value
                   75
Match length
                   45
% identity
                  (AE001400) asparaginyl-tRNA synthetase (OO, TP) [Plasmodium
NCBI Description
                   falciparum]
                   297807
Seq. No.
                   LIB3150-046-Q1-N1-B1
Seq. ID
                   BLASTX
Method
                   g141616
NCBI GI
                   215
BLAST score
                   2.0e-24
E value
                   107
Match length
                   62
% identity
                   ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
NCBI Description
                   >gi 168662 (M12147) 15 kDa zein protein [Zea mays]
                   297808
Seq. No.
                   LIB3150-046-Q1-N1-B8
Seq. ID
Method
                   BLASTX
                   q4204309
NCBI GI
                   255
BLAST score
E value
                   6.0e-22
                   94
Match length
                   56
 % identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                    [Arabidopsis thaliana]
                   297809
 Seq. No.
                   LIB3150-046-Q1-N1-C3
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q1184774
 BLAST score
                   524
                   2.0e-53
 E value
                   119
 Match length
                   88
 % identity
                    (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
 NCBI Description
                   GAPC3 [Zea mays]
```

```
LIB3150-046-Q1-N1-E6
Seq. ID
                   BLASTX
Method
                  g3413165
NCBI GI
                   193
BLAST score
                   2.0e-15
E value
                   74
Match length
% identity
                  (AJ010224) glyceraldehyde 3-phosphate dehydrogenase,
NCBI Description
                   cytosolic [Cicer arietinum]
                   297811
Seq. No.
                   LIB3150-046-Q1-N1-H11
Seq. ID
                   BLASTN
Method
                   g22516
NCBI GI
BLAST score
                   97
                   4.0e-47
E value
                   177
Match length
                   89
% identity
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
                   297812
Seq. No.
                   LIB3150-046-Q1-N1-H3
Seq. ID
                   BLASTN
Method
                   q4874248
NCBI GI
                   39
BLAST score
                   2.0e-12
E value
                   51
Match length
                   94
% identity
                   Zea mays defender against cell death 1 (dad1) mRNA, partial
NCBI Description
                   297813
Seq. No.
                   LIB3150-047-Q1-N1-E9
Seq. ID
                   BLASTX
Method
                   q2498077
NCBI GI
                   154
BLAST score
                   2.0e-23
E value
                   87
Match length
                   76
 % identity
                   NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
 NCBI Description
                    (PP18) >gi_1777930 (U55019) nucleoside diphosphate kinase
                    [Saccharum officinarum]
                   297814
 Seq. No.
 Seq. ID
                   LIB3150-047-Q1-N1-F11
                   BLASTX
 Method
 NCBI GI
                   g123620
                   174
 BLAST score
                    6.0e-13
 E value
                    98
 Match length
                    52
 % identity
                   HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi_100224 pir_ S14950
 NCBI Description
                   heat shock cognate protein 70 - tomato
                    >gi_19258_emb_CAA37971_ (X54030) heat shock protein cognate
```

70 [Lycopersicon esculentum]